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<b>(21) International Application Number:</b> PCT/US00/05883  <b>(22) International Filing Date:</b> 8 March 2000 (08.03.00)  <b>(30) Priority Data:</b> 60/124,270                      12 March 1999 (12.03.99)                      US  <b>(71) Applicant (for all designated States except US):</b> HUMAN GENOME SCIENCES, INC. [US/US]; 9410 Key West Avenue, Rockville, MD 20850 (US).  <b>(72) Inventors; and</b> <b>(75) Inventors/Applicants (for US only):</b> ROSEN, Craig, A. [US/US]; 22400 Rolling Hill Road, Laytonsville, MD 20882 (US). RUBEN, Steven, M. [US/US]; 18528 Heritage Hills Drive, Laytonsville, MD 20882 (US).  <b>(74) Agents:</b> WALES, Michele, M. et al.; Human Genome Sciences, Inc., 9410 Key West Avenue, Rockville, MD 20850 (US).		<b>(81) Designated States:</b> AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).  <b>Published</b> <i>With international search report.</i>
<b>(54) Title:</b> HUMAN COLON CANCER ASSOCIATED GENE SEQUENCES AND POLYPEPTIDES  <b>(57) Abstract</b>  This invention relates to newly identified colon or colon cancer related polynucleotides and the polypeptides encoded by these polynucleotides herein collectively known as "colon cancer antigens", and to the complete gene sequences associated therewith and to the expression products thereof, as well as the use of such colon cancer antigens for detection, prevention and treatment of disorders of the colon, particularly the presence of colon cancer. This invention relates to the colon cancer antigens as well as vectors, host cells, antibodies directed to colon cancer antigens and recombinant and synthetic methods for producing the same. Also provided are diagnostic methods for diagnosing and treating, preventing and/or prognosing disorders related to the colon, including colon cancer, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying agonists and antagonists of colon cancer antigens of the invention. The present invention further relates to methods and/or compositions for inhibiting the production and/or function of the polypeptides of the present invention.		

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## Human Colon Cancer Associated Gene Sequences and Polypeptides

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### *Field of the Invention*

This invention relates to newly identified colon or colon cancer related polynucleotides and the polypeptides encoded by these polynucleotides herein collectively known as "colon cancer antigens," and to the complete gene sequences  
10 associated therewith and to the expression products thereof, as well as the use of such colon cancer antigens for detection, prevention and treatment of disorders of the colon, particularly the presence of colon cancer. This invention relates to the colon cancer antigens as well as vectors, host cells, antibodies directed to colon cancer antigens and recombinant and synthetic methods for producing the same. Also  
15 provided are diagnostic methods for diagnosing and treating, preventing and/or prognosing disorders related to the colon, including colon cancer, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying agonists and antagonists of colon cancer antigens of the invention. The present invention further relates to methods and/or compositions for  
20 inhibiting the production and/or function of the polypeptides of the present invention.

### *Background of the Invention*

Colorectal cancers are among the most common cancers in men and women in the U.S. and are one of the leading causes of death. Other than surgical resection no  
25 other systemic or adjuvant therapy is available. Vogelstein and colleagues have described the sequence of genetic events that appear to be associated with the multistep process of colon cancer development in humans (Trends Genet 9(4):138-41 (1993)). An understanding of the molecular genetics of carcinogenesis, however, has not led to preventative or therapeutic measures. It can be expected that advances in  
30 molecular genetics will lead to better risk assessment and early diagnosis but colorectal cancers will remain a deadly disease for a majority of patients due to the

lack of an adjuvant therapy. Adjuvant or systemic treatments are likely to arise from a better understanding of the autocrine factors responsible for the continued proliferation of cancer cells.

Colorectal carcinoma is a malignant neoplastic disease. There is a high incidence of colorectal carcinoma in the Western world, particularly in the United States. Tumors of this type often metastasize through lymphatic and vascular channels. Many patients with colorectal carcinoma eventually die from this disease. In fact, it is estimated that 62,000 persons in the United States alone die of colorectal carcinoma annually.

At the present time the only systemic treatment available for colon cancer is chemotherapy. However, chemotherapy has not proven to be very effective for the treatment of colon cancers for several reasons, the most important of which is the fact that colon cancers express high levels of the MDR gene (that codes for multi-drug resistance gene products). The MDR gene products actively transport the toxic substances out of the cell before the chemotherapeutic agents can damage the DNA machinery of the cell. These toxic substances harm the normal cell populations more than they harm the colon cancer cells for the above reasons.

There is no effective systemic treatment for treating colon cancers other than surgically removing the cancers. In the case of several other cancers, including breast cancers, the knowledge of growth promoting factors (such as EGF, estradiol, IGF-11) that appear to be expressed or effect the growth of the cancer cells, has been translated for treatment purposes. But in the case of colon cancers this knowledge has not been applied and therefore the treatment outcome for colon cancers remains bleak.

There is a need, therefore, for identification and characterization of such factors that modulate activation and differentiation of colon cells, both normally and in disease states. In particular, there is a need to isolate and characterize additional molecules that mediate apoptosis, DNA repair, tumor-mediated angiogenesis, genetic imprinting, immune responses to tumors and tumor antigens and, among other things, that can play a role in detecting, preventing, ameliorating or correcting dysfunctions or diseases of the colon.

***Summary of the Invention***

The present invention includes isolated nucleic acid molecules comprising, or alternatively, consisting of, a colon and/or colon cancer associated polynucleotide sequence disclosed in the sequence listing (as SEQ ID Nos: 1 to 773) and/or contained in a human cDNA clone described in Tables 1, 2 and 5 and deposited with the American Type Culture Collection ("ATCC"). Fragments, variant, and derivatives of these nucleic acid molecules are also encompassed by the invention. The present invention also includes isolated nucleic acid molecules comprising, or alternatively consisting of, a polynucleotide encoding a colon or colon cancer polypeptide. The present invention further includes colon and/or colon cancer polypeptides encoded by these polynucleotides. Further provided for are amino acid sequences comprising, or alternatively consisting of, colon and/or colon cancer polypeptides as disclosed in the sequence listing (as SEQ ID Nos: 774 to 1546) and/or encoded by a human cDNA clone described in Tables 1, 2 and 5 and deposited with the ATCC. Antibodies that bind these polypeptides are also encompassed by the invention. Polypeptide fragments, variants, and derivatives of these amino acid sequences are also encompassed by the invention, as are polynucleotides encoding these polypeptides and antibodies that bind these polypeptides. Also provided are diagnostic methods for diagnosing and treating, preventing, and/or prognosing disorders related to the colon, including colon cancer, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying agonists and antagonists of colon cancer antigens of the invention.

***Detailed Description***

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**Tables**

Table 1 summarizes some of the colon cancer antigens encompassed by the invention (including contig sequences (SEQ ID NO:X) and the cDNA clone related to the contig sequence) and further summarizes certain characteristics of the colon cancer polynucleotides and the polypeptides encoded thereby. The first column shows the "SEQ ID NO:" for each of the 773 colon cancer antigen polynucleotide sequences of the invention. The second column provides a unique "Sequence/Contig ID"

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identification for each colon and/or colon cancer associated sequence. The third column, "Gene Name," and the fourth column, "Overlap," provide a putative identification of the gene based on the sequence similarity of its translation product to an amino acid sequence found in a publicly accessible gene database and the database accession no. for the database sequence having similarity, respectively. The fifth and sixth columns provide the location (nucleotide position nos. within the contig), "Start" and "End", in the polynucleotide sequence "SEQ ID NO:X" that delineate the preferred ORF shown in the sequence listing as SEQ ID NO:Y. The seventh and eighth columns provide the "% Identity" (percent identity) and "% Similarity" (percent similarity), respectively, observed between the aligned sequence segments of the translation product of SEQ ID NO:X and the database sequence. The ninth column provides a unique "Clone ID" for a cDNA clone related to each contig sequence.

Table 2 summarizes ATCC Deposits, Deposit dates, and ATCC designation numbers of deposits made with the ATCC in connection with the present application.

Table 3 indicates public ESTs, of which at least one, two, three, four, five, ten, fifteen or more of any one or more of these public EST sequences are optionally excluded from certain embodiments of the invention.

Table 4 lists residues comprising antigenic epitopes of antigenic epitope-bearing fragments present in most of the colon or colon cancer associated polynucleotides described in Table 1 as predicted by the inventors using the algorithm of Jameson and Wolf, (1988) Comp. Appl. Biosci. 4:181-186. The Jameson-Wolf antigenic analysis was performed using the computer program PROTEAN (Version 3.11 for the Power MacIntosh, DNASTAR, Inc., 1228 South Park Street Madison, WI). Colon and colon cancer associated polypeptides shown in Table 1 may possess one or more antigenic epitopes comprising residues described in Table 4. It will be appreciated that depending on the analytical criteria used to predict antigenic determinants, the exact address of the determinant may vary slightly. The residues and locations shown in Table 4 correspond to the amino acid sequences for most colon and colon cancer associated polypeptide sequence shown in the Sequence Listing.

Table 5 shows the cDNA libraries sequenced, and ATCC designation numbers and vector information relating to these cDNA libraries.

**Definitions**

The following definitions are provided to facilitate understanding of certain terms used throughout this specification.

5 In the present invention, "isolated" refers to material removed from its original environment (e.g., the natural environment if it is naturally occurring), and thus is altered "by the hand of man" from its natural state. For example, an isolated polynucleotide could be part of a vector or a composition of matter, or could be contained within a cell, and still be "isolated" because that vector, composition of  
10 matter, or particular cell is not the original environment of the polynucleotide. The term "isolated" does not refer to genomic or cDNA libraries, whole cell total or mRNA preparations, genomic DNA preparations (including those separated by electrophoresis and transferred onto blots), sheared whole cell genomic DNA preparations or other compositions where the art demonstrates no distinguishing  
15 features of the polynucleotide/sequences of the present invention.

As used herein, a "polynucleotide" refers to a molecule having a nucleic acid sequence contained in SEQ ID NO:X (as described in column 1 of Table 1) or the related cDNA clone (as described in column 9 of Table 1 and contained within a library deposited with the ATCC). For example, the polynucleotide can contain the  
20 nucleotide sequence of the full length cDNA sequence, including the 5' and 3' untranslated sequences, the coding region, as well as fragments, epitopes, domains, and variants of the nucleic acid sequence. Moreover, as used herein, a "polypeptide" refers to a molecule having an amino acid sequence encoded by a polynucleotide of the invention as broadly defined (obviously excluding poly-Phenylalanine or poly-  
25 Lysine peptide sequences which result from translation of a polyA tail of a sequence corresponding to a cDNA).

In the present invention, "SEQ ID NO:X" was often generated by overlapping sequences contained in multiple clones (contig analysis). A representative clone containing all or most of the sequence for SEQ ID NO:X is deposited at Human  
30 Genome Sciences, Inc. (HGS) in a catalogued and archived library. As shown in column 9 of Table 1, each clone is identified by a cDNA Clone ID. Each Clone ID is unique to an individual clone and the Clone ID is all the information needed to

retrieve a given clone from the HGS library. In addition to the individual cDNA clone deposits, most of the cDNA libraries from which the clones were derived were deposited at the American Type Culture Collection (hereinafter "ATCC"). Table 5 provides a list of the deposited cDNA libraries. One can use the Clone ID to  
5 determine the library source by reference to Tables 2 and 5. Table 5 lists the deposited cDNA libraries by name and links each library to an ATCC Deposit. Library names contain four characters, for example, "HTWE." The name of a cDNA clone ("Clone ID") isolated from that library begins with the same four characters, for example "HTWEP07". As mentioned below, Table 1 correlates the Clone ID names  
10 with SEQ ID NOs. Thus, starting with a SEQ ID NO, one can use Tables 1, 2 and 5 to determine the corresponding Clone ID, from which library it came and in which ATCC deposit the library is contained. Furthermore, it is possible to retrieve a given cDNA clone from the source library by techniques known in the art and described elsewhere herein. The ATCC is located at 10801 University Boulevard, Manassas,  
15 Virginia 20110-2209, USA. The ATCC deposits were made pursuant to the terms of the Budapest Treaty on the international recognition of the deposit of microorganisms for the purposes of patent procedure.

A "polynucleotide" of the present invention also includes those polynucleotides capable of hybridizing, under stringent hybridization conditions, to  
20 sequences contained in SEQ ID NO:X, or the complement thereof (e.g., the complement of any one, two, three, four, or more of the polynucleotide fragments described herein), and/or sequences contained in the related cDNA clone within a library deposited with the ATCC. "Stringent hybridization conditions" refers to an overnight incubation at 42 degree C in a solution comprising 50% formamide, 5x SSC  
25 (750 mM NaCl, 75 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1x SSC at about 65 degree C.

Also included within "polynucleotides" of the present invention are nucleic acid molecules that hybridize to the polynucleotides of the present invention at lower  
30 stringency hybridization conditions. Changes in the stringency of hybridization and signal detection are primarily accomplished through the manipulation of formamide concentration (lower percentages of formamide result in lowered stringency); salt



conditions, or temperature. For example, lower stringency conditions include an overnight incubation at 37 degree C in a solution comprising 6X SSPE (20X SSPE = 3M NaCl; 0.2M NaH<sub>2</sub>PO<sub>4</sub>; 0.02M EDTA, pH 7.4), 0.5% SDS, 30% formamide, 100 ug/ml salmon sperm blocking DNA; followed by washes at 50 degree C with  
5 1XSSPE, 0.1% SDS. In addition, to achieve even lower stringency, washes performed following stringent hybridization can be done at higher salt concentrations (e.g. 5X SSC).

Note that variations in the above conditions may be accomplished through the inclusion and/or substitution of alternate blocking reagents used to suppress  
10 background in hybridization experiments. Typical blocking reagents include Denhardt's reagent, BLOTTO, heparin, denatured salmon sperm DNA, and commercially available proprietary formulations. The inclusion of specific blocking reagents may require modification of the hybridization conditions described above, due to problems with compatibility.

15 Of course, a polynucleotide which hybridizes only to polyA+ sequences (such as any 3' terminal polyA+ tract of a cDNA shown in the sequence listing), or to a complementary stretch of T (or U) residues, would not be included in the definition of "polynucleotide," since such a polynucleotide would hybridize to any nucleic acid molecule containing a poly (A) stretch or the complement thereof (e.g., practically  
20 any double-stranded cDNA clone generated using oligo dT as a primer).

The polynucleotides of the present invention can be composed of any polyribonucleotide or polydeoxribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. For example, polynucleotides can be composed of single- and double-stranded DNA, DNA that is a mixture of single- and double-  
25 stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, the polynucleotide can be composed of triple-stranded regions comprising RNA or DNA or both RNA and DNA. A  
30 polynucleotide may also contain one or more modified bases or DNA or RNA backbones modified for stability or for other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of

modifications can be made to DNA and RNA; thus, "polynucleotide" embraces chemically, enzymatically, or metabolically modified forms.

In specific embodiments, the polynucleotides of the invention are at least 15, at least 30, at least 50, at least 100, at least 125, at least 500, or at least 1000 continuous nucleotides but are less than or equal to 300 kb, 200 kb, 100 kb, 50 kb, 15 kb, 10 kb, 7.5kb, 5 kb, 2.5 kb, 2.0 kb, or 1 kb, in length. In a further embodiment, polynucleotides of the invention comprise a portion of the coding sequences, as disclosed herein, but do not comprise all or a portion of any intron. In another embodiment, the polynucleotides comprising coding sequences do not contain coding sequences of a genomic flanking gene (i.e., 5' or 3' to the gene of interest in the genome). In other embodiments, the polynucleotides of the invention do not contain the coding sequence of more than 1000, 500, 250, 100, 50, 25, 20, 15, 10, 5, 4, 3, 2, or 1 genomic flanking gene(s).

"SEQ ID NO:X" refers to a colon cancer antigen polynucleotide sequence described in Table 1. SEQ ID NO:X is identified by an integer specified in column 1 of Table 1. The polypeptide sequence SEQ ID NO:Y is a translated open reading frame (ORF) encoded by polynucleotide SEQ ID NO:X. There are 773 colon cancer antigen polynucleotide sequences described in Table 1 and shown in the sequence listing (SEQ ID NO:1 through SEQ ID NO:773). Likewise there are 773 polypeptide sequences shown in the sequence listing, one polypeptide sequence for each of the polynucleotide sequences (SEQ ID NO:774 through SEQ ID NO:1546). The polynucleotide sequences are shown in the sequence listing immediately followed by all of the polypeptide sequences. Thus, a polypeptide sequence corresponding to polynucleotide sequence SEQ ID NO:1 is the first polypeptide sequence shown in the sequence listing. The second polypeptide sequence corresponds to the polynucleotide sequence shown as SEQ ID NO:2, and so on. In other words, since there are 773 polynucleotide sequences, for any polynucleotide sequence SEQ ID NO:X, a corresponding polypeptide SEQ ID NO:Y can be determined by the formula  $X + 773 = Y$ . In addition, any of the unique "Sequence/Contig ID" defined in column two of Table 1, can be linked to the corresponding polypeptide SEQ ID NO:Y by reference to Table 4.

The polypeptides of the present invention can be composed of amino acids joined to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres, and may contain amino acids other than the 20 gene-encoded amino acids. The polypeptides may be modified by either natural processes, such as posttranslational processing, or by chemical modification techniques which are well known in the art. Such modifications are well described in basic texts and in more detailed monographs, as well as in a voluminous research literature. Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present in the same or varying degrees at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Polypeptides may be branched, for example, as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched, and branched cyclic polypeptides may result from posttranslation natural processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, pegylation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination. (See, for instance, PROTEINS - STRUCTURE AND MOLECULAR PROPERTIES, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York (1993); POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS, B. C. Johnson, Ed., Academic Press, New York, pgs. 1-12 (1983); Seifter et al., Meth Enzymol 182:626-646 (1990); Rattan et al., Ann NY Acad Sci 663:48-62 (1992).)

The colon and colon cancer polypeptides of the invention can be prepared in any suitable manner. Such polypeptides include isolated naturally occurring polypeptides, recombinantly produced polypeptides, synthetically produced

polypeptides, or polypeptides produced by a combination of these methods. Means for preparing such polypeptides are well understood in the art.

The polypeptides may be in the form of the secreted protein, including the mature form, or may be a part of a larger protein, such as a fusion protein (see below).

5 It is often advantageous to include an additional amino acid sequence which contains secretory or leader sequences, pro-sequences, sequences which aid in purification, such as multiple histidine residues, or an additional sequence for stability during recombinant production.

10 The colon and colon cancer polypeptides of the present invention are preferably provided in an isolated form, and preferably are substantially purified. A recombinantly produced version of a polypeptide, including the secreted polypeptide, can be substantially purified using techniques described herein or otherwise known in the art, such as, for example, by the one-step method described in Smith and Johnson, Gene 67:31-40 (1988). Polypeptides of the invention also can be purified from  
15 natural, synthetic or recombinant sources using techniques described herein or otherwise known in the art, such as, for example, antibodies of the invention raised against the polypeptides of the present invention in methods which are well known in the art.

By a polypeptide demonstrating a "functional activity" is meant, a polypeptide  
20 capable of displaying one or more known functional activities associated with a full-length (complete) protein of the invention. Such functional activities include, but are not limited to, biological activity, antigenicity [ability to bind (or compete with a polypeptide for binding) to an anti-polypeptide antibody], immunogenicity (ability to generate antibody which binds to a specific polypeptide of the invention), ability to  
25 form multimers with polypeptides of the invention, and ability to bind to a receptor or ligand for a polypeptide.

"A polypeptide having functional activity" refers to polypeptides exhibiting activity similar, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as measured in a particular assay, such as,  
30 for example, a biological assay, with or without dose dependency. In the case where dose dependency does exist, it need not be identical to that of the polypeptide, but rather substantially similar to the dose-dependence in a given activity as compared to

the polypeptide of the present invention (i.e., the candidate polypeptide will exhibit greater activity or not more than about 25-fold less and, preferably, not more than about tenfold less activity, and most preferably, not more than about three-fold less activity relative to the polypeptide of the present invention).

5           The functional activity of the colon cancer antigen polypeptides, and fragments, variants derivatives, and analogs thereof, can be assayed by various methods.

For example, in one embodiment where one is assaying for the ability to bind or compete with full-length polypeptide of the present invention for binding to an  
10   antibody to the full length polypeptide antibody, various immunoassays known in the art can be used, including but not limited to, competitive and non-competitive assay systems using techniques such as radioimmunoassays, ELISA (enzyme linked immunosorbent assay), "sandwich" immunoassays, immunoradiometric assays, gel diffusion precipitation reactions, immunodiffusion assays, in situ immunoassays  
15   (using colloidal gold, enzyme or radioisotope labels, for example), western blots, precipitation reactions, agglutination assays (e.g., gel agglutination assays, hemagglutination assays), complement fixation assays, immunofluorescence assays, protein A assays, and immunoelectrophoresis assays, etc. In one embodiment, antibody binding is detected by detecting a label on the primary antibody. In another  
20   embodiment, the primary antibody is detected by detecting binding of a secondary antibody or reagent to the primary antibody. In a further embodiment, the secondary antibody is labeled. Many means are known in the art for detecting binding in an immunoassay and are within the scope of the present invention.

In another embodiment, where a ligand is identified, or the ability of a  
25   polypeptide fragment, variant or derivative of the invention to multimerize is being evaluated, binding can be assayed, e.g., by means well-known in the art, such as, for example, reducing and non-reducing gel chromatography, protein affinity chromatography, and affinity blotting. See generally, Phizicky, E., et al., Microbiol. Rev. 59:94-123 (1995). In another embodiment, physiological correlates polypeptide  
30   of the present invention binding to its substrates (signal transduction) can be assayed.

In addition, assays described herein (see Examples) and otherwise known in the art may routinely be applied to measure the ability of polypeptides of the present

invention and fragments, variants derivatives and analogs thereof to elicit polypeptide related biological activity (either in vitro or in vivo). Other methods will be known to the skilled artisan and are within the scope of the invention.

5

**Colon and Colon Cancer Associated Polynucleotides and Polypeptides of the Invention**

It has been discovered herein that the polynucleotides described in Table 1 are expressed at significantly enhanced levels in human colon and/or colon cancer tissues.

10 Accordingly, such polynucleotides, polypeptides encoded by such polynucleotides, and antibodies specific for such polypeptides find use in the prediction, diagnosis, prevention and treatment of colon related disorders, including colon cancer as more fully described below.

15 Table 1 summarizes some of the polynucleotides encompassed by the invention (including contig sequences (SEQ ID NO:X) and the related cDNA clones) and further summarizes certain characteristics of these colon and/or colon cancer associated polynucleotides and the polypeptides encoded thereby.

Table 1

Seq ID No.	Sequence/ Contig ID	Gene Name	Overlap	HCS Nucleotide Start End	% Identity	% Similarity	Clone ID
1	500802	Immunoglobulin kappa light chain variable region L25 [Homo sapiens] >pir S41816 S41816 Ig kappa chain V region L25 - human Length = 119 (AB008790) Grb7V protein [Homo sapiens] >sp D103000 D103000 GRB7V PROTEIN. >gi 1526535 Grb7 protein [Homo sapiens] {SUB 130-343} Length = 447	gi 415381	2 304	73	86	HGBA183
2	531091			2 292			HUKDY21
3	553147			3 440			HCASG85
4	558860	(AF039700) antigen NY-CO-38 [Homo sapiens] >sp G3170200 G3170200 ANTIGEN NY-CO-38. >gi 3170198 (AF039699) antigen NY-CO-37 [Homo sapiens] {SUB 1-403} Length = 652 MDA-7 [Homo sapiens] >sp Q13007 MDA7_HUMAN MDA-7 PROTEIN PRECURSOR (MELANOMA DIFFERENTIATION ASSOCIATED PROTEIN 7). Length = 206 disintegrin-protease [Homo sapiens] >sp O15204 O15204 DISINTEGRIN- PROTEASE. Length = 470	gnl PID d1030000	33 635	97	98	HCEGY28
5	561730	(AF039700) antigen NY-CO-38 [Homo sapiens] >sp G3170200 G3170200 ANTIGEN NY-CO-38. >gi 3170198 (AF039699) antigen NY-CO-37 [Homo sapiens] {SUB 1-403} Length = 652 MDA-7 [Homo sapiens] >sp Q13007 MDA7_HUMAN MDA-7 PROTEIN PRECURSOR (MELANOMA DIFFERENTIATION ASSOCIATED PROTEIN 7). Length = 206 disintegrin-protease [Homo sapiens] >sp O15204 O15204 DISINTEGRIN- PROTEASE. Length = 470	gi 3170200	34 393	98	98	HSDFA48
6	585938	(AF039700) antigen NY-CO-38 [Homo sapiens] >sp G3170200 G3170200 ANTIGEN NY-CO-38. >gi 3170198 (AF039699) antigen NY-CO-37 [Homo sapiens] {SUB 1-403} Length = 652 MDA-7 [Homo sapiens] >sp Q13007 MDA7_HUMAN MDA-7 PROTEIN PRECURSOR (MELANOMA DIFFERENTIATION ASSOCIATED PROTEIN 7). Length = 206 disintegrin-protease [Homo sapiens] >sp O15204 O15204 DISINTEGRIN- PROTEASE. Length = 470	gi 1141751	206 538	81	81	HMQBR31
7	587785	(AF039700) antigen NY-CO-38 [Homo sapiens] >sp G3170200 G3170200 ANTIGEN NY-CO-38. >gi 3170198 (AF039699) antigen NY-CO-37 [Homo sapiens] {SUB 1-403} Length = 652 MDA-7 [Homo sapiens] >sp Q13007 MDA7_HUMAN MDA-7 PROTEIN PRECURSOR (MELANOMA DIFFERENTIATION ASSOCIATED PROTEIN 7). Length = 206 disintegrin-protease [Homo sapiens] >sp O15204 O15204 DISINTEGRIN- PROTEASE. Length = 470	gnl PID e332729	2 331	100	100	HOSBO86

8	588916	Human apoC-II gene for preapoplipoprotein C-II [Homo sapiens] >gi 757915 apoCII protein [Homo sapiens] >gi 178836 apolipoprotein C-II [Homo sapiens] >pir A24238 LPHUC2 apolipoprotein C- II precursor - human	gi 296636	5	376	100	100	100	HLIDQU56
9	613825			3	260				HMSHB03
10	639090			254	559				HCME22
11	651644			63	194				HCFO73
12	659544			109	249				HMBU15
13	659739	KHSI [Homo sapiens] >sp G185733 G185733 KHSI. Length = 846	gi 185733	238	1140	94		94	HSYAM68
14	661057	protein kinase Dyrk2 [Homo sapiens] >sp Q92630 Q92630 PROTEIN KINASE DYRK2 (PROTEIN KINASE, DYRK2). >gnl PID e280618 Dyrk2 [Homo sapiens] {SUB 320-528} Length = 528	gnl PID e321513	3	425	100		100	HCDBX83
15	661313			894	1118				HHEMN11
16	666316			193	369				HCDC84
17	669229			430	762				HOHDD51
18	670471	(AJ003061) most expressed alternative spliced form [Homo sapiens] >sp O60852 O60852 PROTEIN ENCODED BY SACCHAROMYCES CEREVISIAE SPC98 HOMOLOGUE. Length = 907	gnl PID e1293754	203	937	92		93	HAGGX21
19	676611			207	530				HCE5C73
20	691240			2	385				HISAN54



21	702977	26-kDa cell surface protein TAPA-1 [Homo sapiens] >pir A35649 A35649 cell surface protein TAPA-1 - human >sp P18582 CD81_HUMAN CD81 ANTIGEN (26 KD CELL SURFACE PROTEIN TAPA-1). Length = 236	gi 338678	34	819	80	80	HGCMV09
22	709517	(AF062476) retinoic acid-responsive protein; STRA6 [Mus musculus] >sp O70491 O70491 RETINOIC ACID- RESPONSIVE PROTEIN. Length = 670	gi 3126975	344	478			HWLJX38
23	714730			1	534	75	88	HCRND05
24	714834			1	657			IIA'PTL75
25	715016			1	411			HCEOQ15
26	719584	(AF076856) small espin [Rattus norvegicus] >sp G33818569 G33818569 SMALL ESPIN. Length = 253	gi 3818569	530	886	62	64	HWLFA47
27	724637	muskelin [Mus musculus] >sp O89050 O89050 MUSKELIN. Length = 735	gi 3493462	1	444	92	95	HUSXP30
28	728392	(AB015318) gamma2-adaptin [Homo sapiens] >sp O75843 O75843 GAMMA2-ADAPTIN. Length = 785	gn PI D d1034356	160	801	100	100	HBJIG25
29	738716			137	289			HCRMQ71
30	739056	similar to ADP-ribosylation factor; (AF054179) H beta 58 homolog [Homo sapiens] >sp O75436 O75436 H BETA 58 HOMOLOG. Length = 327	gn PI D e1350748	2	502	87	97	HSDZB27
31	739143		gi 3342000	1	1083	100	100	HKABV36
32	742329			2	277			HSRDE23
33	742557			2	814			HWHGD94
34	745481			1229	1396			HPMFL67
35	746035			414	959			HCHCJ20
36	753731			1	357			HPTTL69



54	784446	(AB002086) p47 [Rattus norvegicus]	gnl PID d1022509	19	282	19	83	85	HBJFL85
55	784832	>gnl PID e294068 XY40 protein [Rattus norvegicus] >sp O35987 O35987 P47, COMPLETE CDS. Length = 370		134	751				HCGMI84
56	786813			114	347				HE2OI55
57	792139			32	334				H6EEC65
58	793987	steroidogenic acute regulatory protein [Mus musculus] >pir A55455 A55455		100	564				HICAEI8
59	805715	steroidogenic acute regulatory protein precursor, mitochondrial - mouse Length = 284		513	1226				HDPKI64
60	811111			1	438				HCEDF72
61	811113		gil 236243	2	718		28	50	HWBEX78
62	823902	(AF028722) fetal globin inducing factor [Mus musculus] >sp G4103857 G4103857 FETAL GLOBIN INDUCING FACTOR. Length = 238	gil 4103857	36	497		87	94	HDTBD43
63	826518	RNase 4 [Homo sapiens] >pir I52489 I52489 ribonuclease 4 (EC 3.1.-.-) precursor - human Length = 147	gnl PID d1007727	1	231		100	100	HLQCQ62
64	826704			475	726				HCQB118
65	827720			789	1076				HFICY86
66	828102			106	297				HSRFC02
67	828180	(AB013456) aquaporin 8 [Homo sapiens] >gnl PID d1035202 (AB013456) aquaporin 8 [Homo sapiens] >sp D1035202 D1035202 AQUAPORIN 8. Length = 261	gnl PID d1035202	20	883		83	83	I1WL1FM26

68	828386	(AF093821) RRM RNA binding protein GRY-RBP [Mus musculus] >sp O8899 O8899  RRM RNA BINDING PROTEIN GRY-RBP. Length = 625	gij3694986	3	650	100	100	100	110HAD26
69	828658	protein-tyrosine-phosphatase [Homo sapiens] >gnl PID d1032930 (AB013601) DUSP6 [Homo sapiens] >gnl PID d1035350 (AB013382) DUSP6 [Homo sapiens] >gnl PID d1032930 (AB013601) DUSP6 [Homo sapiens] >sp Q16828 DUS6_HUMAN DUAL SPECIFICITY PROTEIN	gnl PID e218263	2	568	100	100	100	HLHCO24
70	828919	PHOSPHATASE 6 RNA helicase [Homo sapiens] >pir S71758 S71758 DEAD box protein MrDb, Myc-regulated - human >sp Q92732 Q92732 RNA HELICASE. Length = 610	gnl PID e254454	2	661	99	100	100	HFOYL30
71	829572	similar to Glyoxalase [Caenorhabditis elegans] Length = 281		163	411				HSVAK51
72	830138	UbcH5B [Homo sapiens] >gij595668 ubiquitin conjugating enzyme [Rattus norvegicus] >gij1480742 ubiquitin conjugating enzyme [Mus musculus] >pir S53359 S53359 ubiquitin conjugating enzyme (E217kB) - rat Length = 147	gnl PID e1344082	134	475	53	67	67	HYAAH90
73	830208		gij1145689	2	205	92	95	95	HIBCN46
74	830248	A33 antigen precursor [Homo sapiens] >sp Q99795 A33_HUMAN CELL SURFACE A33 ANTIGEN	gij1814277	3	1097	30	39	39	HWLHJ13

PRECURSOR. Length = 319

75	830275	Similar to D.melanogaster parallel sister chromatids protein [Homo sapiens] >sp Q92549 Q92549 MYELOBLAST KIAA0261 (FRAGMENT). Length = 1287	gnl PID d1014081	3	647	100	100	HWLFO28
76	830286	interferon-related putative protein [Homo sapiens] >sp Q12894 Q12894 HYPOTHETICAL_48.0 KD PROTEIN. >gij 209022 interferon-related putative protein [Homo sapiens] {SUB 2-442} Length = 442	gij 2880033	385	1488	91	91	HWLFE46
77	830347	(AF039401) calcium-dependent chloride channel-1 [Homo sapiens] >sp G4009460 G4009460 CALCIUM-DEPENDENT CHLORIDE CHANNEL-1. Length = 914	gij 4009460	3	656	63	76	HWLEL81
78	830348	inorganic pyrophosphatase (EC 3.6.1.1) - bovine >sp P37980 P37980 PYR_BOVIN	3	911				HWLQR45
79	830364	INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO- HYDROLASE) (PPASE). Length = 289	pir A45153 A45153_3	3	1022	67	85	HWLEI47
80	830394			1	951			HDPVF62
81	830398			526	627			HWBCR84

82	830412	SDF2 [Homo sapiens] >pir JC5106 JC5106 stromal cell-derived factor 2 - human >sp Q99470 Q99470 SDF2. Length = 211	gnl PID d1009953	233	928	91	92	HWHHQ57
83	830436	(AJ005821) X-like 1 protein [Homo sapiens] >sp E1291794 E1291794 X- LIKE 1 PROTEIN. Length = 3027	gnl PID e1291794	83	523	65	78	HWABR83
84	830464	CLP36 [Rattus norvegicus] >pir JC4385 JC4385 LIM protein - rat >sp P52944 CL36_RAT LIM PROTEIN CLP36. Length = 327	gil1020151	2	289	72	81	HUSGB72
85	830471	(AF011794) cell cycle progression restoration 8 protein [Homo sapiens] >sp O14712 O14712 CELL CYCLE PROGRESSION RESTORATION 8 PROTEIN. Length = 375	gil2352906	95	229			HUSIK51
86	830477			116	2389	95	96	HULAT84
87	830500	ORF YGR036c [Saccharomyces cerevisiae] >pir S64327 S64327 probable membrane protein YGR036c - yeast (Saccharomyces cerevisiae) Length = 239	gnl PID e243385	185	736	38	54	HJPCP29
88	830509	(AL021813) phenylalanyl-tRNA synthetase alpha chain [Schizosaccharomyces pombe] >sp O42849 O42849 PHENYLALANYL-tRNA SYNTHETASE ALPHA CHAIN. Length = 589	gnl PID e1250585	2	1081	40	63	HUFAU68

89	830528	hepatoma-derived growth factor [Mus musculus] >pir JC5662 JC5662 hepatoma-derived growth factor-related protein 2 - mouse >sp O35540 O35540 HEPATOMA-DERIVED GROWTH FACTOR, RELATED PROTEIN 2 Length = 669	dbj ID63850_1	38	1591	78	87	HUFBF32
90	830542	mitochondrial 3-oxoacyl-CoA thiolase [Homo sapiens] >pir S43440 S43440 3-oxoacyl-CoA thiolase - human Length = 397	gnl PID d1004316	324	1637	92	92	HTTDO45
91	830564	IgM heavy chain VH1 region precursor [Homo sapiens] Length = 146		702	1343			HTPBU79
92	830611		gil 2344934	1	495	78	79	HTJMB38
93	830618			655	915			HDIM121
94	830620			452	754			HTGDM95
95	830630	mitochondrial benzodiazepine receptor [Homo sapiens] >pir 38724 38724 mitochondrial benzodiazepine receptor - human >gil 3411163 (AF075589) peripheral-type benzodiazepine receptor [Homo sapiens] {SUB 27-169} Length = 169	gil 529946	14	259	100	100	HTGFS43
96	830654	RNA-binding protein [Saccharomyces cerevisiae] Length = 497	gil 295631	2	1687	40	51	HSYBQ96
97	830660			122	694			HSYDW13
98	830661			555	779			HSXDG80
99	830704	pp21 [Homo sapiens] >pir 53785 53785 gene pp21 protein - human >sp Q15170 Q15170 (PP21). Length = 157	gil 521207	1	609	51	76	HSUSF13
100	830765			39	236			HSKES11

101	830778	methionine aminopeptidase [Homo sapiens] >gil687243 eIF-2-associated p67 homolog [Homo sapiens] >pirS52112 DPHUM2 methionyl aminopeptidase (EC 3.4.11.18) 2 - human >sp P50579 AMP2_HUMAN METHIONINE AMINOPEPTIDASE 2 (EC 3.4.11.18) (METAP 2) (PEPTIDASE M 2)	gil903982	26	718	99	100	HSPAX18
102	830784			595	858			HSIFY77
103	830800	(AF039918) CD39L4 [Homo sapiens] >sp O75356 O75356 CD39L4. Length = 428	gil3335102	1	990	94	94	HHPDD94
104	830821			449	754			HAQND53
105	830849			464	868			HHHEAA48
106	830903			1	525			HPJCT75
107	830913	tumor necrosis factor type 1 receptor associated protein [Homo sapiens] >pir A55877 A55877 tumor necrosis factor type 1 receptor associated protein TRAP-1 - human microsomal glutathione S-transferase 2 [Homo sapiens] >sp Q99735 GST2_HUMAN MICROSOMAL GLUTATHIONE S-TRANSFERASE II (EC 2.5.1.18) (MICROSOMAL GST- II). Length = 147	gil687237	3	1193	99	99	HPIBH48
108	830920	peroxisome proliferator activated receptor gamma 2 [Homo sapiens] >gil171117 ligand activated transcription factor PPARgamma2 [Homo sapiens]	gil1747521	90	650	87	87	HIPHA84
109	830938		gil1432177	227	610	98	98	HONAE45



110	830980	beta COP [Rattus norvegicus] >pir S13520 S13520 beta-COP protein - rat >sp P23514 COPB_RAT COATOMER BETA SUBUNIT (BETA- COAT PROTEIN) (BETA-COP). >pir S13636 S13636 110K protein - rabbit {SUB 451-500} Length = 953 (AF016687) similar to alpha-actinin [Caenorhabditis elegans] >sp O16785 O16785 T21D12.4 PROTEIN. Length = 375	gil55819	47	289	95	98	HCEG53
111	831014		gil2315828	310	1188	53	73	HOEBV08
112	831026			340	687			HOBAE30
113	831031			526	765			HTXOK56
114	831055	(AF091395) Trio isoform [Homo sapiens] >sp O75962 O75962 TRIO ISOFORM. Length = 3038	gil3644048	674	1921	93	94	HNTAT24
115	831057			3	1106			HNTCW73
116	831062			3	821			HNTBD04
117	831117			400	579			HMWBR70
118	831122	cell surface glycoprotein [Homo sapiens] >gil567110 [Human CD79b/Ig beta/B29 gene, complete coding sequence.]. gene product [Homo sapiens] >bbs 122035 membrane immunoglobulin beta chain, Ig-beta=Ag receptor complex [human, B cells, Peptide, 229 aa] [Homo	gil179312	2	772	91	92	HMWCV70
119	831125			868	1023			HMWFH12
120	831132			36	185			HMUAR55

121	831152	(AC004668) similar to murine cell cycle regulator MIDA1; similar to A57591 (PID:g2137417) [Homo sapiens] >sp O60414 O60414 WUGSC:H_RG276O03.1A PROTEIN (FRAGMENT). Length = 635 (AF030109) regulator of G protein signaling 12 [Homo sapiens] >gi 2766633 (AF030152) regulator of G protein signaling 12 [Homo sapiens] Length = 799	gi 3115346	111	875	90	91	HMVA157
122	831157		gi 2605780	664	1110	100	100	HMVA24
123	831160	ezrin (AA 1-586) [Homo sapiens] >pir A34400 A34400 ezrin - human >sp P15311 EZRL_HUMAN EZRIN (P81) (CYTOVILLIN) (VILLIN-2). {SUB 2-586} >gi 340217 cyto villin 2 [Homo sapiens] {SUB 12-586} Length = 586	gi 31283	3	1907	100	100	HCRPE60
124	831193			256	378			IIM1AG77
125	831197			884	1267			HMELO02
126	831217			152	427			HITAAN07
127	831239			420	638			HAABB67
128	831248			84	443			HCFL08
129	831313	c-fos protein [Homo sapiens] >gi 29904 c-fos gene product [Homo sapiens] >gi 4063509 (AF111167) cfos [Homo sapiens] >pir A01342 TVHUF1 transforming protein fos - human >sp P01100 FOS_HUMAN P55-C-FOS PROTO-ONCOGENE PROTEIN (G0S7 PROTEIN). >sp G4063509 G406	gi 182735	1182	1670	83	88	HAGDZ30
130	831369			31	1464			HDFQB94

131	831371	cytochrome P450j [Homo sapiens] >gil181356 cytochrome P450IIE1 [Homo sapiens] >pir A31949 A31949 cytochrome P450 2E1 - human >sp P05181 CPE1_HUMAN CYTOCHROME P450 2E1 (EC 1.14.14.1) (CYP1IIE1) (P450-J). >gnl PID d1001366 cytochrome P450IIE1 [Homo sapiens] hydroxymethylglutaryl-CoA synthase [Homo sapiens] >gil2463646 3-hydroxy-3-methylglutaryl CoA synthase [Homo sapiens] >pir S71623 S71623 hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5) precursor, mitochondrial - human >sp P54868 HMCN_HUMAN HYDROXYMETHYLGLU	81	344			HLADA28
132	831373		221	1744	94	94	HWADP47
			gil181360				
133	831387	mucin 2 precursor, intestinal - human (fragments) >gil186396 mucin [Homo sapiens] {SUB 626-1895} >gil186398 MUC2 [Homo sapiens] {SUB 2037-3020} >gil188874 intestinal mucin [Homo sapiens] {SUB 1916-2193} >gil188615 mucin-like protein [Homo sapiens] {SUB 23 calcium-modulated protein S100-beta [artificial sequence] >pir A91254 BCBO1B S-100 protein beta chain - bovine {SUB 2-92} Length = 92	2	727	95	96	HCQDM23
			pir A49963 A4393 2				
134	831410		2	727	95	96	HCQDM23
135	831448		gil554574	482	32	60	HKACO81
136	831450		807	1319			HKABK55

137	831472	(AF020043) chromosome-associated	gi 3089368	1	138		HJMBH59
138	831473	polypeptide [Homo sapiens] >sp O60464 O60464 CHROMOSOME- ASSOCIATED POLYPEPTIDE (BAMACAN PROTEIN). >gnl PID e1285055 (AJ005015) bamacan protein [Homo sapiens] {SUB 827-1217} Length = 1217		40	3765	89	HKACE68
139	831474	excision repair protein [Homo sapiens]		1231	1746		HWHPX60
140	831494	>gi 182174 excision repair protein [Homo sapiens] >gi 2583146 (AF001925) excision repair protein [Homo sapiens] >pir A32875 A24781 excision repair protein - human		2	616		HISES08
141	831506	>sp P07992 ERC1_HUMAN DNA EXCISION REPAIR PROTEIN ERC similar to yeast adenylate cyclase (S56776) [Homo sapiens] >sp Q92627 Q92627 MYELOBLAST K1A0231 (FRAGMENT). Length = 476	gi 182177	3	596	100	HIICAF79
142	831533	growth and transformation dependent protein [Rattus norvegicus] >pir A26882 A26882 p11.2 hypothetical protein - rat (fragment) >sp Q63571 Q63571 RAT GROWTH AND TRANSFORMATION- DEPENDENT (FRAGMENT). Length = 175	gnl PID d1013909	1	900	51	HCRPH87
143	831539		gi 207250	102	572	81	HDTT102
144	831556			395	625		HDTLJ87

145	831594	protein serine/threonine kinase [Homo sapiens] >gi 468789 CDK activating kinase [Homo sapiens] >gi 485909 MO15/CDK-activating kinase (CAK) [Homo sapiens] >gnl PID e257806 Cdk-activating kinase [Homo sapiens] >pir A54820 A54820 CDK-activating protein kinase	gi 348243	117	677			HHECU01
146	831598			23	802	99	99	HHEDO14
147	831608	translational initiation factor beta subunit [Homo sapiens] >pir A31226 A31226 translation initiation factor eIF-2 beta chain - human >pir S13147 S13147 protein synthesis factor - rabbit >sp P20042 F2B_HUMAN EUKARYOTIC TRANSLATION INITIATION FACTOR 2 BET	gi 182067	120	1154	87	87	HHEFB46
148	831613	Human giant larvae homologue [Homo sapiens] >pir S55474 S55474 Human giant larvae homolog - human >sp Q14521 Q14521 GIANT LARVAE HOMOLOGUE. Length = 1015	gi 854124	3	104	96	100	HISAU33
149	831622	alpha l-acid glycoprotein [Homo sapiens] >gi 1340138 alpha l-acid glycoprotein [Homo sapiens] {SUB 39-86} Length = 201	gnl PID e222211	46	690	99	99	HGBI1256

150	831631	aldose reductase-like peptide [Homo sapiens] >sp O60218 O60218 ALDOSE REDUCTASE-LIKE PEPTIDE (ALDOSE REDUCTASE-RELATED PROTEIN). >gij3098514 (AF044961) aldose reductase-related protein [Homo sapiens] {SUB 232-316; Length = 316	gij3150035	100	1173	100	100	HGBAX75
151	831632	lambda-crystallin precursor [Oryctolagus cuniculus] >pir A31992 A31992 lambda-crystallin - rabbit		2	226			HGBCC19
152	831653	>sp P14755 CRYL_RABIT LAMBDA-CRYSTALLIN. {SUB 2-320} Length = 320	gij164905	172	927	85	90	HTJNJ73
153	831655	weak similarity to TPR domains [Caenorhabditis elegans] >sp Q23049 Q23049 SIMILARITY TO TPR DOMAINS. Length = 458	gij1465826	3	662	32	54	HFVHF47
154	831708	vascular endothelial growth factor [Homo sapiens] >sp Q16889 Q16889 VASCULAR ENDOTHELIAL GROWTH FACTOR (FRAGMENT). >pir A41551 A41551 vascular endothelial growth factor 206 precursor - human {SUB 23-254} >bbs 85194 vascular endothelial growth factor; VEGF	gij3712671	96	410	98	100	HFIUT25
155	831738			313	573			HFCAL79

156	831741	myelodysplasia/myeloid leukemia factor 2 [Homo sapiens] >gi13387897 (AF070539) myelodysplasia/myeloid leukemia factor 2 [Homo sapiens] >sp Q15773 Q15773	gi1399745	186	974	77	77	HEBT03
		MYELODYSPLASIA/MYELOID LEUKEMIA FACTOR 2. Length = 248						
157	831754	multidrug resistance protein 3 [Homo sapiens] >gnl PID e1288198 multidrug resistance protein 3 [Homo sapiens] >sp O60922 O60922 MULTIDRUG RESISTANCE PROTEIN 3. Length = 1526	gnl PID e1288198	1	924	92	92	HWMIEZ67
158	831760			373	510			HETEH76
159	831780			2	1003			HELGH58
160	831796			892	1158			HE9RY54
161	831800	nuclear protein SA-2 [Homo sapiens] >sp O00540 O00540 NUCLEAR PROTEIN SA-2. Length = 1162	gnl PID e250094	600	1541	93	93	HFIAU59
162	831807			1015	1341			HE9QD17
163	831812			520	765			HE9OY91
164	831813			83	793			HEAIIA84
165	831830	isoleucyl-tRNA synthetase [Homo sapiens] >pir 59314 59314 isoleucine--tRNA ligase (EC 6.1.1.5) - human Length = 1266	gnl PID d1006382	52	2307	98	99	HE8TV13
166	831860	Similarity to S. Pombe BEM1/BUD5 suppressor;	gnl PID e1347870	465	776	69	84	HE8OT93
167	831872			1	1671			HE8CL14
168	831896			1	2121			HDTDX05

169	831928	(AF061795) dynamin-like protein Dymple isoform [Homo sapiens] >sp O60709 O60709 DYNAMIN-LIKE PROTEIN DYMPLE ISOFORM. Length = 699	gi 3126874	2	778	77	77	HSYBO86
170	831949			3	1109			HE8TX12
171	831950			48	521			HAPQS51
172	831953	carbonic anhydrase II [Homo sapiens] >gi 179780 carbonic anhydrase II [Homo sapiens] >gi 179795 carbonic anhydrase II [Homo sapiens] >gi 29587 carbonic anhydrase II (AA 1-260) [Homo sapiens]	gi 179772	106	987	100	100	H'WLHA60
173	831975			555	761			HDTBO06
174	832036	human phosphotyrosine phosphatase kappa [Homo sapiens] Length = 1439	gnl PID e234080	2	490	82	82	H'CYAC13
175	832047			877	1137			H'CWKS85
176	832078			751	1014			HASAB14
177	832100			687	917			HCRNM09
178	832104			95	220			HCRMU71
179	832268			18	191			HTXOU56
180	832270	Ca2+ ATPase of fast-twitch skeletal muscle sarcoplasmic reticulum, adult isoform [Homo sapiens] >sp O14983 O14983 CA2+ ATPASE OF FAST-TWITCH SKELETAL MUSCLE SARCOPLASMIC RETICULUM, ADULT ISOFORM. Length = 1001	gi 2052522	622	1290	90	91	H'BKDW03



181	832279	acetyl-CoA synthetase [Drosophila melanogaster] >pir[S52154]S52154 acetyl-CoA synthetase - fruit fly (Drosophila melanogaster) >sp Q24226 Q24226 ACETYL- COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL-ACTIVATING ENZYME). Length = 581 11kD protein [Homo sapiens] Length = 111	gi 608694	2	1237	65	77	HIBKDN33
182	832317		gi 897917	270	719	100	100	HBIAX17
183	832354			1	408			HBBB52
184	832364			3	1385			HDPQA93
185	832378	sialidase [Homo sapiens] >gi 2773339 (AF040958) lysosomal neuraminidase precursor [Homo sapiens] >gi 4099141 lysosomal sialidase [Homo sapiens] >sp Q99519 Q99519 SIALIDASE PRECURSOR. >sp G4099141 G4099141 LYSOSOMAL SIALIDASE PRECURSOR (EC 3.2.1.18). Lengt (AF048700) gastrointestinal peptide [Homo sapiens] >sp Q60575 Q60575 GASTROINTESTINAL PEPTIDE. Length = 86	gnl PID e303801	3	746	96	96	HATCO72
186	832385		gi 2935440	2	316	90	90	HARAG42
187	832428	APO-1 ANTIGEN, FAS ANTIGEN. Length = 335	sp G249613 G249613	136	846	97	97	HAMGD53
188	832485			202	597			HAGHC54

189	832494	Ku protein subunit [Homo sapiens] >gil78650 p70 autoantigen [Homo sapiens] >gil339667 thyroid autoantigen [Homo sapiens] >bbs107206 Ku autoantigen p70 subunit [human, Peptide, 609 aa] [Homo sapiens] >pir/A30299/A30894 70K thyroid autoantigen - human >sp	gil307095	80	1918	90	90	HAIBY70
190	832512	Similar to Human C219-reactive peptide (L34688) [Homo sapiens] >sp/Q92580/Q92580 MYELOBLAST KIA0268 (FRAGMENT). >gil511639 C219-reactive peptide [Homo sapiens] {SUB 592-727; Length = 1193 integrin alpha6 subunit [Homo sapiens] Length = 1067 nuclear factor RIP140 [Homo sapiens] >pir/S57348/S57348 nuclear factor RIP140 - human Length = 1158 protein tyrosine kinase [Homo sapiens] >pir/A55922/A55922 tyrosine kinase A6 - human >sp/Q12792/Q12792 PROTEIN TYROSINE KINASE. Length = 350	gnlPID d1014138	3	1058	87	87	HDPTT16
191	832515		gil33942	2	1660	96	96	HCRPH70
192	832526		gil940539	34	693	95	95	HADCX04
193	832575		gil451482	49	1203	99	99	H2LAJ21
194	832576	BTG1 gene product [Homo sapiens] >gil293306 BTG1 [Mus musculus] >gil50188 big1 [Mus musculus] >pir/S20947/S20947 BTG1 protein - human >pir/48272/48272 big1 protein - mouse >sp/P31607/BTG1_HUMAN BTG1 PROTEIN (B-CELL TRANSLOCATION GENE 1 PROTEIN). Length	gil29509	388	1050	100	100	HKGAI67

195	832588	mitochondrial ATP synthase subunit 9 precursor [Homo sapiens] >pir 38612 38612 ATP synthase chain 9 precursor, mitochondrial - human >sp P48201 A T93_HUMAN ATP SYNTHASE LIPID-BINDING PROTEIN P3 PRECURSOR (EC 3.6.1.34) (ATPASE PROTEIN 9) (SUBUNIT C). Leng	gi 511450	2	637	85	85	H2LAD51
196	832634			253	924			HCRMZ25
197	832728			3	542			HKAIL83
198	833094	immunoglobulin I from VH4 family [Homo sapiens] >pir S13519 S13519 Ig heavy chain V region precursor - human >gi 553385 immunoglobulin heavy chain [Homo sapiens] {SUB 24-125} Length = 147	gi 37725	2	391	77	81	HRADC46
199	833395	novel stromal cell protein [Mus musculus] >pir JC4761 JC4761 recombination activating gene 1 inducing protein - human >sp Q62275 Q62275 RECOMBINATION ACTIVATING PROTEIN 1 PROTEIN ACTIVATION (NOVEL STROMAL CELL PROTEIN). Length = 221	gn PID e229590	224	853			HHENV68
200	834326			1	744	69	76	HWLEQ41
201	834583	(AF073957) CXCL chemokine BRAC [Homo sapiens] Length = 99	gi 4140394	2	607	98	100	HHGDE66
202	834944	(AF061443) G protein-coupled receptor LGR4 [Rattus norvegicus] >sp G3885470 G3885470 G PROTEIN-COUPLED RECEPTOR 1.GR4. Length	gi 3885470	2	781	85	86	HE8QE56

= 951

203	835012	(AB017169) Slit-3 protein [Homo sapiens] >sp D1036172 D1036172 SLIT-3 PROTEIN. >gnl PID d1033429	gnl PID d1036172	3	344	92	92	HCCMD55
204	835104	(AB011538) MEGF5 [Homo sapiens] {SUB 785-1523} Length = 1523		580	1818			HLHTJ57
205	835332	(AF065389) tetraspan NET-4 [Homo sapiens] >sp O60746 O60746 TETRASPAN NET-4. Length = 268	gi 3152703	268	1080	100	100	HCROP84
206	835487	(AC002528) alpha2(I) collagen [Homo sapiens] >sp G238855 G238855 ALPHA2(I) COLLAGEN (FRAGMENT). Length = 1186	gi 2388555	2218	4239	100	100	HTSGZ29
207	836182	calmodulin-dependent protein kinase II-delta (EC 2.7.1.37) [Rattus norvegicus]		39	398			HFLUE31
208	836522	>pir A34366 A34366 Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) II delta chain - rat		1819	2046			HSLFO17
209	836655	>sp P15791 KCCD_RAT CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II DELTA CII		1	624			HTPCU04
210	836787		gi 203267	767	1549	92	94	HAIED73

211	836789	GP36b glycoprotein [Homo sapiens] >pir G01447 G01447 GP36b glycoprotein - human >sp Q12907 Q12907 GP36B GLYCOPROTEIN PRECURSOR. Length = 356	gij 505652	1	849	99	99	HKAAD74
212	838577	binding protein [Oryctolagus cuniculus] >gij 82628 FK506-binding protein (FKBP) [Homo sapiens] >gij 82633 FKBP-12 protein [Homo sapiens] >gij 82649 FK506-binding protein 12 [Homo sapiens] >gij 288196 FKBP [Homo sapiens] >gij 665650 FK-506 binding protein [H	gij 65023	2	433	100	100	HCRQD09
213	838717			676	900			HE8UJ03
214	839008			2	997			HFOXSS2
215	840063	(AF006751) ES/130 [Homo sapiens] >sp O75300 O75300 ES/130. Length = 977	gij 3299885	3	2729	84	85	HWLHIX68
216	840533			183	482			HWLLU74
217	840669			474	1115			HPMGM71
218	841140	(AF081281) lysophospholipase [Homo sapiens] >sp O75608 O75608 LYSOPHOSPHOLIPASE. Length = 230 polypeptide GalNAc transferase-T4 [Mus musculus] >sp O08832 O08832 POLYPEPTIDE GALNAc TRANSFERASE-T4. Length = 578	gij 3415123	1	789	100	100	HAJCC51
219	841386		gij 2121220	491	1258	66	81	HMCCA66
220	841480			3	212			HDQET68
221	841509			3	662			HTELO87
222	841616			340	660			HWLFT95

223	841900	peptidylarginine deiminase (EC 3.5.3.15) [Rattus norvegicus] >pir A34339 DIRTR1 protein-arginine deiminase (EC 3.5.3.15) I - rat >sp P20717 PARD_RAT PROTEIN- ARGININE DEIMINASE (EC 3.5.3.15) (PEPTIDYLARGININE DEIMINASE). Length = 665	gij205960	2	439	87	90	HWLFR87
224	842054	ubiquinone-binding protein (QP) [Homo sapiens] >gij I90816 ubiquinone-binding protein precursor [Homo sapiens] >gij 37580 ubiquinone-binding protein (AA 1 - 111) [Homo sapiens] >pir A32450 A32450 ubiquinone-binding protein QP-C - human >gij 553631 ubiquinone (AB012933) acyl-CoA synthetase 5 [Rattus norvegicus] >sp O88813 LCFE_RAT LONG- CHAIN-FATTY-ACID--COA LIGASE 5 (EC 6.2.1.3) (LONG-CHAIN ACYL- COA SYNTHETASE 5) (LACS 5). Length = 683	gij I90802	1	369	100	100	HWHPF06
225	843061	(AB012933) acyl-CoA synthetase 5 [Rattus norvegicus] >sp O88813 LCFE_RAT LONG- CHAIN-FATTY-ACID--COA LIGASE 5 (EC 6.2.1.3) (LONG-CHAIN ACYL- COA SYNTHETASE 5) (LACS 5). Length = 683	gnl PID d1034547	23	2308	81	92	HDAAV92
226	843544	(AF045573) FLI-LRR associated protein- I [Mus musculus] >sp O70323 O70323 FLIGHTLESS-I ASSOCIATED PROTEIN 1 (LRR DOMAIN) (FLI-LRR ASSOCIATED PROTEIN-1). Length = 628	gij 3025718	28	391 837	65	83	HFLNB80 HTEKO43
227	844092							

228	844270	nuclear antigen EBNA-3B [Human herpesvirus 4] >pir[S2792]S2792.1 nuclear antigen EBNA-3B - human herpesvirus 4 >sp Q69139 Q69139 NUCLEAR ANTIGEN EBNA-3B. Length = 946	gi 330409	2	373	47	52	HWLBL06
229	844604	(AF071186) WW domain binding protein 11 [Mus musculus] >sp O88539 O88539 WW DOMAIN BINDING PROTEIN 11. Length = 389	gi 3550082	170	2110	66	70	HNTAD40
230	844685	immunoglobulin lambda heavy chain [Homo sapiens] >gi 567132 This CDS feature is included to show the translation of the corresponding C_region. Presently translation qualifiers on C_region features are illegal [Homo sapiens] {SUB 148-177} Length = 477	gnl PID e1227585	539	1564	94	94	HASAC08
231	844855	titin [Oryctolagus cuniculus] >sp E135530 E135530.1 TITIN (FRAGMENT). Length = 2000	gnl PID e1355301	3	1634	34	54	HAICQ70
232	845101	(AF089814) growth suppressor related [Homo sapiens] >sp O75956 O75956 GROWTH SUPPRESSOR RELATED. Length = 126	gi 3661529	46	627	94	94	HHESZ77
233	845141	(AB011105) KIAA0533 protein [Homo sapiens] >sp O15230 O15230 KIAA0533	gnl PID d1026389	31	966	100	100	HWMF067
234	845220	PROTEIN (LAMININ ALPHA 5 CHAIN) (FRAGMENT). >gnl PID e317479 laminin alpha 5 chain [Homo sapiens] {SUB 693-1645} Length = 1645	2	1096	100	100	100	HKADF64

235	845434	glutathione peroxidase [Synecocystis sp.] >pir[S75885 S75885 glutathione peroxidase homolog - Synecocystis sp. (PCC 6803) >sp P74250 P74250 GLUTATHIONE PEROXIDASE (EC 1.11.1.9). Length = 169	gnl PID d1019077	3	590	50	61	HWAF112
236	845510	dipeptidyl peptidase III [Rattus norvegicus] >sp O55096 O55096 DIPEPTIDYL PEPTIDASE (EC 3.4.14.4) (DIPEPTIDYL PEPTIDASE III) (DIPEPTIDYL AMINOPEPTIDASE III) (DIPEPTIDYL ARYLAMIDASE III) (RED CELL ANGIOTENSINASE) (ENKEPHALINASE B). Length = 827	gnl PID d1025528	3	683	96	98	HEONN92
237	845600	procathepsin B [Homo sapiens] >pir A26498 K11HUB cathepsin B (EC 3.4.22.1) precursor - human >sp P07858 CATB_HUMAN CATHEPSIN B PRECURSOR (EC 3.4.22.1) (CATHEPSIN B1) (APP SECRETASE). >gij 181178 lysosomal proteinase cathepsin B [Homo sapiens] {SUB 131-33 (AF055666) kincsin light chain 2 [Mus musculus] >sp O88448 O88448 KINESIN LIGHT CHAIN 2. Length = 599	gij 181192	223	1254	99	99	HOEMIE38
238	845882		gij 347848	4	1155	68	75	HL.HCE82



239	846007	alpha-1-acid glycoprotein 2 [Homo sapiens] >pir JT0326 OMHU2 alpha-1-acid glycoprotein 2 precursor - human >sp P19652 A1A11_HUMAN ALPHA-1-ACID GLYCOPROTEIN 2 PRECURSOR (AGP 2) (OROSOMUCOID 2) (OMD 2). >gi 388511 alpha 1-acid glycoprotein [Homo sapiens] (SU)	gi 177840	1	390	98	100	HILDBS16
240	846280			31	105			HCNAK57
241	846286	epididymal apical protein 1-precursor [Macaca fascicularis] >pir S28258 S28258 androgen-regulated epididymal protein precursor - crab-eating macaque >sp Q28475 Q28475 EPIDIDYMAL APICAL PROTEIN 1- PRECURSOR. Length = 776	gi 38063	203	901	36	54	HASDA19
242	846388			3	1721			HIL3AA32
243	HCRNG17R			154	288			HCRNG17
244	HWMFG64R			1	315			HWMFG64
245	HAGCZ94R			13	102			HAGCZ94
246	HBJEJ74R			72	287			HBJEJ74
247	HUFBE67R			355	525			HUFBE67
248	HUTHM43R			2	55			HUTHM43
249	HLTGU75R			2	274			HLTGU75
250	HWLKF77R			51	134			HWLKF77
251	HWLLK67R			1	180			HWLLK67
252	HDQIE85R			3	203			HDQIE85
253	HWLFA67R			1	213			HWLFA67
254	HWLGX29R			136	351			HWLGX29
255	HWMFZ29R			324	404			HWMFZ29



265	HCDMC32R	(AF014118) membrane-associated kinase [Homo sapiens] >sp O14731 O14731 MEMBRANE-ASSOCIATED KINASE. Length = 499	g 2460023	3	272	100	100	HCDMC32
266	HCROF25R	(AF034800) liprin-alpha3 [Homo sapiens] >sp G3309535 G3309535 LIPRIN-ALPHA3 (FRAGMENT). Length = 443	g 3309535	70	381	60	65	HCROF25
267	HTEQO80R	(AF035840) NADH:ubiquinone oxidoreductase B17 subunit [Homo sapiens] >sp G3800740 G3800740 NADH:UBIQUINONE. OXIDOREDUCTASE B17 SUBUNIT. Length = 128	g 3800740	1	327	100	100	HTEQO80
268	H2LAU18R	(AF035940) similar to mago nashi [Homo sapiens] >g 2330011 (AF007862) mm-Mago [Mus musculus] >g 2909828 (AF035939) similar to mago nashi [Mus musculus] >sp O35169 O35169 MM-MAGO. >sp G2909830 G2909830 MAGOH. >sp P50606 MGN_HUMAN MAGO NASHI PROTEIN HOMOL	g 2909830	2	592	100	100	H2LAU18
269	HTXPO87R	(AF038129) polyubiquitin [Ovis aries] >sp O46543 O46543 POLYUBIQUITIN. >gn PID e1263307 unnamed protein product [unidentified] {SUB 77-305} >g 163575 polyubiquitin [Bos taurus] {SUB 142-305} >g 1762374 polyubiquitin [Gallus gallus] {SUB 1-71} >gn PID	g 2707837	1	330	97	97	HTXPO87

270	H2LAR08R (AF040642) contains similarity to RNA recognition motifs (RNP) [Caenorhabditis elegans] >sp O44795 O44795 C50D2.5 PROTEIN. Length = 200	gj 2746787	188	514	75	90	H2LAR08
271	HADAF94R (AF044957) NADH:ubiquinone oxidoreductase B15 subunit [Homo sapiens] Length = 129	gj 4164446	88	135	88	88	HADAF94
272	HEMDA91R (AF047473) testis mitotic checkpoint BUB3 [Homo sapiens] >sp O43685 O43685 TESTIS MITOTIC CHECKPOINT BUB3. Length = 326	gj 3378104	132	431	85	85	HEMDA91
273	HWMFN58R (AF051426) slow delayed rectifier channel subunit [Homo sapiens] >sp O60607 O60607 SLOW DELAYED RECTIFIER CHANNEL SUBUNIT. Length = 548	gj 2961249	3	344	100	100	HWMFN58
274	HCNDJ66R (AF054643) lambda 1 immunoglobulin light chain variable region [Homo sapiens] >gj 3023109 (AF054643) lambda 1 immunoglobulin light chain variable region [Homo sapiens] Length = 125	gj 3023109	1	276	72	73	HCNDJ66
275	HOHDH05R (AF061833) aldehyde dehydrogenase; retinal dehydrogenase; class I aldehyde dehydrogenase; ALDH1 [Xenopus laevis] >sp G3818533 G3818533 ALDEHYDE DEHYDROGENASE (EC 1.2.1.3). >pir S1188 S1188 aldehyde dehydrogenase (NAD+) (EC 1.2.1.3), cytosolic - clawed f	gj 3818533	59	331	53	80	HOHDH05

276	HUFBP63R (AF062137) immunoglobulin heavy chain variable region [Homo sapiens] Length = 143	gi 3170737	17	463	92	96	HUFBP63
277	HUFBN90R (AF062211) immunoglobulin heavy chain variable region [Homo sapiens] Length = 149	gi 3170885	26	463	94	96	HUFBN90
278	HEBEJ57R (AF062214) immunoglobulin heavy chain variable region [Homo sapiens] Length = 142	gi 3170895	1	165	81	90	HEBEJ57
279	HDTDK65R (AF069048) immunoglobulin light chain variable region [Homo sapiens] Length = 120	gi 3328006	3	434	76	78	HDTDK65
280	HAIAD82R (AF069711) urokinase [Oryctolagus cuniculus] >sp G3982741 G3982741 UROKINASE (FRAGMENT). Length = 128	gi 3982741	1	156	68	71	HAIAD82
281	HFKHD61R (AF073298) 4F5rel [Homo sapiens] >gi 3641536 (AF073297) 4F5rel [Mus musculus] >sp O75918 O75918 4F5REL. >sp O88891 O88891 4F5REL. Length = 59	gi 3641538	3	203	100	100	HFKHD61
282	H2LAX28R (AF078817) high mobility group protein [Nannospalax ehrenbergi] >sp O88611 O88611 HIGH MOBILITY GROUP PROTEIN. Length = 215	gi 3342571	206	568	97	97	H2LAX28
283	HWLMY93R (AF078839) Rho related protein Rnd3/Rho8 [Sus scrofa] >sp O77683 O77683 RHO RELATED PROTEIN RND3/RHO8. Length = 244	gi 3386532	3	173	91	91	HWLMY93
284	HTXNL13R		3	356			HTXNL13

285	HDPWR89R	(AJ005259) homologous to Bombyx mori multiprotein bridging factor (EMBL: AB001078) [Homo sapiens] >sp O60869 O60869 EDF-1 PROTEIN. Length = 148	gnl PID e 286414	1	312	79	83	HDPWR89
286	H2LAK62R			22	165			H2LAK62
287	HWLKT15R	UBIQUINONE/MENAQUINONE BIOSYNTHESIS METHYLTRANSFERASE UBIE (ubiE) [Rickettsia prowazekii]	gnl PID e 342961	2	301	50	76	HWLKT15
288	HATAR77R	(AL021546) Cytochrome C Oxidase Polypeptide VIa-liver precursor (EC 1.9.3.1) [Homo sapiens]	gnl PID e 248288	3	413	70	73	HATAR77
289	HWLWN07R	(AL022237) bK1191B2.2 (BCL2-interacting killer (apoptosis-inducing) (NBK, BP4, BIP1)) [Homo sapiens] >sp E1359316 E1359316 BK1191B2.2 (BCL2-INTERACTING KILLER (APOPTOSIS-INDUCING) (NBK, BP4, BIP1)) (FRAGMENT). >gi 929655 NBK [Homo sapiens] {SUB 14-173} Le	gnl PID e 359316	1	183	82	88	HWLWN07
290	HWLD118R	(AL023554) ribosomal protein [Schizosaccharomyces pombe] >sp O60118 O60118 RIBOSOMAL PROTEIN. Length = 157	gnl PID e 292696	3	206	43	59	HWLD118
291	HWMEC68R			3	419			HWMEC68

292	HTXFO53R	11 beta-hydroxysteroid dehydrogenase type II [Homo sapiens] >pir 38858 38858.1 beta-hydroxysteroid dehydrogenase (EC 1.1.1.146) type 2 - human >sp P80365 DHI2_HUMAN CORTICOSTEROID 11-BETA-DEHYDROGENASE, ISOZYME 2 (EC 1.1.1.146) (11-DH2) (11-BETA-HYDROX	gij565082	3	236	88	94	HTXFO53
293	HWMEH18R	3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) alpha chain - human >gij3513491 (AF022380) rod photoreceptor cGMP phosphodiesterase alpha subunit [Homo sapiens] {SUB 1-122} Length = 859	pir B3461 B3461.1	3	203	92	92	HWMEH18
294	HCWFF03R	5' half of the product is homologues to Bacillus subtilis SAICAR synthetase, 3' half corresponds to the catalytic subunit of AIR carboxylase [Homo sapiens] >pir S14147 S14147 multifunctional purine biosynthesis protein - human Length = 425	gij28384	3	296	83	90	HCWFF03
295	HCNDP66R	A33 antigen precursor [Homo sapiens] >sp Q99795 A33_HUMAN CELL SURFACE A33 ANTIGEN PRECURSOR. Length = 319	gij1814277	3	503	73	75	HCNDP66
296	HCRMK82R	adenosine A2b receptor [Homo sapiens] >gij757911 A2b adenosine receptor [Homo sapiens] >pir JC1229 JC1229 adenosine receptor A2b - human >sp P29275 A2B_HUMAN	gij178150	2	427	100	100	HCRMK82

ADENOSINE A2B RECEPTOR. Length  
= 332

297	HCDANI6R	alpha-1 collagen (I) [Gallus gallus] Length = 143	gij555432	2	133	77	88	HCDANI6
298	HCEOE88R	amplaxin [Homo sapiens] >pir A48063 A48063 mammary tumor/squamous cell carcinoma- associated protein EMS1 - human Length = 550	gij182087	1	291	93	94	HCEOE88
299	HALSK30R	angiogenin [Homo sapiens] >pir A90498 NRHUAG angiogenin precursor - human >sp P03950 ANG1_HUMAN ANGIOGENIN PRECURSOR (EC 3.1.27.-). Length = 147	gij178250	189	416	74	76	HALSK30
300	HDRME43R	anonymous [Homo sapiens] >pir 39463 39463 gene anonymous protein - human >sp Q13769 Q13769 ANONYMOUS. Length = 683	gij388012	2	346	94	95	HDRME43
301	HHEFA24R	APP-binding protein 1 [Rattus norvegicus] >sp G4099878 G4099878 APP-BINDING PROTEIN 1. Length = 534	gij4099878	10	177	63	65	HHEFA24
302	HSSGC52R	argininosuccinate synthetase [Bos taurus] >sp P14568 ASSY_BOVIN ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5) (CITRULLINE-- ASPARTATE LIGASE). Length = 412	gij162697	1	438	94	95	HSSGC52



303	HCYBN49R	ATP synthase beta subunit precursor [Homo sapiens] >pir A33370 A33370 H+-transporting ATP synthase (EC 3.6.1.34) beta chain precursor, mitochondrial - human >sp P06576 ATPB_HUMAN ATP SYNTHASE BETA CHAIN. MITOCHONDRIAL PRECURSOR (EC 3.6.1.34). >gil28931 be	gil179281	56	445	97	97	HCYBN49
304	HWMGB90R	ATP synthase subunit e [Homo sapiens] >sp P56385 ATPJ_HUMAN ATP SYNTHASE E CHAIN, MITOCHONDRIAL (EC 3.6.1.34). {SUB 2-69} Length = 69	gil2605592	1	165	58	61	HWMGB90
305	HTEAW21R	ATPase coupling factor 6 subunit [Homo sapiens] >pir JT0563 JT0563 coupling factor 6 precursor, mitochondrial - human >sp P18859 ATPR_HUMAN ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (EC 3.6.1.34) (F6). Length = 108	gil179275	47	259	93	93	HTEAW21
306	HCQCV96R	ATPase subunit 6 [Homo sapiens] >sp Q34772 Q34772 ATP SYNTHASE A CHAIN (EC 3.6.1.34). Length = 226	gnl PID d1007873	147	368	58	61	HCQCV96
307	HLTDN74R	autotaxin-t [Homo sapiens] >sp Q13822 Q13822 AUTOTAXIN-T. >gnl PID d1008938 phosphodiesterase I alpha [Homo sapiens] {SUB 1-45} Length = 863	gil1160616	2	118	85	85	HLTDN74
308	HDABV61R	B-creatine kinase [Gallus gallus] Length = 65	gil211524	3	230	93	100	HDABV61

309	H2LAQ68R	beta prime cop [Bos taurus] >pir S35312 S35312 coatmer complex beta' chain - bovine >sp P35605 COPP_BOVIN COATOMER BETA' SUBUNIT (BETA'-COAT PROTEIN) (BETA'- COP) (PI02). {SUB 2-906} Length = 906	gil 312732	127	558	100	100	H2LAQ68
310	HDTLN42R	beta-2-microglobulin [Pan troglodytes] >gil 177065 beta-2-microglobulin [Gorilla gorilla] >gn PID d1036168 (AB021288) beta 2-microglobulin [Homo sapiens] >pir A90976 MGHUB2 beta-2- microglobulin precursor - human >pir 136963 136963 beta-2-microglobulin pre	gil 176827	2	361	86	86	HDTLN42
311	HULFN47R	beta-2-microglobulin [Pan troglodytes] >gil 177065 beta-2-microglobulin [Gorilla gorilla] >gn PID d1036168 (AB021288) beta 2-microglobulin [Homo sapiens] >pir A90976 MGHUB2 beta-2- microglobulin precursor - human >pir 136963 136963 beta-2-microglobulin pre	gil 176827	3	449	88	89	HULFN47
312	HCRM141R			1	528			HCRM141
313	HWLIP53R			2	499			HWLIP53
314	HBAAD60R			2	463			HBAAD60
315	HCROA35R			3	500			HCROA35
316	HCROM64R			201	512			HCROM64
317	HEOPS84R			2	388			HEOPS84
318	HKBAG82R			32	265			HKBAG82
319	HUTSB76R			188	418			HUTSB76

320	HWLJS67R	384	662	HWLJS67
321	HWLLZ82R	2	133	HWLLZ82
322	HCROM20R	351	557	HCROM20
323	HDQMC24R	1	144	HDQMC24
324	HOCTD89R	212	352	HOCTD89
325	HTGAZ53R	198	341	HTGAZ53
326	HWLKZ47R	429	626	HWLKZ47
327	HWLLLS1R	204	416	HWLLLS1
328	HIRLAJ54R	207	548	HIRLAJ54
329	HBAAD69R	1	456	HBAAD69
330	HWLJZ72R	25	453	HWLJZ72
331	HWMFG06R	43	321	HWMFG06
332	HPRTO65R	2	166	HPRTO65
	biliary glycoprotein a [Homo sapiens] >gnl PID d1015047 biliary glycoprotein, BGPg [Homo sapiens] >gi 3172151 (AC004785) BGPg_HUMAN [Homo sapiens] >pir JH0394 JH0394 biliary glycoprotein g precursor - human Length = 417	gil179438	93	97
333	HUFDC01R	108	326	HUFDC01
	biliary glycoprotein l precursor [Homo sapiens] >gi 37198 TM1-CEA preprotein [Homo sapiens] >gi 3172148 (AC004785) BGPI_HUMAN [Homo sapiens] >pir A32164 A32164 biliary glycoprotein l precursor - human >sp P13688 BGPI_HUMAN BILIARY GLYCOPROTEIN l PRECURSOR	gil179440	87	87
334	HWLHY44R	3	413	HWLHY44
	bone-derived growth factor [Homo sapiens] >sp Q13876 Q13876 BONE- DERIVED GROWTH FACTOR (FRAGMENT). Length = 793	gil1203965	75	79

335	HWLGR92R	brain glycogen phosphorylase [Homo sapiens] >pir A29949 A29949 glycogen phosphorylase (EC 2.4.1.1), brain (astrocytoma cell line) - human Length = 863	gil307200	122	238	100	100	100	HWLGR92
336	HCNCQ71R	CAG-isl 7 [Homo sapiens] Length = 213	gil3126984	1	93	66	77	77	HCNCQ71
337	HBMCI28R	carbonic anhydrase I (EC 4.2.1.1) [Homo sapiens] >gil29600 carbonic anhydrase I (AA 1-261) [Homo sapiens] >pir Q0786 CRHU1 carbonate dehydratase (EC 4.2.1.1) I - human >sp P00915 CAH1_HUMAN CARBONIC ANHYDRASE I (EC 4.2.1.1) (CARBONATE DEHYDRATASE I). ;SU	gil179793	81	293	84	84	84	HBMCI28
338	HWLENI1R	carbonic anhydrase I (EC 4.2.1.1) [Homo sapiens] >gil29600 carbonic anhydrase I (AA 1-261) [Homo sapiens] >pir Q0786 CRHU1 carbonate dehydratase (EC 4.2.1.1) I - human >sp P00915 CAH1_HUMAN CARBONIC ANHYDRASE I (EC 4.2.1.1) (CARBONATE DEHYDRATASE I). ;SU	gil179793	84	347	80	80	80	HWLENI1
339	HMSDU92R	carbonic anhydrase II [Homo sapiens] >gil179780 carbonic anhydrase II [Homo sapiens] >gil179795 carbonic anhydrase II [Homo sapiens] >gil29587 carbonic anhydrase II (AA 1-260) [Homo sapiens] >pir A27175 CRHU2 carbonate dehydratase (EC 4.2.1.1) II - human	gil179772	1	360	76	83	83	HMSDU92

340	HCDBF89R	carbonic anhydrase IV [Homo sapiens] >gil409726 carbonic anhydrase IV [Homo sapiens] {SUB 73-294} Length = 294	gil409725	11	160	87	90	HCDBF89
341	HCNDP16R	carboxylesterase hCE-2 [Homo sapiens] >sp Q16859 Q16859 CARBOXYLESTERASE (EC 3.1.1.1) (AL1-ESTERASE) (B-ESTERASE) (MONOBUTYRASE) (COCAINE ESTERASE) (PROCAINE ESTERASE) (METHYLBUTYRASE). Length = 550	gil407780	1	252	70	71	HCNDP16
342	HWLGX53R	carcinoembryonic antigen [Homo sapiens] >gil178677 carcinoembryonic antigen precursor [Homo sapiens] >pir A36319 A36319 carcinoembryonic antigen precursor - human >sp P06731 CCEM_HUMAN CARCINOEMBRYONIC ANTIGEN PRECURSOR (CEA) (MECONIUM ANTIGEN 100) (CD66E)	gil180223	19	138	73	73	HWLGX53
343	HWLEH56R	carcinoembryonic antigen [Homo sapiens] >gnl PID e24945 carcinoembryonic antigen [Homo sapiens] >gil3702266 (AC005797) carcinoembryonic antigen CGM2 precursor - human [Homo sapiens] >pir A55811 A55811 carcinoembryonic antigen CGM2 precursor - human >sp Q	gil471077	1	453	86	87	HWLEH56

344	H2LAD26R	CaRG box-binding factor [Mus musculus] >gnl PID d1014884 CaRG-binding factor-A [Mus musculus] >pir Q0448 Q0448 CaRG-binding factor-A - mouse >sp Q99020 CABA_MOUSE CaRG-BINDING FACTOR-A (CBF-A). Length = 285	gi 840648	43	387	98	98	H2LAD26
345	HADAF48R	CD99 typell [Homo sapiens] >sp O00518 O00518 CD99 TYPEII. Length = 160	gi 2149135	2	151	59	59	HADAF48
346	HCRNV62R	Cdc6-related protein [Homo sapiens] >gi 2465437 (AF022109) HsCdc18p [Homo sapiens] >sp Q99741 Q99741 CDC6-RELATED PROTEIN. Length = 560	gi 1684903	2	442	90	91	HCRNV62
347	HCDC117R	chaperonin-like protein [Homo sapiens] >pir S48087 S48087 I-complex-type molecular chaperone CCT6 - human >gi 184462 chaperonin-like protein [Homo sapiens] {SUB 143-531; Length = 531	gi 517065	3	137	97	100	HCDC117
348	HJUAA02R	CksI protein homologue [Homo sapiens] >pir A36670 A36670 protein kinase cdc2 complex subunit CKS1 - human >sp P33551 CKS1_HUMAN CYCLIN-DEPENDENT KINASES REGULATORY SUBUNIT 1 (CKS-1). Length = 79	gi 29977	186	386	96	96	HJUAA02

349	HKAKO78R	Cks1 protein homologue [Homo sapiens] >pir B36670 B36670 protein kinase cdc2 complex subunit CKS2 - human >sp P33552 CKS2_HUMAN CYCLIN- DEPENDENT KINASES REGULATORY SUBUNIT 2 (CKS-2). Length = 79	gij29979	2	193	77	77	HKAKO78
350	H2CBD02R			58	522			H2CBD02
351	HWLCR90R	contains similarity to ATP/GTP-binding site motif (PS:PS00017) [Caenorhabditis elegans] >sp Q94180 Q94180 SIMILARITY TO ATP/GTP-BINDING SITE MOTIF. Length = 398	gij1519671	1	351	34	60	HWLCR90
352	H2LAK66R	core protein II precursor [Homo sapiens] >pir A32629 A32629 ubiquinol-- cytochrome-c reductase (EC 1.10.2.2) core protein II - human Length = 453	gij180928	126	632	79	79	H2LAK66
353	HSDKC65R	CoxII/D-loop DNA fusion protein [Homo sapiens] >sp Q34777 Q34777 COXII/D- LOOP DNA FUSION PROTEIN (FRAGMENT). Length = 125	gij1374867	179	346	95	97	HSDKC65
354	H2LAK52R	CUL-2 [Homo sapiens] >sp Q13617 CUL2_HUMAN CULLIN HOMOLOG 2 (CUL-2). Length = 745	gij1923243	24	608	100	100	H2LAK52
355	HKAEI2R	cyclin B1 - human >sp P14635 CGB1_HUMAN G2/MITOTIC-SPECIFIC CYCLIN B1. Length = 433	pir A32992 A32992 2	3	392	98	98	HKAEI2
356	HKADP43R	cyclin F [Homo sapiens] >sp P41002 CG2F_HUMAN G2/MITOTIC-SPECIFIC CYCLIN F. Length = 786	gij576781	1	375	71	71	HKADP43

357	HLXND10R	cystatin B [Homo sapiens] >gi 1235678 cystatin B [Homo sapiens] >sp P04080 CYTB_HUMAN CYSTATIN B (LIVER THIOL PROTEINASE INHIBITOR) (CPI-B) (STEFIN B). Length = 98	gi 291927	2	355	100	100	100	HLXND10
358	HUSJE17R	cytochrome c oxidase subunit II [Pan troglodytes] >sp P26457 COX2_PANPA CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1). Length = 227	gi 336514	17	208	97	98		HUSJE17
359	HLHGH82R	cytochrome c oxidase subunit Va preprotein [Mus musculus] >pir S05495 S05495 cytochrome-c oxidase (EC 1.9.3.1) chain Va precursor - mouse >sp P12787 COXA_MOUSE CYTOCHROME C OXIDASE POLYPEPTIDE VA PRECURSOR (EC 1.9.3.1). Length = 145	gi 50527	2	106	94	94		HLHGH82
360	HHBEF06R	cytochrome oxidase III [Homo sapiens] >pir A00482 OTHU3 cytochrome-c oxidase (EC 1.9.3.1) chain III - human mitochondrion (SGC1) >sp P00414 COX3_HUMAN CYTOCHROME C OXIDASE POLYPEPTIDE III (EC 1.9.3.1). >gi 2245564 (AF004341) cytochrome c oxidase subunit I	gi 13010	167	373	75	80		HHBEF06



361	HISCW28R	cytochrome oxidase subunit II [Homo sapiens] >gi 530071 cytochrome oxidase subunit II [Homo sapiens] >gi 530073 cytochrome oxidase subunit II [Homo sapiens] >gi 530077 cytochrome oxidase subunit II [Homo sapiens] >gi 337187 cytochrome oxidase subunit II [	gil530069	121	312	83	86	HISCW28
362	HODEN42R	cytochrome oxidase subunit II [Homo sapiens] >gi 530071 cytochrome oxidase subunit II [Homo sapiens] >gi 530073 cytochrome oxidase subunit II [Homo sapiens] >gi 530077 cytochrome oxidase subunit II [Homo sapiens] >gi 337187 cytochrome oxidase subunit II [	gil530069	302	469	68	71	HODEN42
363	HOEMM43R	cytochrome oxidase subunit II [Homo sapiens] >gi 530071 cytochrome oxidase subunit II [Homo sapiens] >gi 530073 cytochrome oxidase subunit II [Homo sapiens] >gi 530077 cytochrome oxidase subunit II [Homo sapiens] >gi 337187 cytochrome oxidase subunit II [	gil530069	1	180	64	67	HOEMM43
364	HPIAK29R	cytochrome oxidase subunit II [Homo sapiens] >gi 530071 cytochrome oxidase subunit II [Homo sapiens] >gi 530073 cytochrome oxidase subunit II [Homo sapiens] >gi 530077 cytochrome oxidase subunit II [Homo sapiens] >gi 337187 cytochrome oxidase subunit II [	gil530069	295	441	63	70	HPIAK29

365	HUFAR71R	cytochrome oxidase subunit II [Homo sapiens] >gi 530071  cytochrome oxidase subunit II [Homo sapiens] >gi 530073  cytochrome oxidase subunit II [Homo sapiens] >gi 530077  cytochrome oxidase subunit II [Homo sapiens] >gi 337187  cytochrome oxidase subunit II [Homo sapiens]	gi 530069	128	367	82	85	HUFAR71
366	HHEUL74R	cytochrome oxidase subunit II [Homo sapiens] >sp Q37526 Q37526  CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1). Length = 227	gi 530075	3	227	70	74	HHEUL74
367	H2LAY36R	cytosolic malate dehydrogenase [Homo sapiens] >gi 3133269  malate dehydrogenase [Homo sapiens] >sp P40925 MDHC_HUMAN MALATE DEHYDROGENASE, CYTOPLASMIC (EC 1.1.1.37). {SUB 2-334} Length = 334	gnl P D d 010156	10	609	84	88	H2LAY36
368	HOECI21R	decay-accelerating factor precursor [Homo sapiens] >gnl P D d 023771  (AB003312) decay accelerating factor [Homo sapiens] {SUB 286-340} Length = 376	gi 181463	3	548	73	75	HOECI21
369	HKAFY51R	desmoglein 2 [Homo sapiens] >pir S38673 S38673  desmoglein 2 - human >sp Q14126 DSG2_HUMAN DESMOGLEIN 2 PRECURSOR (HDGC). Length = 1117	gi 416178	1	429	100	100	HKAFY51
370	HMCAR63R	diazepam binding inhibitor [Homo sapiens] Length = 104	gi 181478	3	335	100	100	HMCAR63

371	HWMAN06R	dopamine- and cAMP-regulated neuronal phosphoprotein [Sus scrofa] >sp Q29277 IPPD_PIG DOPAMINE- AND CAMP-REGULATED NEURONAL PHOSPHOPROTEIN (DARPP-32) (FRAGMENT). Length = 137	gi 972053	1	222	83	83	HWMAN06
372	HDPLD04R	early growth response 2 protein (EGR2) - human >gi 181987 early growth response 2 protein [Homo sapiens] {SUB 51-456} Length = 456	pir A40492 A40492	1	459	69	70	HDPLD04
373	HCEGK04R	elongation factor 2 [Gallus gallus] >sp Q90705 EF2_CHICK ELONGATION FACTOR 2 (EF-2). {SUB 2-858} Length = 858	gi 1184958	87	182	95	95	HCEGK04
374	HWLMB57R	epidermal growth factor receptor kinase substrate [Homo sapiens] >pir 38728 38728 epidermal growth factor receptor kinase substrate - human >sp Q12929 EPS8_HUMAN EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8. Length = 822	gi 530823	1	186	93	93	HWLMB57
375	HHFHF93R	epidermal growth factor receptor precursor [Homo sapiens] >sp P21860 ERB3_HUMAN ERBB-3 RECEPTOR PROTEIN-TYROSINE KINASE PRECURSOR (EC 2.7.1.112). >gi P1D e304809 unnamed protein product [Homo sapiens] {SUB 1-27} Length = 1342	gi 181980	1	180	89	89	HHFHF93

376	HCDEM69R	epiligrin alpha 3 subunit [Homo sapiens] >pir A55347 A55347 adhesive ligand epiligrin, alpha-3 chain form A precursor - human >sp Q16787 LMA3_HUMAN LAMININ ALPHA-3 CHAIN PRECURSOR (EPI IGRIN 170 KD SUBUNIT) (E170). Length = 1713	gij 551597	136	282	95	95	HCDEM69
377	HCHNP50R	epithelial cell marker protein 1 [Homo sapiens] >pir S38956 S38956 epithelial cell marker protein 1 - human Length = 248	gij 187302	54	218	94	94	HCHNP50
378	HAJAW27R	ERF-1 gene product [Homo sapiens] >pir S34854 S34854 epidermal growth factor-response factor 1 - human >gij 972116 ERF-1 protein [Sus scrofa] {SUB 299-337} Length = 338	gij 825653	3	488	100	100	HAJAW27
379	HAICY55R	G-rich sequence factor-1 [Homo sapiens] >gij 517196 G-rich sequence factor-1 [Homo sapiens] [Homo sapiens] >sp Q12849 GRF1_HUMAN G-RICH SEQUENCE FACTOR-1 (GRSF-1). >pir S48081 S48081 GRSF-1 protein - human (fragment) {SUB 94-424} Length = 424	gij 517196	3	374	50	50	HAICY55
380	HWLIA38R	gap junction protein (aa 1-283) [Homo sapiens] >pir B29005 B29005 gap junction protein Cx32 - human >sp P08034 CX32_HUMAN GAP JUNCTION BETA-1 PROTEIN (CONNEXIN 32) (CX32) (GAP JUNCTION 28 KD LIVER PROTEIN). Length = 283	gij 31647	3	455	82	85	HWLIA38

381	HBXCL69R	glutamine--phenylpyruvate aminotransferase [Homo sapiens] >pir S6900 S52790 glutamine-- phenylpyruvate transaminase (EC 2.6.1.64) - human >sp Q16773 Q16773 GLUTAMINE--PIENYLPYRUVATE AMINOTRANSFERASE (EC 2.6.1.64) (GLUTAMINE TRANSAMINASE K). Length = 422	gi 758591	81	419	61	67	HBXCL69
382	H2LAP90R	glutathione peroxidase [Homo sapiens] Length = 202	gi 488476	234	545	97	97	H2LAP90
383	HCQCR94R	glutathione peroxidase-G1 [Homo sapiens] Length = 190	gi 579930	1	114	95	95	HCQCR94
384	HTELE03R	glutathione peroxidase-G1 [Homo sapiens] Length = 190	gi 579930	14	202	100	100	HTELE03
385	HJMBN86R	glutathione-insulin transhydrogenase (216 AA) [Homo sapiens] Length = 216	gi 31746	2	202	97	100	HJMBN86
386	HSKJC32R	GTP:AMP phosphotransferase (EC 2.7.4.10) [Bos taurus] >gnl P1D d1001680 mitochondrial adenylate kinase isozyme 3 [Bos taurus] >pir A34442 A34442 nucleoside- triphosphate--adenylate kinase (EC 2.7.4.10) 3, mitochondrial - bovine >sp P08760 KAD3_BOVIN GTP:AM	gi 63528	1	642	89	94	HSKJC32
387	HOEAZ62R	GTP_binding protein [Sus scrofa] >sp Q29222 Q29222 GTP_BINDING PROTEIN (FRAGMENT). Length = 92	gi 971836	2	100	89	92	HOEAZ62

388	HAOAG76R	guanine nucleotide-binding protein G-s-alpha-4 [Homo sapiens] >gil31913 alpha-S1 (AA 1-380) [Homo sapiens] >pir C31927 RGHUA1 GTP-binding regulatory protein Gs alpha chain (adenylate cyclase-stimulating), splice form 4 - human Length = 380	gil386746	1	369	86	86	86	HAOAG76
389	HCIAD45R	guanylin [Homo sapiens] >gil306824 guanylin [Homo sapiens] >pir A46279 A46279 guanylin precursor - human >sp Q02747 GUAN_HUMAN GUANYLIN PRECURSOR (GUANYLATE CYCLASE ACTIVATOR 2A). Length = 115	gil183415	2	262	75	81	81	HCIAD45
390	H2MAC82R	H+-ATP synthase subunit b [Homo sapiens] >pir Q1144 Q1144 H+-transporting ATP synthase (EC 3.6.1.34) chain b precursor, mitochondrial - human >sp P24539 ATPF_HUMAN ATP SYNTHASE B CHAIN, MITOCHONDRIAL PRECURSOR (EC 3.6.1.34). Length = 256	gil509291	214	513	95	96	96	H2MAC82
391	H2LAJ41R	heat shock protein [Homo sapiens] >pir A32319 H1H1U86 heat shock protein 90-alpha - human >gil184419 heat shock protein 86 [Homo sapiens] {SUB 1-312} >gnl PID d1014121 heat shock protein 90 [Homo sapiens] {SUB 582-732} Length = 732	gil703087	75	632	98	98	98	H2LAJ41
392	HWLGH40R	HKL1 [Homo sapiens] >sp O60765 O60765 HKL1. Length = 605	gnl PID d1026110	1	597	92	93	93	HWLGH40

393	HBJFH33R	HLA DP4 beta-chain [Homo sapiens] >gi296648 pot. hla-dp-beta 1 [Homo sapiens] >pir A02229 HL.HUPB MHC class II histocompatibility antigen HLA-DP beta 1 chain (allele DPB4.1) precursor - human >sp P04440 HB2P_HUMAN HLA CLASS II HISTOCOMPATIBILITY ANTIGEN.	gij306858	97	369	88	92	HBJFH33
394	HISDV92R	homeobox c1 protein [Homo sapiens] >sp Q64081 Q64081 HOX-B HOX-2 {CLONE 17A1}. {SUB 137-196; Length = 217	gij306878	51	404	72	72	HISDV92
395	HMQCG89R	Hox5.4 gene product (AA 1-95) [Homo sapiens] >pir B32830 B32830 homeotic protein Hox D8 - human (fragment) >sp P13378 HDXD8_HUMAN HOMEBOX PROTEIN HOX-D8 (HOX-4E) (HOX-5.4) (FRAGMENT). Length = 95	gij32400	158 1	388 345	100	100	HMQCG89 HIE9QB35
396	HIE9QB35R							
397	HDABQ50R	hsOrc2p [Homo sapiens] >sp Q13416 ORC2_HUMAN ORIGIN RECOGNITION COMPLEX PROTEIN. SUBUNIT 2. Length = 577	gij1113107	204	368	91	91	HDABQ50

398	HNTEG83R	hydroxymethylglutaryl-CoA lyase [Homo sapiens] >pir A45470 A45470 hydroxymethylglutaryl-CoA lyase (EC 4.1.3.4) - human >sp P35914 HMGL_HUMAN HYDROXYMETHYLGLUTARYL- COA LYASE PRECURSOR (EC 4.1.3.4) (HMG-COA LYASE) (HL) (3- HYDROXY-3-METHYLGLUTARATE- COA LYASE	gil 84503	2	391	83	83	HNTEG83
399	HFVHM90R	hydroxymethylglutaryl-CoA synthase [Homo sapiens] >gil 2463646 3-hydroxy- 3-methylglutaryl CoA synthase [Homo sapiens] >pir S71623 S71623 hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5) precursor, mitochondrial - human >sp P54868 HMCM_HUMAN HYDROXYMETHYLGLU	gil 619877	2	319	92	94	HFVHM90
400	HOSNF90R	hypothetical 18K protein (rRNA) - goldfish mitochondrion (SGC1) Length = 166	pir JC1348 JC1348	257	340	59	62	HOSNF90
401	HSDIE56R	hypothetical 18K protein (rRNA) - goldfish mitochondrion (SGC1) Length = 166	pir JC1348 JC1348	2	70	67	73	HSDIE56
402	HWLGC87R	hypothetical protein 2 (rRNA external transcribed spacer) - mouse Length = 153	pir S12206 S12206	1	135	96	96	HWLGC87



403	HTPAC28R	I-plastin [Homo sapiens] >pir A56536 A56536 plastin, intestine-specific - human >sp Q14651 PLSI_HUMAN I-PLASTIN (INTESTINE-SPECIFIC PLASTIN). Length = 629	gi 405230	68	325	92	93	HTPAC28
404	IIMCGN07R	ICK=INTRON-CONTAINING KALLIKREIN {ALTERNATIVELY SPLICED, INTRON 2}. Length = 216	sp G998972 G998972	1	498	98	99	IIMCGN07
405	HFIBV16R	Id1 gene product [Homo sapiens] >pir S47524 S47524 gene Id1 protein - human Length = 154	gi 457785	2	238	89	89	HFIBV16
406	HBMTT01R	Ig alpha-2 chain C region (allotype A2m(1)) - human >sp P01877 ALC2_HUMAN IG ALPHA-2 CHAIN C REGION. >gi 184761 Ig alpha-2 H-chain constant region (aa at 166) [Homo sapiens] {SUB 2-340} Length = 340	pir B22360 B22360	2	154	80	80	HBMTT01
407	HBMVM66R	Ig gamma chain C region - chimpanzee >gnl PIJ40518 CH2 domain of IgG [Pan troglodytes] {SUB 25-134} >gnl PIJ40517 CH3 domain of IgG [Pan troglodytes] {SUB 135-234} Length = 234	pir PT0207 PT0207	148	435	70	77	HBMVM66
408	HABGC21R	Ig heavy chain (DOT) - human (fragment) >gnl PID4381 reading frame CH1 [Homo sapiens] {SUB 121-218} Length = 241	pir S69131 S69131	1	228	50	56	HABGC21
409	HWLGE72R	Ig kappa light chain (VJ) [Homo sapiens] >pir S40343 S40343 Ig kappa chain V-J region - human Length = 128	gi 441375	11	421	75	79	HWLGE72

410	HLJBX69R	IgM B-cell receptor associated protein (BAP) 37 [Mus musculus] >pir S46996 S46996 B-cell receptor-associated protein [BAP]37 - mouse >sp Q61336 Q61336 BCR-ASSOCIATED PROTEIN 37 (IGM B-CELL RECEPTOR ASSOCIATED PROTEIN 37) (BAP). Length = 298	gij541734	1	279	100	100	HLJBX69
411	HWAFW14R	immunoglobulin from VH4 family [Homo sapiens] >pir S13519 S13519 Ig heavy chain V region precursor - human >gij553385 immunoglobulin heavy chain [Homo sapiens] {SUB 24-125} Length = 147	gij37725	2	139	94	100	HWAFW14
412	HWAFK04R	immunoglobulin heavy chain [Homo sapiens] >pir E36005 E36005 Ig heavy chain V region (M72) - human {SUB 36-157} Length = 157	gij567126	48	473	78	86	HWAFK04
413	HEPNA09R	immunoglobulin heavy chain [Homo sapiens] >pir G36005 G36005 Ig heavy chain V region (M74) - human {SUB 38-158} Length = 158	gij567127	3	206	81	87	HEPNA09
414	HCRQD03R	immunoglobulin heavy chain [Homo sapiens] Length = 152	gij567128	1	573	76	82	HCRQD03
415	HAPSK08R	immunoglobulin heavy chain variable region [Homo sapiens] >gij903667 Ig heavy chain variable region VH [Homo sapiens] {SUB 1-97} >gij976311 This CDS feature is included to show the translation of the corresponding V_segment. Presently translation qualifie	gij1791017	1	363	79	81	HAPSK08

416	HBM1S11R	immunoglobulin IgH heavy chain Fd fragment [Homo sapiens] Length = 221	gi 468237	1	375	68	70	HBM1S11
417	HCNDR62R	immunoglobulin kappa light chain [Homo sapiens] >pir A37927 A37927 Ig kappa chain C region (allotype Inv(1.2)) - human (fragment) {SUB 138-236} Length = 236	gn PI e224083	245	337	100	100	IICNDR62
418	HNJBF13R	immunoglobulin lambda light chain gene product [Homo sapiens] >pir S25738 S25738 Ig lambda chain - human Length = 231	gi 33702	3	308	90	93	HNJBF13
419	HL YCD69R	immunoglobulin lambda light chain gene product [Homo sapiens] >pir S25743 S25743 Ig lambda chain - human (fragment) Length = 145	gi 33712	2	481	86	89	III.YCD69
420	HWAFK89R	immunoglobulin lambda light chain gene product [Homo sapiens] >pir S25750 S25750 Ig lambda chain - human Length = 235	gi 33730	2	460	87	92	IHWAFK89
421	HWCAA53R	immunoglobulin light chain variable region [Homo sapiens] >gi 3142470 (AF063703) immunoglobulin lambda light chain variable region [Homo sapiens] {SUB 20-127} >gi 575243 immunoglobulin lambda chain precursor [Homo sapiens] {SUB 26-127} >gn PI d1020826 V	gi 465170	1	342	74	88	HWCAA53
422	HYAAY47R	immunoglobulin light chain variable region [Homo sapiens] Length = 154	gi 465168	2	292	70	74	HYAAY47
423	IIMCJF14R			21	596			IIMCJF14
424	HE8QU88R			13	141			HE8QU88

425	HFVGP11R	L-FABP [Homo sapiens] >pir A22289 FZHU.L fatty acid-binding protein, hepatic - human >sp P07148 FABL_HUMAN FATTY ACID-BINDING PROTEIN, LIVER (L- FABP). Length = 127	gij 182358	29	322	98	98	HFVGP11
426	HWLQH07R			3	554			HWLQH07
427	HSIGN24R	Irp gene product [Homo sapiens] >pir SS7723 SS7723 Irp protein - human >sp Q14764 MVP_HUMAN MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN). Length = 896	gij 895840	2	250	89	93	HSIGN24
428	HWLKH07R	lysophosphatidic acid acyltransferase- beta [Homo sapiens] Length = 278	gij 2155240	74	298	96	97	HWLKH07
429	HAPQC14R	macrophage capping protein [Homo sapiens] >pir A43358 A43358 macrophage capping protein - human >sp P40121 CAPG_HUMAN MACROPHAGE CAPPING PROTEIN (ACTIN-REGULATORY PROTEIN CAP-G). >gij 515505 Cap-G [Homo sapiens] {SUB 1-172} Length = 348	gij 187456	2	538	96	98	HAPQC14
430	HSODB48R	malonyl-CoA decarboxylase (EC 4.1.1.9) - goose >gij 305323 malonyl CoA decarboxylase [Anser anser] {SUB 33- 462} Length = 462	pir A33313 A33313 3	32	466	77	81	HSODB48
431	HBEAC75R	membrane glycoprotein [Homo sapiens] Length = 385	gij 307132	2	217	73	79	HBEAC75
432	HBGMJ24R	mitochondrial RNA polymerase [Homo sapiens] Length = 1230	gij 2114396	3	479	100	100	HBGMJ24

433	HBJEN94R	mitotic kinase-like protein-1 [Homo sapiens] >pir S28262 S28262 kinesin-related protein MKLP-1 - human >sp Q02241 MKLP_HUMAN MITOTIC KINESIN-LIKE PROTEIN-1. Length = 960	gij34672	1	327	89	89	HBJEN94
434	HCIAE73R	motor protein [Homo sapiens] Length = 721	gn PIPI d1005183	73	324	100	100	HCIAE73
435	HCNDN88R	mucin 2 precursor, intestinal - human (fragments) >gij186396 mucin [Homo sapiens] {SUB 626-1895} >gij186398 MUC2 [Homo sapiens] {SUB 2037-3020} >gij188874 intestinal mucin [Homo sapiens] {SUB 1916-2193} >gij188615 mucin-like protein [Homo sapiens] {SUB 23}	pir A49963 A4393 2	1	171	95	97	HCNDN88
436	HSIDX70R	N-benzoyl-L-tyrosyl-p-amino-benzoic acid hydrolase alpha subunit [Homo sapiens] >pir S60193 H_YHUMA meprin A (EC 3.4.24.18) alpha chain precursor - human >sp Q16819 MEPA_HUMAN MEPRIN A ALPHA-SUBUNIT PRECURSOR (EC 3.4.24.18) (ENDOPEPTIDASE-2) (N-BENZOYL-L-	gij535475	2	253	94	94	HSIDX70

437	HILWBC39R	Na <sup>+</sup> /H <sup>+</sup> exchanger NHE-1 isoform [human, heart, Peptide, 815 aa] [Homo sapiens] >pir 57487  57487 Na <sup>+</sup> /H <sup>+</sup> - exchanging protein NHE-1 - human >sp P19634 NAH1_HUMAN SODIUM/HYDROGEN EXCHANGER 1 (NA <sup>+</sup> /H <sup>+</sup> ) EXCHANGER 1 (NHE- 1) (NA <sup>+</sup> /H <sup>+</sup> ANTIporter, AMILORIDE-SENSI	bbs 43522	2	388	77	77	HILWBC39
438	HWLAA06R	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - chimpanzee mitochondrion (S611) (fragment) >sp P03906 NU4M_PANTR NADH- UBIQUINONE OXIDOREDUCTASE CHAIN 4 (EC 1.6.5.3) (FRAGMENT). Length = 152	pir A00435 A0043 5	66	194	86	97	HWLAA06
439	HASCH25R	NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-39KD) (CI-39KD). >gi 189049 NADH dehydrogenase (ubiquinone) [Homo sapiens] {SUB 3- 377} Length = 377	sp Q16795 NUEM _HUMAN	57	143	78	82	HASCH25
440	HILQGB87R	NADPH--ferrihemoprotein reductase (EC 1.6.2.4) - human >sp P16435 NCPR_HUMAN NADPH- CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR). {SUB 2-677} Length = 677	pir A3342  A6055 7	1	411	92	93	HILQGB87

441	IIIDMD17R	neutrophil gelatinase associated lipocalin [Homo sapiens] >sp P80188 NGAL_HUMAN NEUTROPHIL GELATINASE- ASSOCIATED LIPOCALIN PRECURSOR (NGAL) (P25) (25 KD ALPHA-2-MICROGLOBULIN- RELATED SUBUNIT OF MMP-9) (LIPOCALIN-2) (ONCOGENE 24P3). Length = 198	gi 929657	1	621	74	78	IIIDMD17
442	IIAOC69R	nuclear autoantigen [Homo sapiens] >pir A37244 A37244 nuclear autoantigen Sp-100 - human Length = 480	gi 178689	3	209	88	88	IIAOC69
443	IIWLEQ08R	Nuclear localization signal at AA 569- 573, 576-580, 579-583; acidic transer. activ. domain 620-640.; homeobox motif 653-676 [Homo sapiens] >pir A47456 A47456 down-regulated in adenoma (DRA) - human >sp P40879 DRA_HUMAN DRA PROTEIN (DOWN-REGULATED IN ADENO	gi 291964	191	364	75	84	IIWLEQ08
444	HKAAV70R	nucleic acid binding protein [Homo sapiens] >pir I38191 I38191 nucleic acid binding protein - human (fragment) >sp Q15410 Q15410 NUCLEIC ACID BINDING PROTEIN (FRAGMENT). Length = 163	gi 431953	1	432	73	73	HKAAV70

445	HOCTB64R	ORIGINAL PIGR [unidentified] >gi 456346 Polymetric immunoglobulin receptor [Homo sapiens] >bbs 62408 transmembrane secretory component, poly-Ig receptor, SC [human, colonic adenocarcinoma cell line, Peptide, 764 aa] [Homo sapiens] >bbs 113253 transmembrane	gn P D e 307278	3	212	85	90	HOC1B64
446	HOFNB62R	ornithine decarboxylase [Bos taurus] >gi 163449 ornithine decarboxylase [Bos taurus] >sp P27117 DCOR_BOVIN ORNITHINE DECARBOXYLASE (EC 4.1.1.17) (ODC). >gi 604513 ornithine decarboxylase [Bos taurus] (SUB 1-34) Length = 461	gi 1036793	1	312	85	90	HOFNB62
447	HAUAU04R	p22 phagocyte b-cytochrome [Homo sapiens] >pir A28201 A28201 cytochrome b-245 alpha chain - human >sp P13498 C24A_HUMAN CYTOCHROME B-245 LIGIT CIIAIN (P22 PHAGOCYTE B-CYTOCHROME) (NEUTROPHIL CYTOCHROME B, 22 KD POLYPEPTIDE) (P22-PHOX) (CYTOCHROME B(558) AL	gi 189106	1	267	87	88	HAUAU04
448	HNFJE41R	p47-phox [Homo sapiens] >sp O43842 O43842 P47-PHOX. Length = 390	gi 2754713	1	423	94	97	HNFJE41
449	IICFOH92R	phosphoprotein phosphatase (EC 3.1.3.16) catalytic beta chain - pig (fragment) Length = 293	pir B27430 B2743 0	2	88	93	93	IICFOH92
450	HOUIDS3R	phosphorylation regulatory protein HP-10 - human Length = 492	pir A61382 A6138 2	85	213	45	49	HOUIDS3



451	HCRMW41R	polypeptide BM28 [Homo sapiens] Length = 892	gi 468704	1	282	100	100	100	HCRMW41
452	HOVAX78R	porin [Homo sapiens] >pir A45972 A45972 mitochondrial porin, long form - human >sp P45880 POR2_HUMAN VOLTAGE-DEPENDENT ANION- SELECTIVE CHANNEL PROTEIN 2 (VDAC2) (OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN). >gi 190201 porin [Homo sapiens] {SUB 27-347} Len	gi 190200	2	214	94	98	98	HOVAX78
453	HWAEH57R	precursor [Homo sapiens] >sp P06314 KV4C_HUMAN IG KAPPA CHAIN PRECURSOR V-IV REGION (B17). Length = 134 >pir S63683 S63683 presenilin 1-463 - human Length = 463	gi 37910	1	462	91	93	93	HWAEH57
454	HHBJU76R	prosomal P27K protein [Homo sapiens] >gnl P1D1d1002062 proteasome subunit R-IOTA [Rattus sp.] >pir S30274 S30274 multicatalytic endopeptidase complex (EC 3.4.99.46) iota chain - human >pir JX0230 JX0230 multicatalytic endopeptidase complex (EC 3.4.99.46)	gi 1244638	1	303	98	98	98	HHBJU76
455	HBJFA18R	protein kinase [Homo sapiens] >sp P51956 NEK3_HUMAN SERINE/THREONINE-PROTEIN KINASE NEK3 (EC 2.7.1.-) (NIMA- RELATED PROTEIN KINASE 3) (HSPK 36) (FRAGMENT). Length = 459	gi 35682	178	402	79	83	83	HBJFA18
456	HCRNF16R		gi 479173	336	473	73	79	79	HCRNF16

457	HAHEK76R	putative surface glycoprotein [Homo sapiens] >sp P53801 C211_HUMAN PUTATIVE SURFACE GLYCOPROTEIN C21ORF1	gn PID e188111	33	440	83	86	HAHEK76
458	HEOPT38R	PRECURSOR (C21ORF3), Length = 180 renin-binding protein [Homo sapiens] >gi 1302662 renin-binding protein [Homo sapiens] >pir JX0188 JX0188 renin-binding protein - human Length = 417	gn PID d1001551	2	316	100	100	HEOPT38
459	HOSCG81R	ribonucleoprotein La [Homo sapiens] >sp Q15367 Q15367 RIBONUCLEOPROTEIN (LA) (FRAGMENT). >gi 338496 SS-B/La protein [Homo sapiens] {SUB 121-171} Length = 355	gi 337457	1	297	96	96	HOSCG81
460	HTFMD43R	ribosomal protein L39 [Homo sapiens] >gn PID d1012131 ribosomal protein L39 [Homo sapiens] >gi 575382 ribosomal protein L39 [Rattus norvegicus] >pir JC4229 R6RT39 ribosomal protein L39 - rat >pir G02654 G02654 ribosomal protein L39 - human Length = 51	gi 1373419	3	242	100	100	HTFMD43
461	HDTGQ68R	ribosomal protein L7a large subunit [Homo sapiens] >gi 34203 L7a protein [Homo sapiens] >gi 35512 PLA-X polypeptide [Homo sapiens] >gi 36647 ribosomal protein L7a [Homo sapiens] >gi 56956 ribosomal protein L7a (AA 1- 266) [Rattus rattus] >pir S19717 R5HU7A	gi 337495	43	291	100	100	HDTGQ68

462	H2LAR73R	ribosomal protein S15a [Rattus norvegicus] >pir JC2234 JC2234 ribosomal protein S15a - rat Length = 130	gij495273	23	505	100	100	100	H2LAR73
463	HAMFM26R	ribosomal protein S6 kinase 1 [Homo sapiens] >pir S1901 S1901 ribosomal protein S6 kinase 2 - human >sp Q15418 KS61_HUMAN RIBOSOMAL PROTEIN S6 KINASE II ALPHA 1 (EC 2.7.1.-) (S6KII-ALPHA 1) (P90-RSK 1) (RIBOSOMAL S6 KINASE 1) (RSK1) (PP90RSK1). Length =	gij292457	3	458	97	97	97	HAMFM26
464	HBMTM61R	Rieske Fe-S protein [Homo sapiens] Length = 274	gij488299	1	219	53	53	55	HBMTM61
465	I1W1IPK71R	RIP [Homo sapiens] >pir 38992 38992 receptor interacting protein RIP - human (fragment) Length = 372	gij829617	198	320	56	56	64	I1W1IPK71
466	HWBBJ39R	Sec23 protein [Homo sapiens] Length = 767	gnl PID e236014	2	127	81	81	84	HWBBJ39
467	HSLJJ36R	selenium donor protein [Homo sapiens] Length = 383	gij1000284	2	319	96	96	98	HSLJJ36
468	HSODD94R	selenoprotein P [Homo sapiens] Length = 381	gnl PID e1192260	2	232	61	61	70	HSODD94
469	HMIAG25R	serine kinase [Homo sapiens] >pir S45337 S45337 serine protein kinase SRPK1 - human >sp Q12890 Q12890 SERINE KINASE. Length = 655	gij507213	1	330	82	82	82	HMIAG25
470	HWLEM94R	serine protease [Homo sapiens] Length = 492	gij2507613	2	304	78	78	82	HWLEM94

471	HCNDW17R	Sm protein G [Homo sapiens] >pir S55054 S55054 Sm protein G - human >sp Q15357 Q15357 SM PROTEIN G. Length = 76	gi 806366	1	240	100	100	HCNDW17
472	HWLEY08R	SNAP23A protein [Homo sapiens] >gnl PID e1331767 (AJ011915) synaptosome associated protein of 23 kilodaltons, isoform A [Homo sapiens] >pir JC5296 JC5296 vesicle-membrane fusion protein SNAP-23A - human >sp O00161 O00161 VESICLE-MEMBRANE FUSION PROTEIN SN	gnl PID e290695	222	608	97	97	HWLEY08
473	HULFN68R	sorcin CP-22 [Homo sapiens] >gi 459836 sorcin [Homo sapiens] >pir S52094 S52094 sorcin - human >gi 2772536 (AC003991) calcium binding protein amplified in multidrug-resistant cells [Homo sapiens] {SUB 1-68} Length = 198	gi 338482	2	409	88	91	HULFN68
474	HMEJD77R	SRp30c [Homo sapiens] >gnl PID e1248292 (AL021546) pre-mRNA splicing factor SRp30c [Homo sapiens] >gi 4099429 splicing factor SRp30c [Homo sapiens] >pir S59075 S59075 splicing factor SRp30c - human >sp G4099429 G4099429 SPLICING FACTOR SRP30C. Length = 22	gi 1049078	3	263	46	48	HMEJD77
475	HS2AD15R	stimulator of TAR RNA binding [Homo sapiens] Length = 539	gi 1200184	1	336	87	88	HS2AD15

476	HTEJJ32R	STM-7 [Homo sapiens] >sp Q92749 Q92749 TYPE I PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE BETA (EC 2.7.1.68) (STM-7 PROTEIN). >gi 1743883 type I phosphatidylinositol- 4-phosphate 5-kinase beta [Homo sapiens] {SUB 112-502} >gi 1743879 type I phosphatidylinosi	gnl PID e206448	3	341	100	100	HTEJJ32
477	HETIF46R	sulfate transporter [Homo sapiens] >sp P50443 DTD_HUMAN SULFATE TRANSPORTER (DIASTROPHIC DYSPLASIA PROTEIN). Length = 739 thrombospondin 2 [Homo sapiens] >pir A47379 TSITUP2 thrombospondin 2 precursor - human Length = 1172	gi 549988	1	228	71	71	HETIF46
478	H2CBS58R	thymosin beta-4 precursor [Rattus norvegicus] >pir I52084 I52084 thymosin beta-4 precursor - rat (fragment) >gi 339689 thymosin beta-4 [Homo sapiens] {SUB 13-56} >pir A01521 TNBOB4 thymosin beta-4 - bovine {SUB 14-56} >gi 825683 open reading frame [Homo s	gi 307506	3	455	96	97	H2CBS58
479	H2LAB77R	thymosin beta-4 precursor [Rattus norvegicus] >pir I52084 I52084 thymosin beta-4 precursor - rat (fragment) >gi 339689 thymosin beta-4 [Homo sapiens] {SUB 13-56} >pir A01521 TNBOB4 thymosin beta-4 - bovine {SUB 14-56} >gi 825683 open reading frame [Homo s	gi 207318	98	265	100	100	H2LAB77
480	IIODAJ23R	tissue-specific secretory protein [unidentified] >gi 32051 HE4 protein [Homo sapiens] >pir S25454 S25454 HE4 protein - human >sp Q14508 EP4_HUMAN MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 PRECURSOR (HE4) (EPIDIDYMAL SECRETORY PROTEIN E4). Length =	gi 583141	2	223	62	62	IIODAJ23

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481	HWAFP88R	TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3). Length = 204	sp Q64152 BTF3_ MOUSE	85	471	92	93	HWAFP88
482	IIDTIIIS1R	transcription factor-like protein 4 - human Length = 298	pir JC5333 JC5333	2	565	82	86	IIDTIIIS1
483	HWMEB67R	tryptase-III [Homo sapiens] >sp Q15664 Q15664 TRYPTASE-III (FRAGMENT). Length = 267	gi 339985	21	218	92	92	HWMEB67
484	HTXOU93R	tumor susceptibility protein [Homo sapiens] >sp Q99816 Q99816 TUMOR SUSCEPTIBILITY PROTEIN. Length = 390	gi 3184258	2	439	100	100	HTXOU93
485	HANKB37R	ubiquitin [Plasmodium falciparum] >sp Q26029 Q26029 UBIQUITIN. Length = 77	gi 552237	11	115	70	73	HANKB37
486	HWLHN38R	ubiquitin-conjugating enzyme [Mus musculus] >sp Q88738 Q88738 UBIQUITIN-CONJUGATING ENZYME. Length = 4845	gn P1D1e1311091	129	347	77	83	HWLHN38

487	HOSDZ35R	UDP-GalNAc:polypeptide N- acetylglucosaminyltransferase [Homo sapiens] >sp Q14435 Q14435 POLYPEPTIDE N- ACETYLGLACTOSAMINYLTRANS FERASE (EC 2.4.1.41) (PROTEIN-UDP ACETYLGLACTOSAMINYLTRANS FERASE) (UDP- GALNAc:POLYPEPTIDE, N- ACETYLGLACTOSAMINYLTRANS FERASE)	gnl PID c209711	2	286	85	85	HOSDZ35
488	HKMAA52R	UDP-glucuronosyltransferase [Homo sapiens] >pir A31340 A31340 glucuronosyltransferase (EC 2.4.1.17) UGT1A1 precursor - human >sp G245274 G245274 PHENOL TRANSFERASE=UGT1F: PRODUCT: {SUB 1-286} >gi 264549  (AF014112) phenol UDP-glucuronosyltransferase [Homo	gi 624725	3	284	98	98	HKMAA52
489	H2LAB37R			93	290			H2LAB37
490	H2LAP46R			206	568			H2LAP46
491	H6BSE61R			67	369			H6BSE61
492	H6EEE76R			149	277			H6EEE76
493	H6EEV26R			2	88			H6EEV26
494	HABAF88R			40	216			HABAF88
495	IIABGD41R			1	147			IIABGD41
496	HACBS75R			5	187			HACBS75
497	HACCA48R			5	91			IIACCA48
498	HACCS19R			3	341			HACCS19
499	IIADAB25R			1	261			IIADAB25
500	HAGGL96R			3	347			HAGGL96

501	HAGGT37R	3	113	IIAGGT37
502	HAHDR66R	27	347	HAHDR66
503	HAIJCC53R	164	418	HAIJCC53
504	HAIJCL80R	3	122	HAIJCL80
505	HANKF43R	372	566	HANKF43
506	HAPCM11R	69	152	HAPCM11
507	HAPNT66R	1	66	HAPNT66
508	HAQAG47R	2	148	HAQAG47
509	HAQBW58R	3	260	HAQBW58
510	HAQMH45R	91	363	HAQMH45
511	HAQMI94R	1	183	HAQMI94
512	HARNC74R	84	272	HARNC74
513	HATBA87R	98	202	HATBA87
514	HATBG77R	174	392	HATBG77
515	HBAGQ79R	1	231	HBAGQ79
516	HBCAN64R	2	82	HBCAN64
517	HBGCA44R	1	123	HBGCA44
518	HBGFX27R	3	281	HBGFX27
519	HBGMU38R	40	429	HBGMU38
520	HBJBO10R	1	93	HBJBO10
521	HBJCC53R	2	106	HBJCC53
522	HBJED55R	1	252	HBJED55
523	HBJGR39R	2	106	HBJGR39
524	HBJLU30R	39	344	HBJLU30
525	HBKEC78R	93	245	HBKEC78
526	HBMST81R	1	192	HBMST81
527	HBMTJ51R	150	323	HBMTJ51
528	HBMWF72R	1	111	HBMWF72
529	HBWBD78R	2	226	HBWBD78
530	HBXCU02R	2	79	HBXCU02
531	HCDAK65R	1	138	HCDAK65



532	HCDBM08R	130	339	HCDBM08
533	HCDCP10R	72	206	HCDCP10
534	HCDDQ63R	3	116	HCDDQ63
535	HCEEH05R	204	380	HCEEH05
536	HCEIQ92R	1	90	HCEIQ92
537	HCPCD01R	28	228	HCPCD01
538	HCFCR43R	64	360	HCFCR43
539	HCFLT83R	3	104	HCFLT83
540	HCHAO92R	193	342	HCHAO92
541	HCHOH49R	183	344	HCHOH49
542	HCHPG05R	365	616	HCHPG05
543	HCIAD24R	98	301	HCIAD24
544	HCNCA90R	380	532	HCNCA90
545	HCNCN80R	120	353	HCNCN80
546	HCNCY51R	184	267	HCNCY51
547	HCNCY63R	1	81	HCNCY63
548	HCNDO71R	1	213	HCNDO71
549	HCNDV83R	64	303	HCNDV83
550	HCNUB26R	119	289	HCNUB26
551	HCQBN22R	2	94	HCQBN22
552	HCQCL27R	116	235	HCQCL27
553	HCQCL48R	57	251	HCQCL48
554	HCQCL96R	287	430	HCQCL96
555	HCQDC74R	145	360	HCQDC74
556	HCQDH94R	20	76	HCQDH94
557	HCQDJ42R	149	388	HCQDJ42
558	HCNMD77R	3	185	HCNMD77
559	HCNME02R	3	293	HCNME02
560	HCNMX88R	3	284	HCNMX88
561	HCNNA70R	40	204	HCNNA70
562	HCNRP66R	3	431	HCNRP66

563	HCRNX32R	2	196	HCRNX32
564	HCROH25R	3	128	HCROH25
565	HCROJ05R	66	170	HCROJ05
566	HCROJ68R	3	239	HCROJ68
567	HCROK68R	2	208	HCROK68
568	HCROK94R	1	210	HCROK94
569	HCROM30R	3	365	HCROM30
570	HCROQ34R	29	136	HCROQ34
571	HCROQ54R	3	98	HCROQ54
572	HCROZ66R	239	427	HCROZ66
573	HCRPC61R	3	194	HCRPC61
574	HCRPG28R	95	229	HCRPG28
575	HCRPL80R	59	235	HCRPL80
576	HCRPN52R	3	191	HCRPN52
577	HCRPS40R	208	321	HCRPS40
578	HCRPV74R	179	409	HCRPV74
579	HCRQC89R	2	85	HCRQC89
580	HCWDS78R	322	558	HCWDS78
581	HDCAA21R	1	120	HDCAA21
582	HDDAA85R	139	258	HDDAA85
583	HDPGO03R	110	352	HDPGO03
584	HDPLB08R	142	360	HDPLB08
585	HDQDB15R	220	417	HDQDB15
586	HDQEX80R	274	492	HDQEX80
587	HDRMI91R	3	116	HDRMI91
588	HDTJO85R	36	197	HDTJO85
589	HDTMJ22R	192	608	HDTMJ22
590	HE6CS28R	40	213	HE6CS28
591	HE6DJ45R	2	64	HE6DJ45
592	HE7TJ40R	62	268	HE7TJ40
593	HE9FH12R	182	307	HE9FH12

594	HE9HJ57R	3	74	HE9HJ57
595	HE9QH08R	360	596	HE9QH08
596	HE9TC50R	198	425	HE9TC50
597	HEAAL59R	1	150	HEAAL59
598	HEGAR32R	448	675	HEGAR32
599	HEGAR85R	361	534	HEGAR85
600	HELFE05R	32	187	HELFE05
601	HEMF188R	26	343	HEMF188
602	HEMFR18R	83	397	HEMFR18
603	HEONL43R	2	76	HEONL43
604	HESAC53R	3	116	HESAC53
605	HETJB05R	1	138	HETJB05
606	HETJC36R	1	102	HETJC36
607	HFADM62R	1	78	HFADM62
608	HFATE31R	2	361	HFATE31
609	HFATZ30R	3	152	HFATZ30
610	HFCEL77R	3	278	HFCEL77
611	HFEBN43R	174	491	HFEBN43
612	HFCAF10R	272	469	HFCAF10
613	HFEC01R	1	144	HFEC01
614	HFIR75R	317	427	HFIR75
615	HFUB90R	2	124	HFUB90
616	HFUM71R	37	159	HFUM71
617	HFOXLS3R	1	117	HFOXLS3
618	HFPBO66R	196	408	HFPBO66
619	HFTBI57R	47	220	HFTBI57
620	HFTCC22R	1	126	HFTCC22
621	HFXGX46R	1	114	HFXGX46
622	HGAME72R	2	199	HGAME72
623	HGBCS53R	142	279	HGBCS53
624	HGBHP81R	87	221	HGBHP81

625	IIICOX03R	323	511	HICOX03
626	HHBES92R	349	483	HHBES92
627	HHBEW72R	13	219	HHBEW72
628	HHERT59R	2	88	HHERT59
629	HHMMD64R	31	252	HHMMD64
630	HHSGT13R	428	619	HHSGT13
631	HISED82R	1	126	HISED82
632	IJMAH76R	2	253	IJMAH76
633	IJMAN56R	1	180	IJMAN56
634	IJMAO54R	1	291	IJMAO54
635	HKDAD56R	2	109	HKDAD56
636	HKLSD93R	89	298	HKLSD93
637	HLMFH16R	1	447	HLMFH16
638	HLQBD52R	1	195	HLQBD52
639	HLQCQ73R	3	350	HLQCQ73
640	HLQEF47R	348	503	HLQEF47
641	HLQFM50R	136	291	HLQFM50
642	HLQFY61R	411	575	HLQFY61
643	HLQGA76R	210	404	HLQGA76
644	HLQGE53R	1	66	HLQGE53
645	HLTEV09R	210	371	HLTEV09
646	HLXNE63R	142	258	HLXNE63
647	HLXTF64R	2	136	HLXTF64
648	HMACF85R	23	430	HMACF85
649	HMAIA15R	108	452	HMAIA15
650	HMCHZ07R	247	402	HMCHZ07
651	HMCIS54R	84	242	HMCIS54
652	HMSFW88R	1	69	HMSFW88
653	HMSMW71R	290	514	HMSMW71
654	HNHMR05R	77	598	HNHMR05
655	HNJBB78R	91	282	HNJBB78

656	HINTMA96R	3	362	HINTMA96
657	INTRL32R	130	291	INTRL32
658	INTST76R	2	397	INTST76
659	HOCNC55R	67	156	HOCNC55
660	HOCND06R	147	275	HOCND06
661	HOCND49R	133	273	HOCND49
662	HODEH30R	2	154	HODEH30
663	HODFA26R	263	550	HODFA26
664	HODHL89R	106	279	HODHL89
665	HOEJM67R	2	364	HOEJM67
666	HOGBN48R	147	380	HOGBN48
667	HOHCX95R	2	364	HOHCX95
668	HORBP43R	3	365	HORBP43
669	HOUHN53R	235	345	HOUHN53
670	HOUJE10R	72	254	HOUJE10
671	HPBEE63R	107	211	HPBEE63
672	HIPEBO20R	1	237	HIPEBO20
673	HPJBE91R	1	312	HPJBE91
674	HPTRW82R	32	133	HPTRW82
675	HPWDC51R	33	272	HPWDC51
676	HPWDK52R	1	330	HPWDK52
677	HRDBJ82R	2	334	HRDBJ82
678	HIRODH93R	2	121	HIRODH93
679	HS2AD53R	1	120	HS2AD53
680	HSATR92R	3	203	HSATR92
681	HSIDZG83R	5	136	HSIDZG83
682	HSICQ60R	2	118	HSICQ60
683	HSIFA64R	3	449	HSIFA64
684	HSKNN36R	108	527	HSKNN36
685	HSKYE52R	2	124	HSKYE52
686	HSLJA55R	2	169	HSLJA55

687	HSODA95R	2	169	HSODA95
688	HSPBSI9R	1	372	HSPBSI9
689	HSSGK43R	3	155	HSSGK43
690	HSXFJ9IR	3	242	HSXFJ9I
691	HTFEMB57R	168	410	HTFEMB57
692	HTGBR05R	37	138	HTGBR05
693	HTLGA72R	3	455	HTLGA72
694	HTLIX6IR	1	102	HTLIX6I
695	HTNTE25R	307	426	HTNTE25
696	HTWCP79R	91	180	HTWCP79
697	HTXFA64R	3	263	HTXFA64
698	HUSJF9IR	218	412	HUSJF9I
699	HUSJN48R	259	462	HUSJN48
700	HUSJX68R	98	493	HUSJX68
701	HUSZN23R	36	131	HUSZN23
702	IUTSD20R	104	256	IUTSD20
703	IHWACHI10R	66	275	IHWACHI10
704	IHWAFI63R	3	272	IHWAFI63
705	IHWAGZ89R	176	385	IHWAGZ89
706	IHWBAQ20R	1	177	IHWBAQ20
707	IWHHM83R	2	298	IWHHM83
708	HWLAC24R	11	133	HWLAC24
709	HWLAC8IR	64	360	HWLAC8I
710	HWLBF27R	3	149	HWLBF27
711	HWLBS90R	195	347	HWLBS90
712	HWLCU10R	55	120	HWLCU10
713	HWLEH13R	2	379	HWLEH13
714	HWLEJ67R	375	527	HWLEJ67
715	HWLEM49R	244	354	HWLEM49
716	HWLFP27R	2	79	HWLFP27
717	HWLGG20R	92	208	HWLGG20

718	HWLGK22R	209	373	HWLGK22
719	HWLGM21R	244	354	HWLGM21
720	HWLGP37R	8	181	HWLGP37
721	HWLGS46R	40	324	HWLGS46
722	HWLGU40R	2	202	HWLGU40
723	HWLGX65R	3	230	HWLGX65
724	HWLHD09R	2	310	HWLHD09
725	HWLHD50R	3	98	HWLHD50
726	HWLHM40R	2	208	HWLHM40
727	HWLHW89R	56	382	HWLHW89
728	HWLJD17R	64	276	HWLJD17
729	HWLJM20R	3	158	HWLJM20
730	HWLJA26R	34	135	HWLJA26
731	HWLJA28R	1	108	HWLJA28
732	HWLJG57R	240	404	HWLJG57
733	HWLJL19R	119	292	HWLJL19
734	HWLJP50R	1	147	HWLJP50
735	HWLKG82R	1	360	HWLKG82
736	HWLKG95R	1	300	HWLKG95
737	HWLKI53R	1	144	HWLKI53
738	HWLKM09R	2	100	HWLKM09
739	HWLKM86R	44	226	HWLKM86
740	HWLKM95R	2	184	HWLKM95
741	HWLKU25R	3	137	HWLKU25
742	HWLQS83R	1	117	HWLQS83
743	HWLQU65R	361	558	HWLQU65
744	HWLRL59R	1	225	HWLRL59
745	HWLRP86R	2	253	HWLRP86
746	HWLRQ49R	3	158	HWLRQ49
747	HWLUF60R	84	218	HWLUF60
748	HWLUI37R	51	263	HWLUI37

749	HWLUR4IR	URF 3 (NADH dehydrogenase subunit)	33	155	HWLUR4I
750	HWLVD60R	[Homo sapiens] >gi 506832 protein 3	1	174	HWLVD60
751	HWLVV50R	[Homo sapiens] >pir A00422 DNHUN3	1	72	HWLVV50
752	HWMAN61R	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 3 - human mitochondrion	3	107	HWMAN61
753	HWMEB47R	(SGC1) >sp P03897 NU3M_HUMAN	87	185	HWMEB47
754	HWMEH13R	NADH-UBIQUINONE	2	256	HWMEH13
755	HWMEH26R	OXIDOREDUCTASE CHAIN 3 (EC 1.6	168	341	HWMEH26
756	HWMEH50R	URF 3 (NADH dehydrogenase subunit)	131	400	HWMEH50
757	HWMEH31R	[Homo sapiens] >gi 506832 protein 3	100	285	HWMEH31
758	HWMEH66R	[Homo sapiens] >pir A00422 DNHUN3	61	153	HWMEH66
759	HWMEH93R	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 3 - human mitochondrion	2	79	HWMEH93
760	HWMEH01R	(SGC1) >sp P03897 NU3M_HUMAN	120	284	HWMEH01
761	HZAAD81R	NADH-UBIQUINONE	1	144	HZAAD81
762	HWLHN70R	OXIDOREDUCTASE CHAIN 3 (EC 1.6	2	160	HWLHN70
763	HFIXK57R	URF 3 (NADH dehydrogenase subunit)	2	211	HFIXK57
		[Homo sapiens] >gi 506832 protein 3	2		
		[Homo sapiens] >pir A00422 DNHUN3			
		NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 3 - human mitochondrion			
		(SGC1) >sp P03897 NU3M_HUMAN			
		NADH-UBIQUINONE			
		OXIDOREDUCTASE CHAIN 3 (EC 1.6			
764	HMAFE48R	URF 3 (NADH dehydrogenase subunit)	47	205	HMAFE48
		[Homo sapiens] >gi 506832 protein 3			
		[Homo sapiens] >pir A00422 DNHUN3			
		NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 3 - human mitochondrion			
		(SGC1) >sp P03897 NU3M_HUMAN			
		NADH-UBIQUINONE			
		OXIDOREDUCTASE CHAIN 3 (EC 1.6			



765	HR0DJ88R	URF 3 (NADH dehydrogenase subunit) [Homo sapiens] >gi 506832 protein 3 [Homo sapiens] >pir A00422 DNHUN3 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 3 - human mitochondrion (SGC1) >sp P03897 NU3M_HUMAN NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 (EC 1.6 URF 3 (NADH dehydrogenase subunit) [Homo sapiens] >gi 506832 protein 3 [Homo sapiens] >pir A00422 DNHUN3 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 3 - human mitochondrion (SGC1) >sp P03897 NU3M_HUMAN NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 (EC 1.6	gi 13011	55	213	83	94	HR0DJ88
766	HWLAR3IR	URF 3 (NADH dehydrogenase subunit) [Homo sapiens] >gi 506832 protein 3 [Homo sapiens] >pir A00422 DNHUN3 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 3 - human mitochondrion (SGC1) >sp P03897 NU3M_HUMAN NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 (EC 1.6	gi 13011	56	214	91	100	HWLAR3I
767	HNHLH26R	v-SNARE [Cricetulus griseus] >sp O08522 O08522 V-SNARE. Length = 250	gi 1912453	73	243	64	76	HNHLH26
768	H2LAU24R	weakly similar to gastrula zinc finger protein [Caenorhabditis elegans] >sp Q09998 Q09998 PUTATIVE 55.5 KD ZINC FINGER PROTEIN R144.3 IN CHROMOSOME III. Length = 492	gi 746495	78	488	45	60	H2LAU24
769	HATDR94R	X box binding protein-1 [Homo sapiens] >pir A36299 A36299 transcription factor hXBP-1 - human Length = 260	gi 306893	2	367	95	100	HATDR94
770	HWLLI85R	X-linked deafness dystonia protein [Homo sapiens] >sp O60220 O60220 X- LINKED DEAFNESS DYSTONIA PROTEIN. Length = 97	gi 3123843	410	580	60	80	HWLLI85

771	HBHMF67R	XP-C repair complementing protein (p58/11HR23B) [Homo sapiens] >pir S44346 S44346 R/A/D23 protein homolog - human Length = 409	gnl PID d1005181	3	191	96	96	HBHMF67
772	HSYCH41R	yeast methionyl-tRNA synthetase homolog [Homo sapiens] >pir JC5224 JC5224 methionine--tRNA ligase (EC 6.1.1.10) - human >gi 804996 mitoxantrone-resistance associated gene [Homo sapiens] {SUB 423-900} Length = 900	gnl PID e218477	2	373	90	90	HSYCH41
773	HWLJR53R	zinc finger protein PZF [Mus musculus] >pir 48724 48724 zinc finger protein PZF - mouse >sp Q62511 Q62511 ZINC FINGER PROTEIN PZF: Length = 455	gi 453376	1	552	81	83	HWLJR53

The first column of Table 1 shows the "SEQ ID NO:" for each of the 773 colon cancer antigen polynucleotide sequences of the invention.

The second column in Table 1, provides a unique "Sequence/Contig ID" identification for each colon and/or colon cancer associated sequence. The third column in Table 1, "Gene Name," provides a putative identification of the gene based on the sequence similarity of its translation product to an amino acid sequence found in a publicly accessible gene database, such as GenBank (NCBI). The great majority of the cDNA sequences reported in Table 1 are unrelated to any sequences previously described in the literature. The fourth column, in Table 1, "Overlap," provides the database accession no. for the database sequence having similarity. The fifth and sixth columns in Table 1 provide the location (nucleotide position nos. within the contig), "Start" and "End", in the polynucleotide sequence "SEQ ID NO:X" that delineate the preferred ORF shown in the sequence listing as SEQ ID NO:Y. In one embodiment, the invention provides a protein comprising, or alternatively consisting of, a polypeptide encoded by the portion of SEQ ID NO:X delineated by the nucleotide position nos. "Start" and "End". Also provided are polynucleotides encoding such proteins and the complementary strand thereto. The seventh and eighth columns provide the "% Identity" (percent identity) and "% Similarity" (percent similarity) observed between the aligned sequence segments of the translation product of SEQ ID NO:X and the database sequence.

The ninth column of Table 1 provides a unique "Clone ID" for a clone related to each contig sequence. This clone ID references the cDNA clone which contains at least the 5' most sequence of the assembled contig and at least a portion of SEQ ID NO:X was determined by directly sequencing the referenced clone. The reference clone may have more sequence than described in the sequence listing or the clone may have less. In the vast majority of cases, however, the clone is believed to encode a full-length polypeptide. In the case where a clone is not full-length, a full-length cDNA can be obtained by methods described elsewhere herein.

Table 3 indicates public ESTs, of which at least one, two, three, four, five, ten, or more of any one or more of these public ESTs are optionally excluded from the invention.

SEQ ID NO:X (where X may be any of the polynucleotide sequences disclosed in the sequence listing as SEQ ID NO:1 through SEQ ID NO:773) and the translated SEQ ID NO:Y (where Y may be any of the polypeptide sequences disclosed in the sequence listing as SEQ ID NO:774 through SEQ ID NO:1546) are sufficiently accurate and otherwise suitable for a

variety of uses well known in the art and described further below. For instance, SEQ ID NO:X has uses including, but not limited to, in designing nucleic acid hybridization probes that will detect nucleic acid sequences contained in SEQ ID NO:X or the related cDNA clone contained in a library deposited with the ATCC. These probes will also hybridize to nucleic acid molecules in biological samples, thereby enabling immediate applications in chromosome mapping, linkage analysis, tissue identification and/or typing, and a variety of forensic and diagnostic methods of the invention. Similarly, polypeptides identified from SEQ ID NO:Y have uses that include, but are not limited to, generating antibodies which bind specifically to the colon cancer antigen polypeptides, or fragments thereof, and/or to the colon cancer antigen polypeptides encoded by the cDNA clones identified in Table 1.

Nevertheless, DNA sequences generated by sequencing reactions can contain sequencing errors. The errors exist as misidentified nucleotides, or as insertions or deletions of nucleotides in the generated DNA sequence. The erroneously inserted or deleted nucleotides cause frame shifts in the reading frames of the predicted amino acid sequence. In these cases, the predicted amino acid sequence diverges from the actual amino acid sequence, even though the generated DNA sequence may be greater than 99.9% identical to the actual DNA sequence (for example, one base insertion or deletion in an open reading frame of over 1000 bases).

Accordingly, for those applications requiring precision in the nucleotide sequence or the amino acid sequence, the present invention provides not only the generated nucleotide sequence identified as SEQ ID NO:X, the predicted translated amino acid sequence identified as SEQ ID NO:Y, but also a sample of plasmid DNA containing the related cDNA clone (deposited with the ATCC, as set forth in Table 1). The nucleotide sequence of each deposited clone can readily be determined by sequencing the deposited clone in accordance with known methods. Further, techniques known in the art can be used to verify the nucleotide sequences of SEQ ID NO:X.

The predicted amino acid sequence can then be verified from such deposits. Moreover, the amino acid sequence of the protein encoded by a particular clone can also be directly determined by peptide sequencing or by expressing the protein in a suitable host cell containing the deposited human cDNA, collecting the protein, and determining its sequence.

The present invention also relates to vectors or plasmids which include such DNA sequences, as well as the use of the DNA sequences. The material deposited with the ATCC on:

5 **Table 2**

ATCC Deposits	Deposit Date	ATCC Designation Number
LP01, LP02, LP03, LP04, LP05, LP06, LP07, LP08, LP09, LP10, LP11,	May-20-97	209059, 209060, 209061, 209062, 209063, 209064, 209065, 209066, 209067, 209068, 209069
LP12	Jan-12-98	209579
LP13	Jan-12-98	209578
LP14	Jul-16-98	203067
LP15	Jul-16-98	203068
LP16	Feb-1-99	203609
LP17	Feb-1-99	203610
LP20	Nov-17-98	203485
LP21	Jun-18-99	PTA-252
LP22	Jun-18-99	PTA-253
LP23	Dec-22-99	PTA-1081

each is a mixture of cDNA clones derived from a variety of human tissue and cloned in either a plasmid vector or a phage vector, as shown in Table 5. These deposits are referred to as "the deposits" herein. The tissues from which the clones were derived are listed in Table 5, and the vector in which the cDNA is contained is also indicated in Table 5. The deposited material includes the cDNA clones which were partially sequenced and are related to the SEQ ID NO:X described in Table 1 (column 9). Thus, a clone which is isolatable from the ATCC Deposits by use of a sequence listed as SEQ ID NO:X may include the entire coding region of a human gene or in other cases such clone may include a substantial portion of the coding region of a human gene. Although the sequence listing lists only a portion of the DNA sequence in a clone included in the ATCC Deposits, it is well within the ability of one skilled in the art to complete the sequence of the DNA included in a clone isolatable from the

ATCC Deposits by use of a sequence (or portion thereof) listed in Table 1 by procedures hereinafter further described, and others apparent to those skilled in the art.

Also provided in Table 5 is the name of the vector which contains the cDNA clone. Each vector is routinely used in the art. The following additional information is provided for  
5 convenience.

Vectors Lambda Zap (U.S. Patent Nos. 5,128,256 and 5,286,636), Uni-Zap XR (U.S. Patent Nos. 5,128, 256 and 5,286,636), Zap Express (U.S. Patent Nos. 5,128,256 and 5,286,636), pBluescript (pBS) (Short, J. M. et al., *Nucleic Acids Res.* 16:7583-7600 (1988); Alting-Mees, M. A. and Short, J. M., *Nucleic Acids Res.* 17:9494 (1989)) and pBK (Alting-  
10 Mees, M. A. et al., *Strategies* 5:58-61 (1992)) are commercially available from Stratagene Cloning Systems, Inc., 11011 N. Torrey Pines Road, La Jolla, CA, 92037. pBS contains an ampicillin resistance gene and pBK contains a neomycin resistance gene. Phagemid pBS may be excised from the Lambda Zap and Uni-Zap XR vectors, and phagemid pBK may be excised from the Zap Express vector. Both phagemids may be transformed into *E. coli* strain  
15 XL-1 Blue, also available from Stratagene.

Vectors pSport1, pCMVSPORT 1.0, pCMVSPORT 2.0 and pCMVSPORT 3.0, were obtained from Life Technologies, Inc., P. O. Box 6009, Gaithersburg, MD 20897. All Sport vectors contain an ampicillin resistance gene and may be transformed into *E. coli* strain DH10B, also available from Life Technologies. See, for instance, Gruber, C. E., et al., *Focus*  
20 15:59 (1993). Vector lafmid BA (Bento Soares, Columbia University, New York, NY) contains an ampicillin resistance gene and can be transformed into *E. coli* strain XL-1 Blue. Vector pCR<sup>®</sup>2.1, which is available from Invitrogen, 1600 Faraday Avenue, Carlsbad, CA 92008, contains an ampicillin resistance gene and may be transformed into *E. coli* strain DH10B, available from Life Technologies. See, for instance, Clark, J. M., *Nuc. Acids Res.*  
25 16:9677-9686 (1988) and Mead, D. et al., *Bio/Technology* 9: (1991).

The present invention also relates to the genes corresponding to SEQ ID NO:X, SEQ ID NO:Y, and/or the cDNA contained in a deposited cDNA clone. The corresponding gene can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include, but are not limited to, preparing probes or primers from the  
30 disclosed sequence and identifying or amplifying the corresponding gene from appropriate sources of genomic material.

Also provided in the present invention are allelic variants, orthologs, and/or species homologs. Procedures known in the art can be used to obtain full-length genes, allelic variants, splice variants, full-length coding portions, orthologs, and/or species homologs of genes corresponding to SEQ ID NO:X, SEQ ID NO:Y, and/or the cDNA contained in the related cDNA clone in the deposit, using information from the sequences disclosed herein or the clones deposited with the ATCC. For example, allelic variants and/or species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source for allelic variants and/or the desired homologue.

The present invention provides a polynucleotide comprising, or alternatively consisting of, the nucleic acid sequence of SEQ ID NO:X, and/or the related cDNA clone (See, e.g., columns 1 and 9 of Table 1). The present invention also provides a polypeptide comprising, or alternatively, consisting of, the polypeptide sequence of SEQ ID NO:Y, a polypeptide encoded by SEQ ID NO:X, and/or a polypeptide encoded by the cDNA in the related cDNA clone contained in a deposited library. Polynucleotides encoding a polypeptide comprising, or alternatively consisting of, the polypeptide sequence of SEQ ID NO:Y, a polypeptide encoded by SEQ ID NO:X, and/or a polypeptide encoded by the cDNA in the related cDNA clone contained in a deposited library, are also encompassed by the invention. The present invention further encompasses a polynucleotide comprising, or alternatively consisting of, the complement of the nucleic acid sequence of SEQ ID NO:X, and/or the complement of the coding strand of the related cDNA clone contained in a deposited library.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence would unduly burden the disclosure of this application. Accordingly, for each "Contig Id" listed in the first column of Table 3, preferably excluded are one or more polynucleotides comprising a nucleotide sequence described in the second column of Table 3 by the general formula of a-b, each of which are uniquely defined for the SEQ ID NO:X corresponding to that Contig Id in Table 1. Additionally, specific embodiments are directed to polynucleotide sequences excluding at least one, two, three, four, five, ten, or more of the specific polynucleotide sequences referenced by the Genbank Accession No. for each Contig Id which may be

included in column 3 of Table 3. In no way is this listing meant to encompass all of the sequences which may be excluded by the general formula, it is just a representative example.



Table 3.

Sequence/ Contig ID	General formula	Genbank Accession No.
500802	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 619 of SEQ ID NO:1, b is an integer of 15 to 633, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:1, and where b is greater than or equal to a + 14.	
531091	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 281 of SEQ ID NO:2, b is an integer of 15 to 295, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:2, and where b is greater than or equal to a + 14.	
553147	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 428 of SEQ ID NO:3, b is an integer of 15 to 442, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:3, and where b is greater than or equal to a + 14.	
558860	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 740 of SEQ ID NO:4, b is an integer of 15 to 754, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:4, and where b is greater than or equal to a + 14.	
561730	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 379 of SEQ ID NO:5, b is an integer of 15 to 393, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:5, and where b is greater than or equal to a + 14.	
585938	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 525 of SEQ ID NO:6, b is an integer of 15 to 539, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:6, and where b is greater than or equal to a + 14.	
587785	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 790 of SEQ ID	

	NO:7, b is an integer of 15 to 804, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:7, and where b is greater than or equal to a + 14.	
588916	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 706 of SEQ ID NO:8, b is an integer of 15 to 720, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:8, and where b is greater than or equal to a + 14.	
613825	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 526 of SEQ ID NO:9, b is an integer of 15 to 540, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:9, and where b is greater than or equal to a + 14.	
639090	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 547 of SEQ ID NO:10, b is an integer of 15 to 561, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:10, and where b is greater than or equal to a + 14.	
651644	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 379 of SEQ ID NO:11, b is an integer of 15 to 393, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:11, and where b is greater than or equal to a + 14.	
659544	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 308 of SEQ ID NO:12, b is an integer of 15 to 322, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:12, and where b is greater than or equal to a + 14.	
659739	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1893 of SEQ ID NO:13, b is an integer of 15 to 1907, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:13, and where b is greater than or equal to a + 14.	
661057	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1126 of SEQ ID NO:14, b is an integer of 15 to 1140, where both a	

	and b correspond to the positions of nucleotide residues shown in SEQ ID NO:14, and where b is greater than or equal to a + 14.	
661313	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1994 of SEQ ID NO:15, b is an integer of 15 to 2008, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:15, and where b is greater than or equal to a + 14.	
666316	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 357 of SEQ ID NO:16, b is an integer of 15 to 371, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:16, and where b is greater than or equal to a + 14.	
669229	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 749 of SEQ ID NO:17, b is an integer of 15 to 763, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:17, and where b is greater than or equal to a + 14.	
670471	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1912 of SEQ ID NO:18, b is an integer of 15 to 1926, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:18, and where b is greater than or equal to a + 14.	
676611	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2287 of SEQ ID NO:19, b is an integer of 15 to 2301, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:19, and where b is greater than or equal to a + 14.	
691240	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 524 of SEQ ID NO:20, b is an integer of 15 to 538, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:20, and where b is greater than or equal to a + 14.	
702977	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1389 of SEQ ID NO:21, b is an integer of 15 to 1403, where both a and b correspond to the positions of nucleotide	

	residues shown in SEQ ID NO:21. and where b is greater than or equal to $a + 14$ .	
709517	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 464 of SEQ ID NO:22, b is an integer of 15 to 478, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:22, and where b is greater than or equal to $a + 14$ .	
714730	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1238 of SEQ ID NO:23, b is an integer of 15 to 1252, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:23, and where b is greater than or equal to $a + 14$ .	
714834	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1060 of SEQ ID NO:24, b is an integer of 15 to 1074, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:24, and where b is greater than or equal to $a + 14$ .	
715016	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1172 of SEQ ID NO:25, b is an integer of 15 to 1186, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:25, and where b is greater than or equal to $a + 14$ .	
719584	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 874 of SEQ ID NO:26, b is an integer of 15 to 888, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:26, and where b is greater than or equal to $a + 14$ .	
724637	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 775 of SEQ ID NO:27, b is an integer of 15 to 789, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:27, and where b is greater than or equal to $a + 14$ .	
728392	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 833 of SEQ ID NO:28, b is an integer of 15 to 847, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:28, and where b is greater than	

	or equal to $a + 14$ .	
738716	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 652 of SEQ ID NO:29, b is an integer of 15 to 666, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:29, and where b is greater than or equal to $a + 14$ .	
739056	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 503 of SEQ ID NO:30, b is an integer of 15 to 517, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:30, and where b is greater than or equal to $a + 14$ .	
739143	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2661 of SEQ ID NO:31, b is an integer of 15 to 2675, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:31, and where b is greater than or equal to $a + 14$ .	
742329	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 263 of SEQ ID NO:32, b is an integer of 15 to 277, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:32, and where b is greater than or equal to $a + 14$ .	
742557	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 907 of SEQ ID NO:33, b is an integer of 15 to 921, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:33, and where b is greater than or equal to $a + 14$ .	
745481	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1453 of SEQ ID NO:34, b is an integer of 15 to 1467, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:34, and where b is greater than or equal to $a + 14$ .	
746035	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2063 of SEQ ID NO:35, b is an integer of 15 to 2077, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:35, and where b is greater than or equal to $a + 14$ .	

753731	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 370 of SEQ ID NO:36, b is an integer of 15 to 384, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:36, and where b is greater than or equal to a + 14.	
754383	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 454 of SEQ ID NO:37, b is an integer of 15 to 468, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:37, and where b is greater than or equal to a + 14.	
756749	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1081 of SEQ ID NO:38, b is an integer of 15 to 1095, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:38, and where b is greater than or equal to a + 14.	
757980	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1743 of SEQ ID NO:39, b is an integer of 15 to 1757, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:39, and where b is greater than or equal to a + 14.	R38216, R63249, R78721, H01441, H02557, H02640, H86258, H86321, N21599, W16868, W31882, W56228, N90610, AA047227, AA056107, AA058568, AA100609, AA115890
764818	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1931 of SEQ ID NO:40, b is an integer of 15 to 1945, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:40, and where b is greater than or equal to a + 14.	
765140	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 574 of SEQ ID NO:41, b is an integer of 15 to 588, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:41, and where b is greater than or equal to a + 14.	
766893	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1554 of SEQ ID NO:42, b is an integer of 15 to 1568, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:42, and where b is greater than or equal to a + 14.	R69702, R76994, R77002, H01357
771338	Preferably excluded from the present invention are	

	one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1046 of SEQ ID NO:43, b is an integer of 15 to 1060, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:43, and where b is greater than or equal to a + 14.	
771412	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1330 of SEQ ID NO:44, b is an integer of 15 to 1344, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:44, and where b is greater than or equal to a + 14.	
772226	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 878 of SEQ ID NO:45, b is an integer of 15 to 892, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:45, and where b is greater than or equal to a + 14.	
773057	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 482 of SEQ ID NO:46, b is an integer of 15 to 496, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:46, and where b is greater than or equal to a + 14.	N41725
773173	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1215 of SEQ ID NO:47, b is an integer of 15 to 1229, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:47, and where b is greater than or equal to a + 14.	
780154	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1397 of SEQ ID NO:48, b is an integer of 15 to 1411, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:48, and where b is greater than or equal to a + 14.	
780768	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1671 of SEQ ID NO:49, b is an integer of 15 to 1685, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:49, and where b is greater than or equal to a + 14.	
780779	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide	

	sequence described by the general formula of a-b, where a is any integer between 1 to 646 of SEQ ID NO:50, b is an integer of 15 to 660, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:50, and where b is greater than or equal to a + 14.	
782394	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1558 of SEQ ID NO:51, b is an integer of 15 to 1572, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:51, and where b is greater than or equal to a + 14.	R24689, R25853, R34457, R66839, R68536, H22874, H45555, N50184, AA015963, AA028939, AA028938
783160	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 621 of SEQ ID NO:52, b is an integer of 15 to 635, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:52, and where b is greater than or equal to a + 14.	
783506	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1353 of SEQ ID NO:53, b is an integer of 15 to 1367, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:53, and where b is greater than or equal to a + 14.	
784446	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 364 of SEQ ID NO:54, b is an integer of 15 to 378, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:54, and where b is greater than or equal to a + 14.	
784832	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1044 of SEQ ID NO:55, b is an integer of 15 to 1058, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:55, and where b is greater than or equal to a + 14.	
786813	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 668 of SEQ ID NO:56, b is an integer of 15 to 682, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:56, and where b is greater than or equal to a + 14.	W44740, AA235981
792139	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b.	



	where a is any integer between 1 to 630 of SEQ ID NO:57, b is an integer of 15 to 644, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:57, and where b is greater than or equal to a + 14.	
793987	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 752 of SEQ ID NO:58, b is an integer of 15 to 766, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:58, and where b is greater than or equal to a + 14.	
805715	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2347 of SEQ ID NO:59, b is an integer of 15 to 2361, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:59, and where b is greater than or equal to a + 14.	
811111	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1458 of SEQ ID NO:60, b is an integer of 15 to 1472, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:60, and where b is greater than or equal to a + 14.	R11325, R11326, R43655, R43655, R72437, R78096, H23850, N20947, N22686, N25829, N27270, N31401, N40002, N46020, W92748, W92871, AA461202, AA461382
811113	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1658 of SEQ ID NO:61, b is an integer of 15 to 1672, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:61, and where b is greater than or equal to a + 14.	
823902	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1526 of SEQ ID NO:62, b is an integer of 15 to 1540, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:62, and where b is greater than or equal to a + 14.	
826518	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1030 of SEQ ID NO:63, b is an integer of 15 to 1044, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:63, and where b is greater than or equal to a + 14.	T60163, T60223, T61894, R12251, T81471, T81679, T95899, R98321, R98322, H52605, H59085, N27268, N31506, N53499, N54486, N58236, N92460, AA027189, AA045077, AA127016, AA418935, AA426582
826704	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 837 of SEQ ID	

	NO:64. b is an integer of 15 to 851, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:64, and where b is greater than or equal to a + 14.	
827720	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2779 of SEQ ID NO:65, b is an integer of 15 to 2793, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:65, and where b is greater than or equal to a + 14.	
828102	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 289 of SEQ ID NO:66, b is an integer of 15 to 303, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:66, and where b is greater than or equal to a + 14.	
828180	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1396 of SEQ ID NO:67, b is an integer of 15 to 1410, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:67, and where b is greater than or equal to a + 14.	
828386	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1010 of SEQ ID NO:68, b is an integer of 15 to 1024, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:68, and where b is greater than or equal to a + 14.	
828658	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1834 of SEQ ID NO:69, b is an integer of 15 to 1848, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:69, and where b is greater than or equal to a + 14.	
828919	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2668 of SEQ ID NO:70, b is an integer of 15 to 2682, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:70, and where b is greater than or equal to a + 14.	T66771, T66772, T71638, R08935, R09044, R09373, T80114, T85695, R00758, R00759, R12645, R19577, R20545, R22041, R22097, R20545, R59701, R59811, R60034, R60096, R60694, R76255, R81371, R81370, H04390, H04415, H05912, H47622, H47647, R83679, H71735, H72298, N25487, N35542, N49731, N52660, N67681, N75596, W03490, AA044638, AA044702, AA165090, AA164628, AA215698, AA215699, AA233182, AA233196, AA236759, AA256822, AA429489.

		AA428534
829572	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 398 of SEQ ID NO:71, b is an integer of 15 to 412, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:71, and where b is greater than or equal to a + 14.	T63032
830138	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1347 of SEQ ID NO:72, b is an integer of 15 to 1361, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:72, and where b is greater than or equal to a + 14.	
830208	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 914 of SEQ ID NO:73, b is an integer of 15 to 928, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:73, and where b is greater than or equal to a + 14.	R01611, N76461, W74577, W79757, AA045350, AA056064, AA190524
830248	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1172 of SEQ ID NO:74, b is an integer of 15 to 1186, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:74, and where b is greater than or equal to a + 14.	
830275	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 919 of SEQ ID NO:75, b is an integer of 15 to 933, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:75, and where b is greater than or equal to a + 14.	
830286	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1950 of SEQ ID NO:76, b is an integer of 15 to 1964, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:76, and where b is greater than or equal to a + 14.	T90376, R46154, R46154, AA224239, AA467906, AA483293, AA502593, AA513313, AA594445, AA594570, AA594876, AA579404, AA720893, AA767344, AA857646, AA877489, AA954868, AA991634, A1014751, C02074, AA093141
830347	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1788 of SEQ ID NO:77, b is an integer of 15 to 1802, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:77, and where b is greater than or equal to a + 14.	

830348	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 981 of SEQ ID NO:78, b is an integer of 15 to 995, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:78, and where b is greater than or equal to a + 14.	AA983601
830364	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1201 of SEQ ID NO:79, b is an integer of 15 to 1215, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:79, and where b is greater than or equal to a + 14.	
830394	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2646 of SEQ ID NO:80, b is an integer of 15 to 2660, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:80, and where b is greater than or equal to a + 14.	
830398	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1776 of SEQ ID NO:81, b is an integer of 15 to 1790, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:81, and where b is greater than or equal to a + 14.	
830412	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1336 of SEQ ID NO:82, b is an integer of 15 to 1350, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:82, and where b is greater than or equal to a + 14.	
830436	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1732 of SEQ ID NO:83, b is an integer of 15 to 1746, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:83, and where b is greater than or equal to a + 14.	T89041, R38418, R51559, R62385, R63785, H21426, N55384, AA009460, AA039527, AA039526, AA490811, AA588539, AA574253, AA827525, AA975094, D79482, D79908, N55964, C14631, C14891, C14892
830464	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1477 of SEQ ID NO:84, b is an integer of 15 to 1491, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:84, and where b is greater than or equal to a + 14.	H06247, H19227, W52470
830471	Preferably excluded from the present invention are	R28064, R28282, AA143044, AA151127.

	one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 954 of SEQ ID NO:85, b is an integer of 15 to 968, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:85, and where b is greater than or equal to a + 14.	AA165093, AA164631, AA256943, AA765384, D80554
830477	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3054 of SEQ ID NO:86, b is an integer of 15 to 3068, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:86, and where b is greater than or equal to a + 14.	T71686, R81413, R81414, H52583, H84987, H87923, H88319, H88319, W74073, W79680, AA021098, AA179389, AA182649, AA188175, AA191449, AA228943, AA228942, AA594459, AA737972, C02737
830500	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2216 of SEQ ID NO:87, b is an integer of 15 to 2230, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:87, and where b is greater than or equal to a + 14.	
830509	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1149 of SEQ ID NO:88, b is an integer of 15 to 1163, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:88, and where b is greater than or equal to a + 14.	
830528	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1925 of SEQ ID NO:89, b is an integer of 15 to 1939, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:89, and where b is greater than or equal to a + 14.	
830542	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2018 of SEQ ID NO:90, b is an integer of 15 to 2032, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:90, and where b is greater than or equal to a + 14.	T60268, T61648, T68371, T88743, R00503, R13392, R40908, R40908, H02114, H07926, H29767, H29768, H38826, H93354, W42415, W42513, W61060, W72566, W76560, AA011078, AA011079, AA031697, AA031863, AA058529, AA100913, AA100912, AA129619, AA129593, AA129330, AA128581, AA160087, AA160675, AA173629, AA173985, AA186698, AA188326, AA480672, AA587251, AA576938, AA743161, AA834774, AA872783, AA877207, AA878505, AA923685, AA934427, AA962214, AA995455, AA995857, N88876
830564	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b.	

	where a is any integer between 1 to 1774 of SEQ ID NO:91, b is an integer of 15 to 1788, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:91, and where b is greater than or equal to a + 14.	
830611	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 481 of SEQ ID NO:92, b is an integer of 15 to 495, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:92, and where b is greater than or equal to a + 14.	
830618	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1363 of SEQ ID NO:93, b is an integer of 15 to 1377, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:93, and where b is greater than or equal to a + 14.	R43709, R43709, H09113, H43746, N92632, AA022453, AA120876, AA120889, AA493651, AA493785, AA494347, AA565392, AA743179, AA769161
830620	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2805 of SEQ ID NO:94, b is an integer of 15 to 2819, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:94, and where b is greater than or equal to a + 14.	
830630	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 691 of SEQ ID NO:95, b is an integer of 15 to 705, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:95, and where b is greater than or equal to a + 14.	
830654	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3458 of SEQ ID NO:96, b is an integer of 15 to 3472, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:96, and where b is greater than or equal to a + 14.	
830660	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1202 of SEQ ID NO:97, b is an integer of 15 to 1216, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:97, and where b is greater than or equal to a + 14.	
830661	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1172 of SEQ ID	

	NO:98, b is an integer of 15 to 1186, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:98, and where b is greater than or equal to a + 14.	
830704	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1106 of SEQ ID NO:99, b is an integer of 15 to 1120, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:99, and where b is greater than or equal to a + 14.	
830765	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1211 of SEQ ID NO:100, b is an integer of 15 to 1225, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:100, and where b is greater than or equal to a + 14.	
830778	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1199 of SEQ ID NO:101, b is an integer of 15 to 1213, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:101, and where b is greater than or equal to a + 14.	
830784	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1550 of SEQ ID NO:102, b is an integer of 15 to 1564, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:102, and where b is greater than or equal to a + 14.	R63323, R66534, AA491630
830800	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1443 of SEQ ID NO:103, b is an integer of 15 to 1457, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:103, and where b is greater than or equal to a + 14.	
830821	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 771 of SEQ ID NO:104, b is an integer of 15 to 785, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:104, and where b is greater than or equal to a + 14.	
830849	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 907 of SEQ ID NO:105, b is an integer of 15 to 921, where both a	AA258128, AA259034, AA262104, AA742612, AA804402

	and b correspond to the positions of nucleotide residues shown in SEQ ID NO:105, and where b is greater than or equal to a + 14.	
830903	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 578 of SEQ ID NO:106, b is an integer of 15 to 592, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:106, and where b is greater than or equal to a + 14.	
830913	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2234 of SEQ ID NO:107, b is an integer of 15 to 2248, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:107, and where b is greater than or equal to a + 14.	R06463, R06517, R48006, R51455, R61502, R72398, R72399, R74489, R74599, H07933, H08039, H61149, H62056, H90758, H90809, N32837, N42283, W40284, W45325, AA079353, AA079592, AA100814, AA102342, AA111844, AA122150, AA134127, AA134128, AA148738, AA148709, AA164240, AA164899, AA164275, AA171881, AA179310, AA179453, AA180811, AA180955, AA187432, AA190377, AA190791, AA190383, AA458475, AA427428, AA468548, AA554518, AA595768, AA595893, AA640601, AA574035, AA658143, AA863401, AA906604, AA995159, C03746, C04875, C05396, AA033510
830920	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 771 of SEQ ID NO:108, b is an integer of 15 to 785, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:108, and where b is greater than or equal to a + 14.	
830938	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 597 of SEQ ID NO:109, b is an integer of 15 to 611, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:109, and where b is greater than or equal to a + 14.	AA053612
830980	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 650 of SEQ ID NO:110, b is an integer of 15 to 664, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:110, and where b is greater than or equal to a + 14.	
831014	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 4051 of SEQ ID NO:111, b is an integer of 15 to 4065, where both a	



	and b correspond to the positions of nucleotide residues shown in SEQ ID NO:111, and where b is greater than or equal to a + 14.	
831026	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1478 of SEQ ID NO:112, b is an integer of 15 to 1492, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:112, and where b is greater than or equal to a + 14.	
831031	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1468 of SEQ ID NO:113, b is an integer of 15 to 1482, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:113, and where b is greater than or equal to a + 14.	R46004, R46004, H06850, N27532, N30567, N30842, N34647, N40349, N41369, N49777, N52708, N62958, W68355, W68490, AA054602, AA193410, AA193648, AA503204, AA688236, AA730103, AA736540, AA747555, AA811522, AA863169, N79861
831055	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3717 of SEQ ID NO:114, b is an integer of 15 to 3731, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:114, and where b is greater than or equal to a + 14.	
831057	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1301 of SEQ ID NO:115, b is an integer of 15 to 1315, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:115, and where b is greater than or equal to a + 14.	R69415, R69546, H14127, H62767, N62927, N63320, W00649, W01189, AA053293, AA058396, AA149075, AA458528, AA418699, AA418770, AA505598, AA576507, AA730033, AA805864, AA988279, AA991217, D82661, C21298
831062	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1306 of SEQ ID NO:116, b is an integer of 15 to 1320, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:116, and where b is greater than or equal to a + 14.	
831117	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2011 of SEQ ID NO:117, b is an integer of 15 to 2025, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:117, and where b is greater than or equal to a + 14.	R80585, R80586, N49020, AA173625, AA173981, AA557142, AA627866, AA847195, A1015673
831122	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1281 of SEQ ID NO:118, b is an integer of 15 to 1295, where both a and b correspond to the positions of nucleotide	R72079, R72128, AA715820, AA804163, AA809123, AA641490

	residues shown in SEQ ID NO:118, and where b is greater than or equal to a + 14.	
831125	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1243 of SEQ ID NO:119, b is an integer of 15 to 1257, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:119, and where b is greater than or equal to a + 14.	N80647, AA114140, AA143553, AA156386, N68188, AA070867
831132	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 383 of SEQ ID NO:120, b is an integer of 15 to 397, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:120, and where b is greater than or equal to a + 14.	
831152	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 862 of SEQ ID NO:121, b is an integer of 15 to 876, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:121, and where b is greater than or equal to a + 14.	AA765155
831157	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1264 of SEQ ID NO:122, b is an integer of 15 to 1278, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:122, and where b is greater than or equal to a + 14.	T57943, R34275, R35472, R77406, R77405, N23203, N59015, AA160841, AA610280, AA857624, A1089936, A1094724, A1094954
831160	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3101 of SEQ ID NO:123, b is an integer of 15 to 3115, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:123, and where b is greater than or equal to a + 14.	
831193	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 365 of SEQ ID NO:124, b is an integer of 15 to 379, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:124, and where b is greater than or equal to a + 14.	
831197	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1253 of SEQ ID NO:125, b is an integer of 15 to 1267, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:125, and where b is	AA134613

	greater than or equal to $a + 14$ .	
831217	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 827 of SEQ ID NO:126, b is an integer of 15 to 841, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:126, and where b is greater than or equal to $a + 14$ .	
831239	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1158 of SEQ ID NO:127, b is an integer of 15 to 1172, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:127, and where b is greater than or equal to $a + 14$ .	T68487, T88923, T88994, R09550, R09663, R26714, R26937, H27046, H28228, H30272, H30335, N27966, N36884, N46156, N93575, W21407, W44513, W44514, W47626, W47627, W56215, W60528, W80465, W80574, W92729, AA002237, AA002076, AA099290, AA099291, AA127753, AA127706, AA128275, AA128572, AA148737, AA149497, AA419078, AA423819, AA506117, AA534694, AA552105, AA552219, AA583468, AA622094, AA633205, AA878663, AA911544, AA916173, AA974873, AA988860, A1056396, A1074163, W92753
831248	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 877 of SEQ ID NO:128, b is an integer of 15 to 891, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:128, and where b is greater than or equal to $a + 14$ .	
831313	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2447 of SEQ ID NO:129, b is an integer of 15 to 2461, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:129, and where b is greater than or equal to $a + 14$ .	T61093, T97774, R13148, R31511, R32943, R33906, R33921, R37053, R44148, R44148, R74449, R79209, R79476, H12271, H27631, H30122, R84834, H63166, H71003, H71015, H83387, N23726, N23730, N23773, N52416, N66497, N67917, N68137, N73801, N99428, W95944, AA018712, AA020879, AA429721, AA470397, AA493243, AA507952, AA515358, AA583463, AA617991, AA618186, AA631437, AA566089, AA746085, AA837997, AA878863, AA922678, AA985597, AA947992, A1074096, C03207, C17030, C18106
831369	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2183 of SEQ ID NO:130, b is an integer of 15 to 2197, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:130, and where b is greater than or equal to $a + 14$ .	
831371	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide	

	sequence described by the general formula of a-b, where a is any integer between 1 to 450 of SEQ ID NO:131, b is an integer of 15 to 464, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:131, and where b is greater than or equal to a + 14.	
831373	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1936 of SEQ ID NO:132, b is an integer of 15 to 1950, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:132, and where b is greater than or equal to a + 14.	T50786, T50949, T53797, T53916, T64650, T71681, T71836, T71876, T71877, T74596, T74656, H30426, H46449, H46671, H46670, H46990, H50500, AA419051, AA423809, AA928986
831387	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2079 of SEQ ID NO:133, b is an integer of 15 to 2093, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:133, and where b is greater than or equal to a + 14.	
831410	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 715 of SEQ ID NO:134, b is an integer of 15 to 729, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:134, and where b is greater than or equal to a + 14.	
831448	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1175 of SEQ ID NO:135, b is an integer of 15 to 1189, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:135, and where b is greater than or equal to a + 14.	
831450	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1452 of SEQ ID NO:136, b is an integer of 15 to 1466, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:136, and where b is greater than or equal to a + 14.	
831472	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 126 of SEQ ID NO:137, b is an integer of 15 to 140, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:137, and where b is greater than or equal to a + 14.	
831473	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b,	

	where a is any integer between 1 to 4128 of SEQ ID NO:138, b is an integer of 15 to 4142, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:138, and where b is greater than or equal to a + 14.	
831474	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1733 of SEQ ID NO:139, b is an integer of 15 to 1747, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:139, and where b is greater than or equal to a + 14.	T66054, T89542, R10967, T78297, T83524, T97793, R13138, H08701, H10662, R82956, R96295, R98912, H66237, H79525, N31425, N36736, W76142, W81053, AA010227, AA011652, AA057613, AA057653, AA069088, AA083946, AA084193, AA126186, H70618, H79526, W72916, W80802, AA011433, AA057699, AA057752, AA069023
831494	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1226 of SEQ ID NO:140, b is an integer of 15 to 1240, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:140, and where b is greater than or equal to a + 14.	H14081, H14102, N34979, N42213, N43740, N68241, W69584, W69583, AA507828, AA877181, AA975100, A1000204
831506	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 657 of SEQ ID NO:141, b is an integer of 15 to 671, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:141, and where b is greater than or equal to a + 14.	AA035596, AA577792, AA903617, AA972775, AA996054, C00084
831533	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3251 of SEQ ID NO:142, b is an integer of 15 to 3265, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:142, and where b is greater than or equal to a + 14.	
831539	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 751 of SEQ ID NO:143, b is an integer of 15 to 765, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:143, and where b is greater than or equal to a + 14.	
831556	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1680 of SEQ ID NO:144, b is an integer of 15 to 1694, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:144, and where b is greater than or equal to a + 14.	H01879, H01880, H43546, H43547, H43548, N58813, N75148, AA428902, AA429101, AA278337, AA662009, AA928907, AA988624
831594	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide	

	sequence described by the general formula of a-b, where a is any integer between 1 to 809 of SEQ ID NO:145, b is an integer of 15 to 823, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:145, and where b is greater than or equal to a + 14.	
831598	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1120 of SEQ ID NO:146, b is an integer of 15 to 1134, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:146, and where b is greater than or equal to a + 14.	
831608	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1472 of SEQ ID NO:147, b is an integer of 15 to 1486, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:147, and where b is greater than or equal to a + 14.	
831613	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 139 of SEQ ID NO:148, b is an integer of 15 to 153, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:148, and where b is greater than or equal to a + 14.	
831622	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 868 of SEQ ID NO:149, b is an integer of 15 to 882, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:149, and where b is greater than or equal to a + 14.	T40013, T40117, T55842, T55892, T58738, T58764, T58805, T58835, T58963, T60293, T60386, T61270, T61322, T61371, T61395, T61404, T61721, T61734, T61735, T61841, T61856, T61857, T61884, T62049, T62065, T62070, T62087, T62113, T62126, T62146, T41021, T62664, T62668, T62669, T62676, T62816, T62819, T62820, T62827, T64118, T64230, T64368, T64422, T64678, T64698, T64747, T67429, T67590, T67709, T67724, T67754, T67785, T67831, T67863, T67888, T67996, T68022, T68038, T68104, T68142, T68217, T68418, T68465, T68484, T68531, T68548, T68557, T68575, T68623, T68633, T68648, T68653, T68760, T68826, T68895, T68969, T68981, T69056, T69126, T69184, T69428, T69605, T69622, T69678, T69699, T70483, T70907, T70960, T71019, T71080, T71224, T71297, T71437, T71660, T71885, T71903, T71985, T72050, T72115, T72129, T72147, T72158, T72263, T72310, T72415, T72769, T72775, T72802, T72897, T72903, T72922, T72924, T73035, T73068, T73167, T73224, T73305, T73392, T73458, T73473, T73482, T73525, T73540, T73541, T73551, T73560, T73599, T73606, T73619, T73637, T73644, T73655, T73659, T73660, T73800,

		T73887, T73913, T73945, T73950, T74048, T74200, T74201, T74423, T74477, T74559, T74706, T74827, T99112, R05781, R05867, H47944, R95831, H60131, H65347, H65551, H68454, H68777, H73380, H73381, H79275, H79386, H82213, H82307, H93202, H93992, H93991, H94491, H94804, H95257, H95307, H95341, N28274, N58244, N68733, N77623, N80767, N91623, W07555, W80697, AA004677, AA004255, AA033869, AA034057, AA234464, AA491842, C20927
831631	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1494 of SEQ ID NO:150, b is an integer of 15 to 1508, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:150, and where b is greater than or equal to a + 14.	
831632	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1218 of SEQ ID NO:151, b is an integer of 15 to 1232, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:151, and where b is greater than or equal to a + 14.	T60158, T60218, T62213, T62652, T62877, T62966, T63329, T63951, T64542, T64634, T65965, T90119, T91565, T91610, T92138, T94160, T94999, T90219, T83025, T84028, T84029, T84511, R22325, R22619, R22620, R25250, R25595, R26992, R27328, R32850, R32954, R33282, R44282, R47779, R48151, R48152, R48322, R48428, R48538, R50415, R52277, R52278, R54608, R44282, R55376, R70352, R72103, R72155, R72280, R72317, R72367, R72368, R72371, R72372, R72716, R73784, R74375, R77393, R77394, R77892, R77987, R81485, R81725, H05676, H15941, H22149, H22193, H24533, H25059, H26810, H27743, H27803, H28012, H28066, H28290, H28291, H30654, H39748, H39761, H41932, H41979, H42063, H42642, H42766, H42767, H44628, H45776, H45777, H46386, H46404, R93135, R93942, R94660, R94661, H50708, H50709, H50720, H50812, H50811, H50826, H61352, H62379, H63665, H63944, H66336, H66385, H70746, H73887, H74080, H74176, H82646, H82647, H86555, H87065, H87719, H91147, H91197, H93078, H93211, H98788, N24993, N25111, N30229, N32159, N34033, N36553, N41829, N42292, N46951, N49340, N52921, N55462, N57121, N69863, N76837, N80667, N92844, N93333, N93683, N94449, N95075, W16427, W15325, W23470, W23480, W25070, W25186, W30795.

		W38675, W39219, W39393, W69270, W69557, AA019864, AA022662, AA022669, AA022768, AA025335, AA024417, AA031282, AA031281, AA032192, AA039752, AA040328, AA040307, AA041359, AA041442, AA057720, AA074855, AA086192, AA099717, AA099716, AA100416, AA142927, AA143150, AA149895, AA150239, AA150313, AA176193, AA459294, AA464165, AA425845, AA425899, AA428397, AA430393, AA427364, AA469113, AA505259, AA515918, AA516032, AA527677, AA533908, AA541266, AA554671, AA555247, AA557794, AA565267, AA582247, AA584415, AA588477, AA593255, AA595311, AA595376, AA604354, AA622137, AA573444, AA574244, AA732469, AA740323, AA741360, AA742872, AA749432, AA807903, AA808285, AA872498, AA873181, AA878139, AA878294, AA909748, AA937058, AA987672, AA994225, A1076066, W07696
831653	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 985 of SEQ ID NO:152, b is an integer of 15 to 999, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:152, and where b is greater than or equal to a + 14.	
831655	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1198 of SEQ ID NO:153, b is an integer of 15 to 1212, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:153, and where b is greater than or equal to a + 14.	N95539, W24228, W37689, AA019086, AA430215
831708	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2347 of SEQ ID NO:154, b is an integer of 15 to 2361, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:154, and where b is greater than or equal to a + 14.	
831738	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1817 of SEQ ID NO:155, b is an integer of 15 to 1831, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:155, and where b is greater than or equal to a + 14.	



831741	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1172 of SEQ ID NO:156, b is an integer of 15 to 1186, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:156, and where b is greater than or equal to a + 14.	T47689, T80213, H11356, H13411, R86865, R87546, N35663, AA081442, AA161001, C17978, C18946
831754	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1434 of SEQ ID NO:157, b is an integer of 15 to 1448, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:157, and where b is greater than or equal to a + 14.	
831760	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 990 of SEQ ID NO:158, b is an integer of 15 to 1004, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:158, and where b is greater than or equal to a + 14.	R73907, R74000, N64405, AA196765, AA232516, AA806432, AA837776, A1017699
831780	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1495 of SEQ ID NO:159, b is an integer of 15 to 1509, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:159, and where b is greater than or equal to a + 14.	AA100654, AA112750, AA594472, AA731487
831796	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2146 of SEQ ID NO:160, b is an integer of 15 to 2160, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:160, and where b is greater than or equal to a + 14.	H14891, W74005, AA623010, D80585, A1096496, W38434
831800	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3595 of SEQ ID NO:161, b is an integer of 15 to 3609, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:161, and where b is greater than or equal to a + 14.	
831807	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1589 of SEQ ID NO:162, b is an integer of 15 to 1603, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:162, and where b is greater than or equal to a + 14.	
831812	Preferably excluded from the present invention are	

	one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 839 of SEQ ID NO:163, b is an integer of 15 to 853, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:163, and where b is greater than or equal to a + 14.	
831813	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1903 of SEQ ID NO:164, b is an integer of 15 to 1917, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:164, and where b is greater than or equal to a + 14.	H14269, AA069213, AA808661
831830	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2406 of SEQ ID NO:165, b is an integer of 15 to 2420, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:165, and where b is greater than or equal to a + 14.	H04695, AA112742, AA251641, AA506539
831860	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2047 of SEQ ID NO:166, b is an integer of 15 to 2061, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:166, and where b is greater than or equal to a + 14.	
831872	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2553 of SEQ ID NO:167, b is an integer of 15 to 2567, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:167, and where b is greater than or equal to a + 14.	R15368, R36227, R36228, R36669, R39751, H12331, H12382, H47986, R84945, R97224, R97223, W78107, AA149874, AA193466, AA193348, AA287444, AA535607, AA687414, AA689396, AA748665, AA809715
831896	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2310 of SEQ ID NO:168, b is an integer of 15 to 2324, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:168, and where b is greater than or equal to a + 14.	R59635, N28389, AA158646, AA158659, AA188594, AA190705, AA459426, AA465652
831928	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1770 of SEQ ID NO:169, b is an integer of 15 to 1784, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:169, and where b is greater than or equal to a + 14.	
831949	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide	

	sequence described by the general formula of a-b, where a is any integer between 1 to 1282 of SEQ ID NO:170, b is an integer of 15 to 1296, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:170, and where b is greater than or equal to a + 14.	
831950	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1883 of SEQ ID NO:171, b is an integer of 15 to 1897, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:171, and where b is greater than or equal to a + 14.	
831953	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1709 of SEQ ID NO:172, b is an integer of 15 to 1723, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:172, and where b is greater than or equal to a + 14.	
831975	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1402 of SEQ ID NO:173, b is an integer of 15 to 1416, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:173, and where b is greater than or equal to a + 14.	
832036	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1942 of SEQ ID NO:174, b is an integer of 15 to 1956, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:174, and where b is greater than or equal to a + 14.	R60820, R78776, R79082, H01912, H04427, N34789, N44513, W20183, W35150, AA159701, AA159628, AA470753, AA659808
832047	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1675 of SEQ ID NO:175, b is an integer of 15 to 1689, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:175, and where b is greater than or equal to a + 14.	R21952, R21968, R26963, R78028, H75703, H75632, H84015, H88136, H88135, H94007, H95012, N24834, N30818, N31761, N41592, N79533, W16686, W24639, W38979, W87777, W87875, AA121146, AA122426, AA131874, AA131978, AA147083, AA147140, AA282507, AA282605, AA558945, H84016, AA587558, AA830662, AA866026, AA917653, AI017813, C06340
832078	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1002 of SEQ ID NO:176, b is an integer of 15 to 1016, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:176, and where b is greater than or equal to a + 14.	

832100	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1350 of SEQ ID NO:177, b is an integer of 15 to 1364, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:177, and where b is greater than or equal to a + 14.	
832104	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 726 of SEQ ID NO:178, b is an integer of 15 to 740, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:178, and where b is greater than or equal to a + 14.	
832268	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1396 of SEQ ID NO:179, b is an integer of 15 to 1410, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:179, and where b is greater than or equal to a + 14.	
832270	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1479 of SEQ ID NO:180, b is an integer of 15 to 1493, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:180, and where b is greater than or equal to a + 14.	
832279	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2026 of SEQ ID NO:181, b is an integer of 15 to 2040, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:181, and where b is greater than or equal to a + 14.	
832317	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 955 of SEQ ID NO:182, b is an integer of 15 to 969, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:182, and where b is greater than or equal to a + 14.	R81508, H12476, H86945, AA053747, AA115783, AA133749, AA134163, AA134164, AA224985, AA228334, AA228423, AA229297, AA640471, AA657793, AA687568, AA904162, AA983632
832354	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1438 of SEQ ID NO:183, b is an integer of 15 to 1452, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:183, and where b is greater than or equal to a + 14.	
832364	Preferably excluded from the present invention are	

	one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2105 of SEQ ID NO:184, b is an integer of 15 to 2119, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:184, and where b is greater than or equal to a + 14.	
832378	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1311 of SEQ ID NO:185, b is an integer of 15 to 1325, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:185, and where b is greater than or equal to a + 14.	
832385	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 419 of SEQ ID NO:186, b is an integer of 15 to 433, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:186, and where b is greater than or equal to a + 14.	
832428	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 845 of SEQ ID NO:187, b is an integer of 15 to 859, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:187, and where b is greater than or equal to a + 14.	AA031420
832485	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 819 of SEQ ID NO:188, b is an integer of 15 to 833, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:188, and where b is greater than or equal to a + 14.	R63025, R66741, H53264, H53265, H53769, H53822, H54405, H54489, H81182, H91282, AA526672, H81181
832494	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2197 of SEQ ID NO:189, b is an integer of 15 to 2211, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:189, and where b is greater than or equal to a + 14.	T61040, T61591, T90055, T90157, T92840, T93714, T96177, T77726, H04686, H05450, H06997, H20176, H20366, R92666, H65144, H92413, N64053, N64060, N66714, N71338, N71388, N79742, N95497, N99884, W07259, W24989, W37394, W37657, W40208, W40260, W40532, W45430, W56165, W60427, W60986, W61080, W63739, W72328, W73757, W74394, AA025512, AA026057, AA065019, AA069295, AA069798, AA069845, AA070441, AA075793, AA083393, AA083394, AA084576, AA086181, AA099019, AA099097, AA099493, AA102003, AA100395, AA100554, AA100555, AA100638, AA101578, AA113226, AA113811, AA115645, AA115646.

		AA115888, AA115889, AA122231, AA121108, AA121596, AA121671, AA121743, AA126075, AA126102, AA126181, AA126295, AA126404, AA129470, AA129665, AA133945, AA133946, AA146752, AA155947, AA157140, AA157228, AA159947, AA160900, AA164889, AA164890, AA164840, AA164839, AA172107, AA182040, AA171714, AA187244, AA187376, AA186418, AA188846, AA189131, AA196155, AA196257, AA196611, AA196789, AA196961, AA223155, AA223415, AA226816, AA226856, AA227026, AA227109, AA227208, AA243161, AA243205, AA428759, AA429347, AA514858, AA535250, AA555125, AA565075, AA565168, AA581531, AA587192, AA576761, AA580523, AA659699, AA688240, AA689484, AA689543, AA689313, AA729979, AA740203, AA747258, AA747399, AA747993, AA837961, AA865930, AA906561, AA910350, AA919085, AA931143, AA999884, A1051141, F19298, W22294, W22759, W22970, W25820, W73709, C02713, C02766, C03390, C03613, C04202, C05262, C05272, R28954, R29028, R29032, AA062628, AA090039, C18989
832512	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1645 of SEQ ID NO:190, b is an integer of 15 to 1659, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:190, and where b is greater than or equal to a + 14.</p>	
832515	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3880 of SEQ ID NO:191, b is an integer of 15 to 3894, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:191, and where b is greater than or equal to a + 14.</p>	
832526	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 681 of SEQ ID NO:192, b is an integer of 15 to 695, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:192, and where b is greater than or equal to a + 14.</p>	
832575	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide</p>	R28543, R28684, R55782, R55862, R62797, R62843, R67670, R71154.

	sequence described by the general formula of a-b, where a is any integer between 1 to 3117 of SEQ ID NO:193, b is an integer of 15 to 3131, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:193, and where b is greater than or equal to a + 14.	R71651, N20642, N24838, N25562, N29014, N31768, N34161, N57560, N72111, W00338, W00374, W30889, W52729, W59982, W68047, W68189, AA019459, AA043870, AA044336, AA045040, AA045041, AA115599, AA115134, AA131177, AA165259, AA165260, AA165191, AA165192, AA164549, AA164550, AA261988, AA424972, AA279863, AA458832, AA459024, AA505193, AA507542, AA514388, AA622542, AA689232, AA689233, AA804910, AA807169, AA832321, AA878091, AA904023, AA936069, AA936071, AA946621, C00143, N86645, AA010988, AA641236, AA641464, C18301
832576	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2044 of SEQ ID NO:194, b is an integer of 15 to 2058, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:194, and where b is greater than or equal to a + 14.	
832588	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 817 of SEQ ID NO:195, b is an integer of 15 to 831, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:195, and where b is greater than or equal to a + 14.	
832634	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 947 of SEQ ID NO:196, b is an integer of 15 to 961, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:196, and where b is greater than or equal to a + 14.	
832728	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 592 of SEQ ID NO:197, b is an integer of 15 to 606, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:197, and where b is greater than or equal to a + 14.	
833094	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 379 of SEQ ID NO:198, b is an integer of 15 to 393, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:198, and where b is greater than or equal to a + 14.	

833395	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1047 of SEQ ID NO:199, b is an integer of 15 to 1061, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:199, and where b is greater than or equal to a + 14.	
834326	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1345 of SEQ ID NO:200, b is an integer of 15 to 1359, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:200, and where b is greater than or equal to a + 14.	
834583	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 712 of SEQ ID NO:201, b is an integer of 15 to 726, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:201, and where b is greater than or equal to a + 14.	
834944	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2700 of SEQ ID NO:202, b is an integer of 15 to 2714, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:202, and where b is greater than or equal to a + 14.	
835012	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 408 of SEQ ID NO:203, b is an integer of 15 to 422, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:203, and where b is greater than or equal to a + 14.	
835104	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2325 of SEQ ID NO:204, b is an integer of 15 to 2339, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:204, and where b is greater than or equal to a + 14.	
835332	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1641 of SEQ ID NO:205, b is an integer of 15 to 1655, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:205, and where b is greater than or equal to a + 14.	
835487	Preferably excluded from the present invention are	



	one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 5131 of SEQ ID NO:206, b is an integer of 15 to 5145, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:206, and where b is greater than or equal to a + 14.	
836182	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 473 of SEQ ID NO:207, b is an integer of 15 to 487, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:207, and where b is greater than or equal to a + 14.	
836522	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2282 of SEQ ID NO:208, b is an integer of 15 to 2296, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:208, and where b is greater than or equal to a + 14.	
836655	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 611 of SEQ ID NO:209, b is an integer of 15 to 625, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:209, and where b is greater than or equal to a + 14.	
836787	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1537 of SEQ ID NO:210, b is an integer of 15 to 1551, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:210, and where b is greater than or equal to a + 14.	W56241, W56321, AA009901, AA521313, AA732599, AA730271, AA766911, AA767313, W27009
836789	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 997 of SEQ ID NO:211, b is an integer of 15 to 1011, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:211, and where b is greater than or equal to a + 14.	T68817, R22374, R27362, H38950, R89148, R91088, H68416, H93594, N33889, N47045, N56761, W19886, W44630, W61370, W86385, AA036993, AA065062, AA101017, AA121107, AA130485, AA147474, AA160596, AA282977
838577	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1625 of SEQ ID NO:212, b is an integer of 15 to 1639, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:212, and where b is greater than or equal to a + 14.	T53501, T40735, T63398, T63985, T64053, T64155, T64284, T93511, T94941, T94995, T96340, R00890, R01553, R12738, R12739, R39790, R54423, R66373, R66595, R67104, R67219, R79151, R79152, R82180, R82224, R82470, R82471, H01963, H02048, H02758, H02759, H05982, H19484, H19567, H19882, H19900, H44901, H44938, H44978, H46289, H46871, H49538.

		H49781, H53114, H53220, H54300, H56079, H56279, H79695, H79696, N23140, N25755, N25850, N26983, N29784, N32719, N36477, N40104, N42924, N44580, N50724, N55052, N67751, N93444, N98425, N98537, W02803, W21105, W23673, W30688, W30899, W35106, W45448, W45449, W45661, W44441, W46823, W46872, W47373, W47374, W52205, W58331, W58652, W96332, AA007386, AA007676, AA011363, AA016311, AA017511, AA018464, AA019899, AA025040, AA025039, AA029796, AA029797, AA031472, AA035395, AA035396, AA037272, AA040791, AA041228, AA042893, AA043029, AA055565, AA056185, AA056186, AA056621, AA056726, AA069193, AA079705, AA082517, AA084044, AA084043, AA115273, AA115056, AA132031, AA132153, AA149267, AA149284, AA149378, AA158093, AA158103, AA158364, AA158904, AA158905, AA165106, AA220957, AA235312, AA251169, AA421302, AA421425, AA428706, AA429291, AA513790, AA531603, AA551736, AA554236, AA605236, AA604674, AA604939, AA612935, AA617731, AA627300, AA687527, AA732095, AA740760, AA765135, AA765136, AA765296, AA765891, AA888144, AA908665, AA928038, AA936934, AA961143, AA987647, AA975856, W03595, C03206, C18055, AA164690, AA218956, AA291352, AA292329, AA293276, AA393988, AA398076, AA410772, D12417, AA442678, AA442969, AA454814, AA454888, AA482370, AA486098, AA486161, AA625879, AA678365, AA679281, AA703505, AA722872, AA732793, AA989559, A1003448, A1014938, A1022070, A1084792, A1092360
838717	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2113 of SEQ ID NO:213, b is an integer of 15 to 2127, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:213, and where b is greater than or equal to a + 14.</p>	
839008	<p>Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1152 of SEQ ID</p>	

	NO:214, b is an integer of 15 to 1166, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:214, and where b is greater than or equal to a + 14.	
840063	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3309 of SEQ ID NO:215, b is an integer of 15 to 3323, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:215, and where b is greater than or equal to a + 14.	
840533	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1394 of SEQ ID NO:216, b is an integer of 15 to 1408, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:216, and where b is greater than or equal to a + 14.	
840669	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2097 of SEQ ID NO:217, b is an integer of 15 to 2111, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:217, and where b is greater than or equal to a + 14.	T71029, T79145, T79226, T99989, R59589, R61735, R61734, R66190, R67070, H16201, H16200, H22960, H84137, H85574, H98850, N23572, N26340, N56614, W72249, W76334, W86530, W87654, W87653, AA057869, AA122103, AA129545, AA136524, AA137122, AA429808, AA525242, AA558970, H99223, AA584317, AA595168, AA825180, AA931521, AA938437, A1017369, N29659, N68604, W86674, AA007246
841140	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2479 of SEQ ID NO:218, b is an integer of 15 to 2493, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:218, and where b is greater than or equal to a + 14.	
841386	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1245 of SEQ ID NO:219, b is an integer of 15 to 1259, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:219, and where b is greater than or equal to a + 14.	AA429393, AA429394, AA493187, AA807096, AA836046
841480	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1835 of SEQ ID NO:220, b is an integer of 15 to 1849, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:220, and where b is greater than or equal to a + 14.	
841509	Preferably excluded from the present invention are	

	one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1253 of SEQ ID NO:221, b is an integer of 15 to 1267, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:221, and where b is greater than or equal to a + 14.	
841616	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 740 of SEQ ID NO:222, b is an integer of 15 to 754, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:222, and where b is greater than or equal to a + 14.	
841900	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1244 of SEQ ID NO:223, b is an integer of 15 to 1258, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:223, and where b is greater than or equal to a + 14.	R87848, AA806230, Z28656
842054	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 570 of SEQ ID NO:224, b is an integer of 15 to 584, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:224, and where b is greater than or equal to a + 14.	
843061	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3435 of SEQ ID NO:225, b is an integer of 15 to 3449, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:225, and where b is greater than or equal to a + 14.	
843544	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1852 of SEQ ID NO:226, b is an integer of 15 to 1866, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:226, and where b is greater than or equal to a + 14.	
844092	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1050 of SEQ ID NO:227, b is an integer of 15 to 1064, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:227, and where b is greater than or equal to a + 14.	
844270	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide	

	sequence described by the general formula of a-b, where a is any integer between 1 to 359 of SEQ ID NO:228, b is an integer of 15 to 373, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:228, and where b is greater than or equal to a + 14.	
844604	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2830 of SEQ ID NO:229, b is an integer of 15 to 2844, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:229, and where b is greater than or equal to a + 14.	
844685	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1784 of SEQ ID NO:230, b is an integer of 15 to 1798, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:230, and where b is greater than or equal to a + 14.	
844855	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1809 of SEQ ID NO:231, b is an integer of 15 to 1823, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:231, and where b is greater than or equal to a + 14.	
845101	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 956 of SEQ ID NO:232, b is an integer of 15 to 970, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:232, and where b is greater than or equal to a + 14.	
845141	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 953 of SEQ ID NO:233, b is an integer of 15 to 967, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:233, and where b is greater than or equal to a + 14.	
845220	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2149 of SEQ ID NO:234, b is an integer of 15 to 2163, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:234, and where b is greater than or equal to a + 14.	R70310, H02204, H28992, H29096, W67797, W67855, W72320, AA459289, AA459519, AA430385, AA746169
845434	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b,	

	where a is any integer between 1 to 1307 of SEQ ID NO:235, b is an integer of 15 to 1321, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:235, and where b is greater than or equal to a + 14.	
845510	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 669 of SEQ ID NO:236, b is an integer of 15 to 683, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:236, and where b is greater than or equal to a + 14.	
845600	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2101 of SEQ ID NO:237, b is an integer of 15 to 2115, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:237, and where b is greater than or equal to a + 14.	
845882	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1628 of SEQ ID NO:238, b is an integer of 15 to 1642, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:238, and where b is greater than or equal to a + 14.	
846007	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 454 of SEQ ID NO:239, b is an integer of 15 to 468, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:239, and where b is greater than or equal to a + 14.	H81424
846280	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1315 of SEQ ID NO:240, b is an integer of 15 to 1329, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:240, and where b is greater than or equal to a + 14.	
846286	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1638 of SEQ ID NO:241, b is an integer of 15 to 1652, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:241, and where b is greater than or equal to a + 14.	
846388	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1932 of SEQ ID	

	NO:242. b is an integer of 15 to 1946, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:242, and where b is greater than or equal to a + 14.	
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*Polynucleotide and Polypeptide Variants*

The present invention is directed to variants of the polynucleotide sequence disclosed in SEQ ID NO:X or the complementary strand thereto, and/or the cDNA sequence contained in a cDNA clone contained in the deposit.

- 5       The present invention also encompasses variants of a colon and/or colon cancer polypeptide sequence disclosed in SEQ ID NO:Y, a polypeptide sequence encoded by the polynucleotide sequence in SEQ ID NO:X, and/or a polypeptide sequence encoded by the cDNA in the related cDNA clone contained in the deposit.

- 10       "Variant" refers to a polynucleotide or polypeptide differing from the polynucleotide or polypeptide of the present invention, but retaining essential properties thereof. Generally, variants are overall closely similar, and, in many regions, identical to the polynucleotide or polypeptide of the present invention.

- 15       The present invention is also directed to nucleic acid molecules which comprise, or alternatively consist of, a nucleotide sequence which is at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100%, identical to, for example, the nucleotide coding sequence in SEQ ID NO:X or the complementary strand thereto, the nucleotide coding sequence of the related cDNA contained in a deposited library or the complementary strand thereto, a nucleotide sequence encoding the polypeptide of SEQ ID NO:Y, a nucleotide sequence encoding a polypeptide sequence encoded by the nucleotide sequence in SEQ ID NO:X, a nucleotide sequence encoding the polypeptide encoded by the cDNA in the related cDNA contained in a deposited library, and/or polynucleotide fragments of any of these nucleic acid molecules (e.g., those fragments described herein). Polypeptides encoded by these nucleic acid molecules are also encompassed by the invention. In another embodiment, the invention encompasses nucleic acid molecules which comprise or alternatively consist of, a polynucleotide which hybridizes under stringent hybridization conditions, or alternatively, under low stringency conditions, to the nucleotide coding sequence in SEQ ID NO:X, the nucleotide coding sequence of the related cDNA clone contained in a deposited library, a nucleotide sequence encoding the polypeptide of SEQ ID NO:Y, a nucleotide sequence encoding a polypeptide sequence encoded by the nucleotide sequence in SEQ ID NO:X, a nucleotide sequence encoding the polypeptide encoded by the cDNA in the related cDNA clone contained in a deposited library, and/or polynucleotide fragments of any of these nucleic acid molecules (e.g., those fragments described herein). Polynucleotides which
- 20
- 25
- 30



hybridize to the complement of these nucleic acid molecules under stringent hybridization conditions or alternatively, under lower stringency conditions. are also encompassed by the invention, as are polypeptides encoded by these polynucleotides.

The present invention is also directed to polypeptides which comprise, or alternatively  
5 consist of, an amino acid sequence which is at least 80%, 85%, 90%, 95%, 96%, 97%, 98%,  
99% or 100% identical to, for example, the polypeptide sequence shown in SEQ ID NO:Y, a  
polypeptide sequence encoded by the nucleotide sequence in SEQ ID NO:X, a polypeptide  
sequence encoded by the cDNA in the related cDNA clone contained in a deposited library,  
and/or polypeptide fragments of any of these polypeptides (e.g., those fragments described  
10 herein). Polynucleotides which hybridize to the complement of the nucleic acid molecules  
encoding these polypeptides under stringent hybridization conditions, or alternatively, under  
lower stringency conditions, are also encompassed by the invention, as are polypeptides  
encoded by these polynucleotides.

By a nucleic acid having a nucleotide sequence at least, for example, 95% "identical"  
15 to a reference nucleotide sequence of the present invention, it is intended that the nucleotide  
sequence of the nucleic acid is identical to the reference sequence except that the nucleotide  
sequence may include up to five point mutations per each 100 nucleotides of the reference  
nucleotide sequence encoding the polypeptide. In other words, to obtain a nucleic acid  
having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to  
20 5% of the nucleotides in the reference sequence may be deleted or substituted with another  
nucleotide, or a number of nucleotides up to 5% of the total nucleotides in the reference  
sequence may be inserted into the reference sequence. The query sequence may be, for  
example, an entire sequence referred to in Table 1, an ORF (open reading frame), or any  
fragment specified as described herein.

25 As a practical matter, whether any particular nucleic acid molecule or polypeptide is  
at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to a nucleotide sequence of  
the present invention can be determined conventionally using known computer programs. A  
preferred method for determining the best overall match between a query sequence (a  
sequence of the present invention) and a subject sequence, also referred to as a global  
30 sequence alignment, can be determined using the FASTDB computer program based on the  
algorithm of Brutlag et al. (Comp. App. Biosci. 6:237-245 (1990)). In a sequence alignment  
the query and subject sequences are both DNA sequences. An RNA sequence can be

compared by converting U's to T's. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB alignment of DNA sequences to calculate percent identity are: Matrix=Unitary, k-tuple=4, Mismatch Penalty=1, Joining Penalty=30. Randomization Group Length=0, Cutoff Score=1, Gap Penalty=5, Gap Size  
5 Penalty 0.05, Window Size=500 or the length of the subject nucleotide sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence because of 5' or 3' deletions, not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for 5' and 3' truncations of the  
10 subject sequence when calculating percent identity. For subject sequences truncated at the 5' or 3' ends, relative to the query sequence, the percent identity is corrected by calculating the number of bases of the query sequence that are 5' and 3' of the subject sequence, which are not matched/aligned, as a percent of the total bases of the query sequence. Whether a nucleotide is matched/aligned is determined by results of the FASTDB sequence alignment.  
15 This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This corrected score is what is used for the purposes of the present invention. Only bases outside the 5' and 3' bases of the subject sequence, as displayed by the FASTDB alignment, which are not matched/aligned with the query sequence, are calculated for the purposes of  
20 manually adjusting the percent identity score.

For example, a 90 base subject sequence is aligned to a 100 base query sequence to determine percent identity. The deletions occur at the 5' end of the subject sequence and therefore, the FASTDB alignment does not show a matched/alignment of the first 10 bases at 5' end. The 10 unpaired bases represent 10% of the sequence (number of bases at the 5' and  
25 3' ends not matched/total number of bases in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 bases were perfectly matched the final percent identity would be 90%. In another example, a 90 base subject sequence is compared with a 100 base query sequence. This time the deletions are internal deletions so that there are no bases on the 5' or 3' of the subject sequence which  
30 are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only bases 5' and 3' of the subject sequence which are not matched/aligned with the query sequence are manually corrected for. No other

manual corrections are to made for the purposes of the present invention.

By a polypeptide having an amino acid sequence at least, for example, 95% "identical" to a query amino acid sequence of the present invention, it is intended that the amino acid sequence of the subject polypeptide is identical to the query sequence except that  
5 the subject polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the query amino acid sequence. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a query amino acid sequence, up to 5% of the amino acid residues in the subject sequence may be inserted, deleted, (indels) or substituted with another amino acid. These alterations of the reference sequence may occur  
10 at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

As a practical matter, whether any particular polypeptide is at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to, for instance, the amino acid sequence in SEQ ID  
15 NO:Y or a fragment thereof, the amino acid sequence encoded by the nucleotide sequence in SEQ ID NO:X or a fragment thereof, or the amino acid sequence encoded by the cDNA in the related cDNA clone contained in a deposited library, or a fragment thereof, can be determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present  
20 invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci.6:237- 245(1990)). In a sequence alignment the query and subject sequences are either both nucleotide sequences or both amino acid sequences. The result of said global sequence alignment is in percent identity. Preferred parameters used in a  
25 FASTDB amino acid alignment are: Matrix=PAM 0, k-tuple=2, Mismatch Penalty=1, Joining Penalty=20, Randomization Group Length=0, Cutoff Score=1, Window Size=sequence length, Gap Penalty=5, Gap Size Penalty=0.05, Window Size=500 or the length of the subject amino acid sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence due to N- or C-terminal  
30 deletions. not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for N- and C-terminal truncations of the subject sequence when calculating global percent identity. For subject sequences

truncated at the N- and C-termini, relative to the query sequence, the percent identity is corrected by calculating the number of residues of the query sequence that are N- and C-terminal of the subject sequence, which are not matched/aligned with a corresponding subject residue, as a percent of the total bases of the query sequence. Whether a residue is  
5 matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This final percent identity score is what is used for the purposes of the present invention. Only residues to the N- and C-termini of the subject sequence, which are not matched/aligned with the  
10 query sequence, are considered for the purposes of manually adjusting the percent identity score. That is, only query residue positions outside the farthest N- and C- terminal residues of the subject sequence.

For example, a 90 amino acid residue subject sequence is aligned with a 100 residue query sequence to determine percent identity. The deletion occurs at the N-terminus of the  
15 subject sequence and therefore, the FASTDB alignment does not show a matching/alignment of the first 10 residues at the N-terminus. The 10 unpaired residues represent 10% of the sequence (number of residues at the N- and C- termini not matched/total number of residues in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 residues were perfectly matched the final percent  
20 identity would be 90%. In another example, a 90 residue subject sequence is compared with a 100 residue query sequence. This time the deletions are internal deletions so there are no residues at the N- or C-termini of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only residue positions outside the N- and C-terminal ends of the subject  
25 sequence, as displayed in the FASTDB alignment, which are not matched/aligned with the query sequence are manually corrected for. No other manual corrections are to made for the purposes of the present invention.

The variants may contain alterations in the coding regions, non-coding regions, or both. Especially preferred are polynucleotide variants containing alterations which produce  
30 silent substitutions, additions, or deletions, but do not alter the properties or activities of the encoded polypeptide. Nucleotide variants produced by silent substitutions due to the degeneracy of the genetic code are preferred. Moreover, variants in which less than 50, less

than 40, less than 30, less than 20, less than 10, or 5-50, 5-25, 5-10, 1-5, or 1-2 amino acids are substituted, deleted, or added in any combination are also preferred. Polynucleotide variants can be produced for a variety of reasons, e.g., to optimize codon expression for a particular host (change codons in the human mRNA to those preferred by a bacterial host such as *E. coli*).

Naturally occurring variants are called "allelic variants," and refer to one of several alternate forms of a gene occupying a given locus on a chromosome of an organism. (Genes II. Lewin, B., ed., John Wiley & Sons, New York (1985).) These allelic variants can vary at either the polynucleotide and/or polypeptide level and are included in the present invention. Alternatively, non-naturally occurring variants may be produced by mutagenesis techniques or by direct synthesis.

Using known methods of protein engineering and recombinant DNA technology, variants may be generated to improve or alter the characteristics of the polypeptides of the present invention. For instance, as discussed herein, one or more amino acids can be deleted from the N-terminus or C-terminus of the polypeptide of the present invention without substantial loss of biological function. The authors of Ron et al., *J. Biol. Chem.* 268: 2984-2988 (1993), reported variant KGF proteins having heparin binding activity even after deleting 3, 8, or 27 amino-terminal amino acid residues. Similarly, Interferon gamma exhibited up to ten times higher activity after deleting 8-10 amino acid residues from the carboxy terminus of this protein. (Dobeli et al., *J. Biotechnology* 7:199-216 (1988).)

Moreover, ample evidence demonstrates that variants often retain a biological activity similar to that of the naturally occurring protein. For example, Gayle and coworkers (*J. Biol. Chem.* 268:22105-22111 (1993)) conducted extensive mutational analysis of human cytokine IL-1a. They used random mutagenesis to generate over 3,500 individual IL-1a mutants that averaged 2.5 amino acid changes per variant over the entire length of the molecule. Multiple mutations were examined at every possible amino acid position. The investigators found that "[m]ost of the molecule could be altered with little effect on either [binding or biological activity]." (See, Abstract.) In fact, only 23 unique amino acid sequences, out of more than 3,500 nucleotide sequences examined, produced a protein that significantly differed in activity from wild-type.

Furthermore, as discussed herein, even if deleting one or more amino acids from the N-terminus or C-terminus of a polypeptide results in modification or loss of one or more

biological functions, other biological activities may still be retained. For example, the ability of a deletion variant to induce and/or to bind antibodies which recognize the secreted form will likely be retained when less than the majority of the residues of the secreted form are removed from the N-terminus or C-terminus. Whether a particular polypeptide lacking N- or C-terminal residues of a protein retains such immunogenic activities can readily be determined by routine methods described herein and otherwise known in the art.

Thus, the invention further includes polypeptide variants which show a functional activity (e.g., biological activity) of the polypeptide of the invention of which they are a variant. Such variants include deletions, insertions, inversions, repeats, and substitutions selected according to general rules known in the art so as have little effect on activity.

The present application is directed to nucleic acid molecules at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% identical to the nucleic acid sequences disclosed herein or fragments thereof, (e.g., including but not limited to fragments encoding a polypeptide having the amino acid sequence of an N and/or C terminal deletion), irrespective of whether they encode a polypeptide having functional activity. This is because even where a particular nucleic acid molecule does not encode a polypeptide having functional activity, one of skill in the art would still know how to use the nucleic acid molecule, for instance, as a hybridization probe or a polymerase chain reaction (PCR) primer. Uses of the nucleic acid molecules of the present invention that do not encode a polypeptide having functional activity include, inter alia, (1) isolating a gene or allelic or splice variants thereof in a cDNA library; (2) in situ hybridization (e.g., "FISH") to metaphase chromosomal spreads to provide precise chromosomal location of the gene, as described in Verma et al., Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York (1988); and (3) Northern Blot analysis for detecting mRNA expression in specific tissues.

Preferred, however, are nucleic acid molecules having sequences at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% identical to the nucleic acid sequences disclosed herein, which do, in fact, encode a polypeptide having a functional activity of a polypeptide of the invention.

Of course, due to the degeneracy of the genetic code, one of ordinary skill in the art will immediately recognize that a large number of the nucleic acid molecules having a sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to, for example, the nucleic acid sequence of the cDNA in the related cDNA clone contained in a

deposited library, the nucleic acid sequence referred to in Table 1 (SEQ ID NO:X), or fragments thereof, will encode polypeptides "having functional activity." In fact, since degenerate variants of any of these nucleotide sequences all encode the same polypeptide, in many instances, this will be clear to the skilled artisan even without performing the above described comparison assay. It will be further recognized in the art that, for such nucleic acid molecules that are not degenerate variants, a reasonable number will also encode a polypeptide having functional activity. This is because the skilled artisan is fully aware of amino acid substitutions that are either less likely or not likely to significantly effect protein function (e.g., replacing one aliphatic amino acid with a second aliphatic amino acid), as further described below.

For example, guidance concerning how to make phenotypically silent amino acid substitutions is provided in Bowie et al., "Deciphering the Message in Protein Sequences: Tolerance to Amino Acid Substitutions," *Science* 247:1306-1310 (1990), wherein the authors indicate that there are two main strategies for studying the tolerance of an amino acid sequence to change.

The first strategy exploits the tolerance of amino acid substitutions by natural selection during the process of evolution. By comparing amino acid sequences in different species, conserved amino acids can be identified. These conserved amino acids are likely important for protein function. In contrast, the amino acid positions where substitutions have been tolerated by natural selection indicates that these positions are not critical for protein function. Thus, positions tolerating amino acid substitution could be modified while still maintaining biological activity of the protein.

The second strategy uses genetic engineering to introduce amino acid changes at specific positions of a cloned gene to identify regions critical for protein function. For example, site directed mutagenesis or alanine-scanning mutagenesis (introduction of single alanine mutations at every residue in the molecule) can be used. (Cunningham and Wells, *Science* 244:1081-1085 (1989).) The resulting mutant molecules can then be tested for biological activity.

As the authors state, these two strategies have revealed that proteins are surprisingly tolerant of amino acid substitutions. The authors further indicate which amino acid changes are likely to be permissive at certain amino acid positions in the protein. For example, most buried (within the tertiary structure of the protein) amino acid residues require nonpolar side

chains, whereas few features of surface side chains are generally conserved. Moreover, tolerated conservative amino acid substitutions involve replacement of the aliphatic or hydrophobic amino acids Ala, Val, Leu and Ile; replacement of the hydroxyl residues Ser and Thr; replacement of the acidic residues Asp and Glu; replacement of the amide residues Asn and Gln, replacement of the basic residues Lys, Arg, and His; replacement of the aromatic residues Phe, Tyr, and Trp, and replacement of the small-sized amino acids Ala, Ser, Thr, Met, and Gly. Besides conservative amino acid substitution, variants of the present invention include (i) substitutions with one or more of the non-conserved amino acid residues, where the substituted amino acid residues may or may not be one encoded by the genetic code, or (ii) substitution with one or more of amino acid residues having a substituent group, or (iii) fusion of the mature polypeptide with another compound, such as a compound to increase the stability and/or solubility of the polypeptide (for example, polyethylene glycol), or (iv) fusion of the polypeptide with additional amino acids, such as, for example, an IgG Fc fusion region peptide, or leader or secretory sequence, or a sequence facilitating purification. Such variant polypeptides are deemed to be within the scope of those skilled in the art from the teachings herein.

For example, polypeptide variants containing amino acid substitutions of charged amino acids with other charged or neutral amino acids may produce proteins with improved characteristics, such as less aggregation. Aggregation of pharmaceutical formulations both reduces activity and increases clearance due to the aggregate's immunogenic activity. (Pinckard et al., Clin. Exp. Immunol. 2:331-340 (1967); Robbins et al., Diabetes 36: 838-845 (1987); Cleland et al., Crit. Rev. Therapeutic Drug Carrier Systems 10:307-377 (1993).)

A further embodiment of the invention relates to a polypeptide which comprises the amino acid sequence of a polypeptide having an amino acid sequence which contains at least one amino acid substitution, but not more than 50 amino acid substitutions, even more preferably, not more than 40 amino acid substitutions, still more preferably, not more than 30 amino acid substitutions, and still even more preferably, not more than 20 amino acid substitutions. Of course it is highly preferable for a polypeptide to have an amino acid sequence which comprises the amino acid sequence of a polypeptide of SEQ ID NO:Y, an amino acid sequence encoded by SEQ ID NO:X, and/or the amino acid sequence encoded by the cDNA in the related cDNA clone contained in a deposited library which contains, in order of ever-increasing preference, at least one, but not more than 10, 9, 8, 7, 6, 5, 4, 3, 2 or 1



amino acid substitutions. In specific embodiments, the number of additions, substitutions, and/or deletions in the amino acid sequence of SEQ ID NO:Y or fragments thereof (e.g., the mature form and/or other fragments described herein), an amino acid sequence encoded by SEQ ID NO:X or fragments thereof, and/or the amino acid sequence encoded by the cDNA in the related cDNA clone contained in a deposited library or fragments thereof, is 1-5, 5-10, 5-25, 5-50, 10-50 or 50-150, conservative amino acid substitutions are preferable.

#### *Polynucleotide and Polypeptide Fragments*

The present invention is also directed to polynucleotide fragments of the colon and/or colon cancer polynucleotides (nucleic acids) of the invention. In the present invention, a "polynucleotide fragment" refers, for example, to a polynucleotide having a nucleic acid sequence which: is a portion of the cDNA contained in a deposited cDNA clone; or is a portion of a polynucleotide sequence encoding the polypeptide encoded by the cDNA contained in a deposited cDNA clone; or is a portion of the polynucleotide sequence in SEQ ID NO:X or the complementary strand thereto; or is a polynucleotide sequence encoding a portion of the polypeptide of SEQ ID NO:Y; or is a polynucleotide sequence encoding a portion of a polypeptide encoded by SEQ ID NO:X or the complementary strand thereto. The nucleotide fragments of the invention are preferably at least about 15 nt, and more preferably at least about 20 nt, still more preferably at least about 30 nt, and even more preferably, at least about 40 nt, at least about 50 nt, at least about 75 nt, at least about 100 nt, at least about 125 nt or at least about 150 nt in length. A fragment "at least 20 nt in length," for example, is intended to include 20 or more contiguous bases from, for example, the sequence contained in the cDNA in a related cDNA clone contained in a deposited library, the nucleotide sequence shown in SEQ ID NO:X or the complementary stand thereto. In this context "about" includes the particularly recited value or a value larger or smaller by several (5, 4, 3, 2, or 1) nucleotides. These nucleotide fragments have uses that include, but are not limited to, as diagnostic probes and primers as discussed herein. Of course, larger fragments (e.g., at least 150, 175, 200, 250, 500, 600, 1000, or 2000 nucleotides in length) are also encompassed by the invention.

Moreover, representative examples of polynucleotide fragments of the invention, include, for example, fragments comprising, or alternatively consisting of, a sequence from about nucleotide number 1-50, 51-100, 101-150, 151-200, 201-250, 251-300, 301-350, 351-

400, 401-450, 451-500, 501-550, 551-600, 651-700, 701-750, 751-800, 800-850, 851-900, 901-950, 951-1000, 1001-1050, 1051-1100, 1101-1150, 1151-1200, 1201-1250, 1251-1300, 1301-1350, 1351-1400, 1401-1450, 1451-1500, 1501-1550, 1551-1600, 1601-1650, 1651-1700, 1701-1750, 1751-1800, 1801-1850, 1851-1900, 1901-1950, 1951-2000, 2001-2050, 2051-2100, 2101-2150, 2151-2200, 2201-2250, 2251-2300, 2301-2350, 2351-2400, 2401-2450, 2451-2500, 2501-2550, 2551-2600, 2601-2650, 2651-2700, 2701-2750, 2751-2800, 2801-2850, 2851-2900, 2901-2950, 2951-3000, 3001-3050, 3051-3100, 3101-3150, 3151-3200, 3201-3250, 3251-3300, 3301-3350, 3351-3400, 3401-3450, 3451-3500, 3501-3550, 3551-3600, 3601-3650, 3651-3700, 3701-3750, 3751-3800, 3801-3850, 3851-3900, 3901-3950, 3951-4000, 4001-4050, 4051-4100, and 4101 to the end of SEQ ID NO:X, or the complementary strand thereto. In this context "about" includes the particularly recited range or a range larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. Preferably, these fragments encode a polypeptide which has a functional activity (e.g., biological activity) of the polypeptide encoded by the polynucleotide of which the sequence is a portion. More preferably, these fragments can be used as probes or primers as discussed herein. Polynucleotides which hybridize to one or more of these nucleic acid molecules under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention, as are polypeptides encoded by these polynucleotides or fragments.

Moreover, representative examples of polynucleotide fragments of the invention, include, for example, fragments comprising, or alternatively consisting of, a sequence from about nucleotide number 1-50, 51-100, 101-150, 151-200, 201-250, 251-300, 301-350, 351-400, 401-450, 451-500, 501-550, 551-600, 651-700, 701-750, 751-800, 800-850, 851-900, 901-950, 951-1000, 1001-1050, 1051-1100, 1101-1150, 1151-1200, 1201-1250, 1251-1300, 1301-1350, 1351-1400, 1401-1450, 1451-1500, 1501-1550, 1551-1600, 1601-1650, 1651-1700, 1701-1750, 1751-1800, 1801-1850, 1851-1900, 1901-1950, 1951-2000, 2001-2050, 2051-2100, 2101-2150, 2151-2200, 2201-2250, 2251-2300, 2301-2350, 2351-2400, 2401-2450, 2451-2500, 2501-2550, 2551-2600, 2601-2650, 2651-2700, 2701-2750, 2751-2800, 2801-2850, 2851-2900, 2901-2950, 2951-3000, 3001-3050, 3051-3100, 3101-3150, 3151-3200, 3201-3250, 3251-3300, 3301-3350, 3351-3400, 3401-3450, 3451-3500, 3501-3550, 3551-3600, 3601-3650, 3651-3700, 3701-3750, 3751-3800, 3801-3850, 3851-3900, 3901-3950, 3951-4000, 4001-4050, 4051-4100, and 4101 to the end of the cDNA nucleotide

sequence contained in the deposited cDNA clone, or the complementary strand thereto. In this context "about" includes the particularly recited range, or a range larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. Preferably, these fragments encode a polypeptide which has a functional activity (e.g., biological activity) of the polypeptide encoded by the cDNA nucleotide sequence contained in the deposited cDNA clone. More preferably, these fragments can be used as probes or primers as discussed herein. Polynucleotides which hybridize to one or more of these fragments under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention, as are polypeptides encoded by these polynucleotides or fragments.

In the present invention, a "polypeptide fragment" refers to an amino acid sequence which is a portion of that contained in SEQ ID NO:Y, a portion of an amino acid sequence encoded by the polynucleotide sequence of SEQ ID NO:X, and/or encoded by the cDNA contained in the related cDNA clone contained in a deposited library. Protein (polypeptide) fragments may be "free-standing," or comprised within a larger polypeptide of which the fragment forms a part or region, most preferably as a single continuous region. Representative examples of polypeptide fragments of the invention, include, for example, fragments comprising, or alternatively consisting of, an amino acid sequence from about amino acid number 1-20, 21-40, 41-60, 61-80, 81-100, 102-120, 121-140, 141-160, 161-180, 181-200, 201-220, 221-240, 241-260, 261-280, 281-300, 301-320, 321-340, 341-360, 361-380, 381-400, 401-420, 421-440, 441-460, 461-480, 481-500, 501-520, 521-540, 541-560, 561-580, 581-600, 601-620, 621-640, 641-660, 661-680, 681-700, 701-720, 721-740, 741-760, 761-780, 781-800, 801-820, 821-840, 841-860, 861-880, 881-900, 901-920, 921-940, 941-960, 961-980, 981-1000, 1001-1020, 1021-1040, 1041-1060, 1061-1080, 1081-1100, 1101-1120, 1121-1140, 1141-1160, 1161-1180, 1181-1200, 1201-1220, 1221-1240, 1241-1260, 1261-1280, 1281-1300, 1301-1320, 1321-1340, 1341-1360, and 1361 to the end of SEQ ID NO:Y. Moreover, polypeptide fragments of the invention may be at least about 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 100, 110, 120, 130, 140, or 150 amino acids in length. In this context "about" includes the particularly recited ranges or values, or ranges or values larger or smaller by several (5, 4, 3, 2, or 1) amino acids, at either terminus or at both termini. Polynucleotides encoding these polypeptide fragments are also encompassed by the invention.

Even if deletion of one or more amino acids from the N-terminus of a protein results in modification of loss of one or more biological functions of the protein, other functional activities (e.g., biological activities, ability to multimerize, ability to bind a ligand) may still be retained. For example, the ability of shortened muteins to induce and/or bind to antibodies  
5 which recognize the complete or mature forms of the polypeptides generally will be retained when less than the majority of the residues of the complete or mature polypeptide are removed from the N-terminus. Whether a particular polypeptide lacking N-terminal residues of a complete polypeptide retains such immunologic activities can readily be determined by routine methods described herein and otherwise known in the art. It is not unlikely that a  
10 mutein with a large number of deleted N-terminal amino acid residues may retain some biological or immunogenic activities. In fact, peptides composed of as few as six amino acid residues may often evoke an immune response.

Accordingly, polypeptide fragments of the invention include the secreted protein as well as the mature form. Further preferred polypeptide fragments include the secreted protein  
15 or the mature form having a continuous series of deleted residues from the amino or the carboxy terminus, or both. For example, any number of amino acids, ranging from 1-60, can be deleted from the amino terminus of either the secreted polypeptide or the mature form. Similarly, any number of amino acids, ranging from 1-30, can be deleted from the carboxy terminus of the secreted protein or mature form. Furthermore, any combination of the above  
20 amino and carboxy terminus deletions are preferred. Similarly, polynucleotides encoding these polypeptide fragments are also preferred.

The present invention further provides polypeptides having one or more residues deleted from the amino terminus of the amino acid sequence of a polypeptide disclosed herein (e.g., a polypeptide of SEQ ID NO:Y, a polypeptide encoded by the polynucleotide  
25 sequence contained in SEQ ID NO:X, and/or a polypeptide encoded by the cDNA contained in the related cDNA clone contained in a deposited library). In particular, N-terminal deletions may be described by the general formula m-q, where q is a whole integer representing the total number of amino acid residues in a polypeptide of the invention (e.g., the polypeptide disclosed in SEQ ID NO:Y), and m is defined as any integer ranging from 2  
30 to q-6. Polynucleotides encoding these polypeptides are also encompassed by the invention.

Also as mentioned above, even if deletion of one or more amino acids from the C-terminus of a protein results in modification of loss of one or more biological functions of

the protein, other functional activities (e.g., biological activities, ability to multimerize, ability to bind a ligand) may still be retained. For example the ability of the shortened mutein to induce and/or bind to antibodies which recognize the complete or mature forms of the polypeptide generally will be retained when less than the majority of the residues of the complete or mature polypeptide are removed from the C-terminus. Whether a particular polypeptide lacking C-terminal residues of a complete polypeptide retains such immunologic activities can readily be determined by routine methods described herein and otherwise known in the art. It is not unlikely that a mutein with a large number of deleted C-terminal amino acid residues may retain some biological or immunogenic activities. In fact, peptides composed of as few as six amino acid residues may often evoke an immune response.

Accordingly, the present invention further provides polypeptides having one or more residues from the carboxy terminus of the amino acid sequence of a polypeptide disclosed herein (e.g., a polypeptide of SEQ ID NO:Y, a polypeptide encoded by the polynucleotide sequence contained in SEQ ID NO:X, and/or a polypeptide encoded by the cDNA contained in the related cDNA referenced in Table 1). In particular, C-terminal deletions may be described by the general formula 1-n, where n is any whole integer ranging from 6 to q-1, and where n corresponds to the position of an amino acid residue in a polypeptide of the invention. Polynucleotides encoding these polypeptides are also encompassed by the invention.

In addition, any of the above described N- or C-terminal deletions can be combined to produce a N- and C-terminal deleted polypeptide. The invention also provides polypeptides having one or more amino acids deleted from both the amino and the carboxyl termini, which may be described generally as having residues m-n of a polypeptide encoded by SEQ ID NO:X (e.g., including, but not limited to, the preferred polypeptide disclosed as SEQ ID NO:Y), and/or the cDNA in the related cDNA clone contained in a deposited library, where n and m are integers as described above. Polynucleotides encoding these polypeptides are also encompassed by the invention.

Any polypeptide sequence contained in the polypeptide of SEQ ID NO:Y, encoded by the polynucleotide sequences set forth as SEQ ID NO:X, or encoded by the cDNA in the related cDNA clone contained in a deposited library may be analyzed to determine certain preferred regions of the polypeptide. For example, the amino acid sequence of a polypeptide encoded by a polynucleotide sequence of SEQ ID NO:X, or the cDNA in a deposited cDNA

clone may be analyzed using the default parameters of the DNASTAR computer algorithm (DNASTAR, Inc., 1228 S. Park St., Madison, WI 53715 USA; <http://www.dnastar.com/>).

Polypeptide regions that may be routinely obtained using the DNASTAR computer algorithm include, but are not limited to, Garnier-Robson alpha-regions, beta-regions, 5 turn-regions, and coil-regions, Chou-Fasman alpha-regions, beta-regions, and turn-regions, Kyte-Doolittle hydrophilic regions and hydrophobic regions, Eisenberg alpha- and beta-amphipathic regions, Karplus-Schulz flexible regions, Emini surface-forming regions and Jameson-Wolf regions of high antigenic index. Among highly preferred polynucleotides of the invention in this regard are those that encode polypeptides comprising regions that 10 combine several structural features, such as several (e.g., 1, 2, 3 or 4) of the features set out above.

Additionally, Kyte-Doolittle hydrophilic regions and hydrophobic regions, Emini surface-forming regions, and Jameson-Wolf regions of high antigenic index (i.e., containing 15 four or more contiguous amino acids having an antigenic index of greater than or equal to 1.5, as identified using the default parameters of the Jameson-Wolf program) can routinely be used to determine polypeptide regions that exhibit a high degree of potential for antigenicity. Regions of high antigenicity are determined from data by DNASTAR analysis by choosing values which represent regions of the polypeptide which are likely to be exposed on the surface of the polypeptide in an environment in which antigen recognition may occur in the 20 process of initiation of an immune response.

Preferred polypeptide fragments of the invention are fragments comprising, or alternatively consisting of, an amino acid sequence that displays a functional activity of the polypeptide sequence of which the amino acid sequence is a fragment.

By a polypeptide demonstrating a "functional activity" is meant, a polypeptide 25 capable of displaying one or more known functional activities associated with a full-length (complete) protein of the invention. Such functional activities include, but are not limited to, biological activity, antigenicity [ability to bind (or compete with a polypeptide for binding) to an anti-polypeptide antibody], immunogenicity (ability to generate antibody which binds to a specific polypeptide of the invention), ability to form multimers with polypeptides of the 30 invention, and ability to bind to a receptor or ligand for a polypeptide.

Other preferred polypeptide fragments are biologically active fragments. Biologically active fragments are those exhibiting activity similar, but not necessarily identical, to an

activity of the polypeptide of the present invention. The biological activity of the fragments may include an improved desired activity, or a decreased undesirable activity.

In preferred embodiments, polypeptides of the invention comprise, or alternatively consist of, one, two, three, four, five or more of the antigenic fragments of the polypeptide of  
5 SEQ ID NO:Y, or portions thereof. Polynucleotides encoding these polypeptides are also encompassed by the invention.

Table 4.

Sequence/ Contig ID	Predicted Epitopes
500802	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 774 as residues: Gln-1 to Ser-17, Ser-19 to Ile-25, Leu-29 to Arg-41, Ser-46 to Glu-57.
553147	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 776 as residues: Phe-1 to Ile-20.
558860	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 777 as residues: Ser-6 to Arg-11.
561730	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 778 as residues: Asn-1 to Arg-7, Leu-28 to Pro-45.
585938	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 779 as residues: Arg-10 to Ser-23, Gln-69 to His-74.
587785	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 780 as residues: Ile-1 to Ser-11, Leu-20 to Thr-30, Cys-74 to Cys-82, Leu-94 to Glu-110.
588916	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 781 as residues: Val-43 to Pro-55, Glu-92 to Ser-99.
613825	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 782 as residues: Asn-1 to Trp-11, Ser-15 to Gln-22, Ser-43 to Ala-51, Lys-58 to Gly-66.
639090	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 783 as residues: Ser-29 to Ser-35, Pro-43 to Gly-48, Gln-60 to Ser-65.
659544	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 785 as residues: Leu-10 to Glu-15, His-19 to Glu-26.
659739	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 786 as residues: Lys-70 to His-78, Lys-149 to Asn-154, Gly-209 to Leu-217, Lys-248 to Val-255, Ile-259 to Arg-264, Arg-280 to Ala-287.
661057	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 787 as residues: Cys-59 to Arg-64, Gly-110 to Asp-115, Pro-127 to Trp-132.
661313	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 788 as residues: Glu-1 to Phe-7, Lys-42 to Leu-48.
666316	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 789 as residues: Lys-27 to Asn-52.
669229	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 790 as residues: Asp-1 to Phe-12, Val-92 to Ser-103.
670471	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 791 as residues: Lys-75 to Asp-81, Glu-145 to Gln-156, Glu-163 to Arg-170, Lys-225 to Leu-231.
676611	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 792 as residues: Tyr-4 to Lys-12, Thr-23 to Asn-31, Val-52 to Thr-63, Arg-90 to Met-95.
691240	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 793 as residues: Pro-74 to Glu-79, Ser-116 to Lys-121.
702977	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 794 as residues: Pro-8 to Tyr-20.
709517	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 795 as residues: Leu-7 to Gly-12, Cys-20 to His-27.
714730	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 796 as residues: Pro-14 to Arg-23, Ala-171 to Ser-178.
714834	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 797 as residues: Ala-6 to Gly-12, Gln-18 to Arg-32.
719584	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 799 as residues: Pro-22 to Ile-31.
724637	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 800 as residues: Val-11 to Arg-34, Asn-54 to Cys-59.
728392	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 801 as



	residues: Arg-31 to Glu-45, Glv-76 to Pro-88, Asn-143 to Asp-148.
738716	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 802 as residues: Pro-40 to Pro-46.
739056	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 803 as residues: Ser-28 to Ala-33, Pro-44 to Phe-49, Arg-113 to Gly-118, Pro-131 to Arg-142, Asp-155 to Leu-166.
739143	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 804 as residues: Ala-1 to Gly-14, Glu-21 to Gly-27, Asp-54 to Lys-59, Lys-64 to Glu-71, Gln-92 to Leu-97, Asn-114 to His-120, Leu-135 to Asp-142, Glu-149 to Ser-154, Ser-256 to Thr-261, Asp-290 to Lys-301, Glu-315 to Gln-323, Lys-331 to Asn-342, Arg-346 to Met-361.
742329	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 805 as residues: Arg-7 to Ala-13, Gln-21 to Ser-27, Gln-68 to Glv-73, Pro-75 to Val-88.
745481	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 807 as residues: Asn-1 to Lys-14, Arg-32 to His-39, Asn-46 to Gly-51.
753731	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 809 as residues: Arg-22 to Ser-39, Val-42 to Thr-54, Gln-61 to His-69.
754383	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 810 as residues: Ala-2 to Glv-12.
756749	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 811 as residues: His-1 to Thr-11, Thr-13 to Ser-18, Gly-25 to Gly-30, Pro-63 to Pro-69, Glu-84 to Tyr-101, Asn-110 to Ala-140.
757980	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 812 as residues: Phe-9 to His-21.
764818	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 813 as residues: Pro-12 to Trp-17, Asn-22 to Ala-37, Arg-45 to Gly-54, Asp-72 to Thr-95, Pro-97 to Glu-116, Gly-137 to Lys-151, Glu-164 to Asp-171, Ser-175 to Gly-185, Glu-187 to Gly-213, Lys-270 to Glu-276, Leu-281 to Lys-286, Asp-314 to Gly-321, Glu-324 to Glu-331, Val-333 to Arg-340.
765140	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 814 as residues: Thr-15 to Asp-27.
766893	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 815 as residues: Arg-6 to Leu-11, Arg-21 to Tyr-27, Phe-37 to Lys-46, Gly-59 to Glv-64.
771412	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 817 as residues: Pro-1 to His-6, Pro-37 to Arg-47.
772226	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 818 as residues: Phe-16 to Arg-30, Glu-35 to Trp-58, Lys-60 to Gln-68, Pro-80 to Tyr-85.
773057	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 819 as residues: Gly-37 to Arg-43.
773173	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 820 as residues: Pro-19 to Asn-26.
780154	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 821 as residues: Arg-20 to Ile-31, Pro-34 to Ala-59, Glu-66 to Pro-125, Leu-132 to Lys-137, Lys-155 to Arg-259.
780768	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 822 as residues: Phe-12 to Lys-17.
780779	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 823 as residues: Ser-1 to Ser-11, Gln-64 to Gln-69, Arg-117 to Arg-127.
782394	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 824 as residues: Phe-18 to Gly-24.
783160	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 825 as residues: Lys-35 to Lys-41, Thr-50 to His-56, Thr-110 to Gly-119.
783506	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 826 as residues: Thr-3 to Thr-9.
792139	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 830 as residues: Arg-1 to Thr-13, Arg-21 to Pro-30, Ser-70 to Arg-79, Asp-89 to Arg-101.

805715	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 832 as residues: Met-7 to Ala-17, Arg-26 to Leu-32, Lys-47 to Lys-52, Asn-67 to Asn-72, Val-77 to Tyr-82, Pro-101 to Arg-107, Arg-137 to Arg-146, Ser-168 to Thr-173, Asp-189 to Lys-199.
811111	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 833 as residues: His-24 to Asn-31.
811113	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 834 as residues: Gln-1 to Ala-9, Cys-56 to Gly-61, Trp-105 to Thr-110, Arg-150 to Thr-155, Leu-189 to Lys-195.
823902	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 835 as residues: Thr-18 to Glu-23.
826518	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 836 as residues: Ile-20 to Lys-26, Cys-39 to Arg-46.
826704	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 837 as residues: His-14 to Phe-20, Glu-70 to Leu-83.
828180	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 840 as residues: Glu-38 to Arg-52, Ser-56 to Val-62.
828658	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 842 as residues: Asp-1 to Pro-12, Gly-59 to Lys-64, Asp-70 to Leu-76, Pro-160 to Pro-166, Thr-174 to Asn-179.
828919	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 843 as residues: Thr-49 to Val-54, Leu-83 to Lys-91, Gly-121 to Thr-130, Asp-165 to Glu-172, Thr-180 to Gly-188.
830208	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 846 as residues: Lys-49 to Asn-56, Glu-61 to Ala-67.
830248	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 847 as residues: Pro-17 to Asp-36, Pro-102 to Glu-108, Pro-122 to Lys-128, His-150 to Gly-155, Asn-162 to Tyr-168, Pro-186 to Gln-193, Ser-205 to Pro-211, Gln-305 to Gly-317.
830275	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 848 as residues: Ser-16 to Glu-22, Asn-45 to Ser-50, Thr-121 to Gly-136, Lys-150 to Arg-157, Ser-175 to Cys-181, Glu-198 to Ser-203.
830286	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 849 as residues: His-11 to Pro-18, Thr-241 to Thr-258, Ala-352 to Ala-365.
830347	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 850 as residues: Asp-33 to Ala-39.
830348	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 851 as residues: Gln-5 to Arg-15, Ile-96 to Asn-101, Asp-122 to Gly-128.
830364	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 852 as residues: Val-76 to Asn-82, Lys-87 to Tyr-94, Glu-118 to Gln-125, Pro-140 to Ile-145, Gly-149 to Pro-173, Ala-215 to Lys-222, Lys-230 to Gly-235, Pro-250 to Asn-256, Ser-302 to Arg-307, Ser-321 to Glu-332.
830394	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 853 as residues: Thr-37 to Thr-44, Leu-57 to Ser-63, Ser-74 to Lys-86, Gln-107 to Leu-112, Lys-140 to Ala-145, Asp-154 to Ser-163.
830412	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 855 as residues: His-65 to Gly-74, Asp-85 to Ser-97, Leu-133 to Glu-138, Glu-144 to Asp-153, Arg-170 to Ser-175, Gly-184 to Arg-189, Gln-202 to Tyr-208.
830464	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 857 as residues: Val-3 to Val-11, Gln-16 to Gln-27, Glu-41 to Asp-51.
830471	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 858 as residues: Glu-10 to His-22, Ser-37 to Lys-45.
830477	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 859 as residues: Lys-1 to Cys-13, Thr-32 to Cys-37, Ser-44 to Glu-50, Glu-57 to Asn-64, Glu-85 to Glu-93, Ala-129 to Ser-139, Gln-157 to Thr-185, Gln-199 to Gly-215, Ile-241 to Leu-247, Asp-254 to Leu-263, Gln-265 to Gln-270, Glu-298 to Gln-309, Glu-316 to Ala-321, Leu-325 to Glu-334, Glu-340 to Ser-345, Leu-348 to His-367, Lys-384 to Arg-391.

	Leu-409 to Asn-417, Arg-431 to Arg-437, Phe-441 to Leu-448, Ala-456 to Glu-484, Lys-509 to Val-519, Glu-521 to Asp-528, Asp-546 to Phe-553, Glu-558 to Phe-567, Pro-573 to Thr-588.
830500	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 860 as residues: Gln-27 to Gly-34.
830509	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 861 as residues: Pro-2 to Asp-7, Gln-13 to Gln-29, Pro-35 to Trp-41.
830528	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 862 as residues: Gln-1 to Arg-12, Asp-22 to Pro-44, Lys-52 to Asp-62, Pro-68 to Lys-93, Pro-99 to Pro-129, Ala-138 to Ser-150, Lys-156 to Val-194, Ile-197 to Glu-210, Ala-213 to Ala-287, Leu-289 to Lys-327, Lys-330 to Gly-340, Asp-344 to Gln-360, Ile-396 to Thr-401, Lys-409 to Asp-418, Met-450 to Ala-460, Glu-468 to Gly-475.
830542	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 863 as residues: Val-1 to Gly-10, Arg-24 to Asp-36, Leu-225 to Trp-231, Val-249 to Met-258, Glu-262 to Thr-269, Val-279 to Gly-284, Asp-307 to Asn-313, Arg-411 to Lys-416.
830564	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 864 as residues: Trp-103 to Glu-113, Lys-118 to Tyr-125.
830611	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 865 as residues: Glu-51 to Ser-57, Arg-128 to Ala-133.
830620	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 867 as residues: Lys-54 to Arg-59, Arg-66 to Arg-71.
830630	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 868 as residues: Pro-12 to Gly-17.
830654	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 869 as residues: Leu-1 to Asp-6.
830660	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 870 as residues: Lys-111 to Trp-116, Glu-139 to Gly-148, Arg-182 to Ser-189.
830704	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 872 as residues: Asn-1 to Glu-8, Ala-38 to Gly-46, Gln-58 to Asp-71, Ala-75 to Cys-103, Met-106 to Ala-140, Gln-153 to Ile-159.
830765	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 873 as residues: Ser-19 to Thr-26, Pro-47 to Thr-59.
830778	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 874 as residues: Asp-35 to Gly-40, Glu-104 to Glu-109, Ser-226 to Tyr-231.
830784	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 875 as residues: Pro-34 to Leu-41.
830800	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 876 as residues: Ser-16 to Lys-24, Gly-91 to Thr-96.
830821	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 877 as residues: Leu-2 to Thr-8, Asp-15 to Gly-26, Phe-64 to Ser-70, Pro-77 to Trp-82, Pro-85 to Lys-90.
830849	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 878 as residues: Leu-2 to Ser-18, Gly-31 to Ser-40, Asn-56 to Thr-86, Asp-114 to Arg-120.
830903	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 879 as residues: Thr-21 to Thr-33.
830913	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 880 as residues: Gly-48 to Pro-53, Gln-66 to Pro-74, Thr-151 to Gly-156, Asn-292 to Asn-297.
830920	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 881 as residues: Asp-15 to Ser-25, Ser-33 to Val-38, Lys-181 to Phe-187.
830938	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 882 as residues: Thr-65 to Asp-70, Leu-89 to Ala-95.
831014	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 884 as residues: Ala-2 to Gln-11, Glu-71 to Leu-78, Leu-89 to Trp-98, Ser-163 to Ala-170, Glu-261 to Asp-269, Phe-286 to Val-292.
831026	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 885 as residues: Lys-41 to Gly-46, Tyr-64 to Phe-75.

831055	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 887 as residues: Trp-37 to His-50, Lys-108 to Phe-114, Lys-131 to Thr-137, Arg-351 to Ser-356, Pro-363 to Cys-369, Glu-390 to Asp-397.
831057	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 888 as residues: Arg-1 to Gly-14, Thr-19 to Gly-25, Ala-31 to Ala-41, Glu-53 to Ile-62, Val-66 to Glu-75, Ser-103 to Asp-113, Ala-135 to Asp-140.
831062	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 889 as residues: Ser-24 to Ala-31.
831117	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 890 as residues: Lys-50 to Tyr-55.
831122	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 891 as residues: Phe-8 to Gly-14, Arg-58 to Gly-68, Lys-107 to Ser-131, Gln-151 to Val-160, Lys-180 to Lys-186, Lys-211 to Thr-223.
831132	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 893 as residues: Gly-1 to Ser-16.
831152	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 894 as residues: Ser-8 to Arg-13, Lys-59 to Ala-65, Glu-71 to Glu-86, Leu-98 to His-108, Arg-118 to Ile-126, His-138 to Ala-145, Pro-148 to Tyr-156, Pro-170 to Ala-175, Val-187 to Lys-194, Glu-206 to Val-217, Gly-221 to Ser-226, Asp-250 to Lys-255.
831157	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 895 as residues: Val-1 to Asn-11, Glu-13 to Gly-25, Ser-31 to Ala-49, Arg-61 to Gly-66, Ala-84 to Ala-90.
831160	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 896 as residues: His-1 to Ala-7, Asp-43 to Lys-52, Tyr-98 to Gly-103, Glu-118 to Leu-125, Phe-183 to Tyr-195, Gln-209 to Arg-220, Ile-257 to Gly-262, Glu-278 to Thr-284, Ile-309 to Pro-314, Leu-339 to Asp-347, Ala-358 to Gln-388, Gln-401 to Leu-414, Glu-425 to Ala-440, Ala-448 to Glu-453, Ile-460 to Gln-465, Glu-482 to Glu-492, Ala-498 to Glu-511, Pro-520 to Val-526, Gly-556 to Gln-577, Leu-587 to His-598, Glu-605 to Asp-630.
831197	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 898 as residues: Ser-28 to Leu-39, Phe-48 to Phe-55, Pro-60 to Gln-66, Arg-73 to Thr-78.
831217	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 899 as residues: Asp-52 to Val-63, Asn-75 to Glu-83.
831248	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 901 as residues: Pro-24 to Gly-34, Lys-108 to Arg-118.
831369	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 903 as residues: Ala-1 to Gly-8.
831371	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 904 as residues: Arg-39 to Ser-44, Arg-66 to Arg-76.
831373	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 905 as residues: Gly-7 to Ser-13, Gln-40 to Trp-45, Lys-109 to Gly-116, Gly-134 to Arg-141, Arg-149 to Arg-164, Arg-174 to Phe-181, Lys-202 to Lys-210, Glu-263 to Leu-272, Pro-274 to Leu-280, Glu-289 to Glu-296, Pro-334 to His-341, Tyr-413 to Pro-426, Glu-432 to Lys-449.
831387	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 906 as residues: Tyr-21 to Leu-28, Cys-51 to Phe-72, Ser-107 to Leu-113, Leu-125 to Leu-134, Ser-142 to Ala-152, His-159 to Tyr-164, Arg-276 to Val-290.
831410	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 907 as residues: Arg-7 to Lys-13, Pro-28 to Cys-34, Gly-100 to Asn-109, Cys-155 to Arg-162.
831448	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 908 as residues: Ala-10 to Cys-20, Tyr-36 to Lys-41, Asp-68 to Ala-75, Ala-84 to Arg-89, Glu-112 to Ser-119.
831450	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 909 as residues: Pro-23 to Gly-28, Thr-52 to Pro-63.
831472	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 910 as residues: Ser-16 to Ala-26.

831473	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 911 as residues: Arg-37 to Gln-42, Asn-59 to Asn-65, Asn-109 to Val-121, Arg-191 to Glu-199, Lys-205 to Ile-214.
831474	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 912 as residues: Glu-1 to Leu-8, Ser-50 to Arg-56, Thr-61 to Arg-66, Val-69 to Arg-82.
831494	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 913 as residues: Arg-21 to Ser-27, Arg-77 to Asp-82, Glu-116 to Ile-134, Ser-139 to Ser-162, Leu-167 to Gly-190, Cys-192 to Gly-205.
831506	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 914 as residues: Val-6 to Tyr-12, Lys-77 to Ala-82, Ser-102 to Arg-108, Ser-145 to Ser-151.
831533	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 915 as residues: Thr-9 to Cys-16, Arg-52 to Tyr-57, Ser-61 to Ser-69.
831539	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 916 as residues: Thr-32 to Arg-39, Cys-44 to Arg-60, Lys-65 to Gln-70, Gly-78 to Ile-86, Lys-126 to Thr-134, Leu-140 to Glu-148.
831556	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 917 as residues: Gly-45 to Asp-52.
831598	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 919 as residues: Asn-1 to Val-6, Phe-76 to Tyr-83, Gly-129 to Gln-135, Thr-145 to Asp-153, Pro-213 to Gln-220, Thr-230 to Asn-236, Lys-242 to Ala-248.
831608	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 920 as residues: Thr-23 to Pro-34, Glu-39 to Asp-83, Asn-89 to Lys-99, Asp-118 to Asp-128, Asn-135 to Glu-150, Glu-153 to Gly-168, Gly-181 to Thr-187, Arg-200 to Asp-205, Arg-273 to Ile-279, Thr-295 to Asp-300, Thr-316 to Cys-321.
831613	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 921 as residues: Pro-1 to Glu-7, Arg-9 to Phe-15, Thr-27 to Gly-34.
831655	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 926 as residues: Tyr-31 to Gln-38.
831708	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 927 as residues: Glu-22 to Ile-27, Gly-43 to Gly-49, His-83 to Arg-105.
831741	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 929 as residues: Asp-22 to Asp-27, Pro-64 to Gln-74, Ser-126 to Gly-131, Lys-134 to Arg-143, Arg-150 to Gly-162, Gln-180 to Tyr-196, Asp-209 to Leu-224, Gly-233 to Gly-241, Pro-246 to Arg-251.
831754	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 930 as residues: Arg-40 to Glu-50, Gly-57 to Gly-68, Phe-72 to Tyr-79.
831760	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 931 as residues: His-24 to Asp-39.
831780	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 932 as residues: Arg-92 to Thr-101.
831796	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 933 as residues: Pro-1 to Ser-8.
831800	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 934 as residues: Asp-1 to Ser-6, Glu-16 to Ser-26, Lys-66 to Pro-76, Leu-93 to Arg-99, Val-153 to Lys-164, Glu-177 to Asp-183, Ser-188 to Leu-193, Arg-210 to Ser-220, Thr-229 to Ser-244, Pro-283 to Phe-297.
831813	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 937 as residues: Pro-20 to Ala-30.
831830	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 938 as residues: Arg-12 to Lys-17, Gln-51 to Phe-60, Asp-97 to Trp-102, Glu-132 to Cys-137, Asp-160 to Leu-168, Glu-210 to Gln-219, Lys-302 to Pro-308, Phe-416 to Asp-421, Leu-444 to Leu-449, Val-457 to Asn-464, Leu-466 to Trp-472, Ile-474 to Trp-480, Ser-527 to Ser-533, Pro-558 to Phe-565, Ile-578 to Trp-584, Asp-614 to Asp-627, Asn-698 to Asp-710, Pro-738 to Ser-744.
831860	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 939 as residues: Pro-19 to Tyr-25.

831896	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 941 as residues: Ser-18 to Phe-30, Leu-34 to Asn-41, Ala-48 to Tyr-56, Leu-103 to Ala-110, Asp-124 to Val-130, Ile-141 to Leu-150, Leu-188 to Ser-196, Glu-229 to Asn-238, Thr-248 to Cys-259.
831928	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 942 as residues: Asn-55 to Asp-60.
831949	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 943 as residues: Arg-1 to Glu-9, Glu-19 to Arg-32, Ala-77 to Thr-90, Thr-95 to Thr-104, Lys-106 to Ser-119, Leu-136 to Arg-141, Tyr-165 to Asn-174.
831950	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 944 as residues: Ser-18 to Glu-26, Phe-93 to Arg-102, Leu-137 to Gln-143, Pro-148 to Glv-157.
831975	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 946 as residues: His-41 to Thr-48.
832047	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 948 as residues: Arg-57 to Glu-62, Pro-73 to Gly-80.
832078	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 949 as residues: Pro-14 to Leu-21, Cys-34 to Gly-39.
832100	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 950 as residues: Tyr-37 to Val-45.
832104	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 951 as residues: Thr-1 to Ser-6, Arg-14 to Cys-20.
832279	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 954 as residues: Ser-28 to Pro-34, Pro-134 to Ser-139, Gln-178 to Gly-183, Thr-193 to Gly-198, His-244 to Gly-257, Asp-263 to Tyr-273, Lys-337 to Arg-347, Pro-366 to Lys-372, Ala-382 to Asp-387.
832317	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 955 as residues: Thr-32 to Gln-39, Asn-58 to Trp-71, Glu-96 to Trp-108, Cys-126 to Glv-133.
832364	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 957 as residues: Glu-2 to Met-9, Asp-17 to Asn-22, Leu-27 to Val-35.
832428	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 960 as residues: Arg-35 to Glv-41.
832485	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 961 as residues: Ser-121 to Cys-127.
832494	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 962 as residues: Ser-10 to Leu-28, Ser-31 to Asp-40, Ser-55 to Thr-62, Thr-94 to Asn-102, Asp-124 to Phe-135, Asn-175 to Lys-193, Glu-238 to Leu-243, Val-250 to Ala-259, Lys-291 to Asn-308, Ser-318 to Gly-327, Lys-335 to Asp-346, Tyr-404 to Ile-410, Gln-420 to Gln-430, Thr-476 to Phe-482, Pro-536 to Val-561, Tyr-563 to Leu-568.
832512	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 963 as residues: Arg-1 to Ala-7, Leu-9 to Ser-24, Glu-32 to Asp-43, Glu-71 to Glu-86, Val-92 to Ile-104, Asp-143 to Ser-154, Lys-190 to Glu-202, Glu-218 to Lys-241.
832515	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 964 as residues: Glu-3 to Gly-12, Arg-20 to Gln-30, Leu-34 to Gln-39, Asp-51 to Arg-58, Gln-69 to Val-77, Gly-105 to Lys-117, Cys-123 to Phe-132.
832526	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 965 as residues: Pro-15 to Asn-25, Glu-48 to Phe-59.
832575	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 966 as residues: Thr-24 to Arg-29, Ala-55 to Tyr-60, Tyr-77 to Asp-89, Leu-108 to Gly-115, Thr-142 to Gly-149.
832576	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 967 as residues: Arg-1 to Leu-11, Pro-21 to Gly-28, Pro-37 to His-47, Lys-79 to Gln-88, Pro-108 to Glv-116, Pro-179 to Thr-188, Arg-207 to Asn-213.
832634	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 969 as residues: Leu-2 to Ser-12, Pro-125 to Asp-133.
832728	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 970 as residues: Gln-16 to Glv-32, Leu-100 to Gly-106, Glv-118 to Lys-132, Pro-156 to Leu-

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833395	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 972 as residues: Ser-3 to Gly-9.
834326	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 973 as residues: Ser-1 to Trp-19, Asn-148 to Leu-153, Tyr-235 to Trp-244.
834944	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 975 as residues: Glu-42 to Gln-51, Pro-115 to Asp-120, Arg-127 to Gly-133, Gln-199 to Gln-211.
835104	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 977 as residues: Thr-1 to Arg-14, Val-18 to Pro-23, Thr-37 to Met-44, Gln-51 to Leu-57.
835332	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 978 as residues: Thr-1 to Glu-13, Arg-135 to Asp-142, Thr-150 to Gln-155, Cys-173 to Cys-183, Cys-203 to Asp-214.
835487	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 979 as residues: Ala-13 to Arg-22, Pro-43 to Glu-57, Ala-73 to Pro-90, Arg-102 to Ser-109, Pro-114 to Gly-122, Arg-127 to Arg-138, Glu-153 to Gly-158, Pro-165 to Pro-171, Gly-185 to Arg-190, Pro-211 to Pro-216, Glu-231 to Asn-261, Ala-280 to Pro-291, Pro-303 to Gly-311, Arg-313 to Gly-326, Ala-358 to Ala-364, Pro-369 to Gly-377, Pro-390 to Gly-407, Tyr-420 to Tyr-441, Glu-461 to Thr-470, Pro-479 to Trp-487, Asp-489 to Cys-494, Gln-515 to Lys-532, Ala-572 to Asn-582, Asp-588 to Leu-594, Cys-625 to Trp-632, Tyr-639 to Arg-646.
836182	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 980 as residues: Ala-7 to Thr-17, Arg-31 to Thr-36.
836522	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 981 as residues: Gly-59 to Cys-65.
836789	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 984 as residues: Gly-18 to Gly-25, Glu-59 to Glu-64.
838577	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 985 as residues: Pro-15 to Trp-20, Pro-46 to Gln-57, Glu-68 to Phe-83.
839008	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 987 as residues: Arg-1 to Arg-13, Gln-125 to Glu-131, Asn-137 to Val-142, Gly-183 to Tyr-188, Asn-245 to Ser-251, Gln-302 to Asn-311.
840063	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 988 as residues: Gly-1 to Gly-31.
840533	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 989 as residues: Thr-16 to Pro-23, Pro-39 to Trp-48, Arg-50 to Lys-55, Gly-73 to Gly-79.
840669	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 990 as residues: Met-27 to Gln-33, Gln-49 to Gly-56, Thr-63 to Leu-70, Thr-115 to Arg-127, Pro-174 to Asn-184.
841140	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 991 as residues: Arg-17 to Phe-24, Pro-113 to Gly-121, Thr-235 to Met-240.
841386	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 992 as residues: Val-58 to Met-66, Pro-134 to Lys-143, Tyr-163 to Ala-170, Val-178 to Lys-187, Pro-207 to Gly-212.
841900	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 996 as residues: Ile-2 to Phe-12.
842054	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 997 as residues: Asp-27 to Trp-32, Pro-89 to Glu-99, Arg-112 to Lys-123.
843061	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 998 as residues: Leu-3 to Gly-18, His-36 to His-57, Lys-136 to Leu-145, Gly-174 to Trp-184, Lys-188 to Tyr-196, Lys-204 to Asp-211, Pro-293 to Ser-305, Glu-321 to Asp-333, Gly-342 to Lys-348, Ala-371 to Asp-377, Asp-439 to Leu-449, Ala-521 to Gly-529, Tyr-583 to Trp-599, Asn-639 to Ser-644, Leu-738 to Leu-745.
843544	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 999 as residues: Tyr-11 to Phe-18, Ser-34 to Lys-43.
844092	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1000 as

	residues: Gln-1 to Lys-6, Glu-30 to Glu-37, Glu-40 to Thr-53.
844270	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1001 as residues: Thr-10 to Glu-20, Pro-44 to Thr-50.
844604	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1002 as residues: Gly-8 to Phe-20, Pro-23 to Arg-43, Asp-62 to Asp-67, Pro-73 to Asn-80, Val-83 to Phe-95, Glu-103 to Ile-109, Tyr-120 to Ala-125, Thr-176 to Thr-183, Pro-200 to Pro-214, Pro-232 to Met-240, Gln-248 to Asp-292, Arg-297 to Ser-310, Pro-320 to Glu-332, Glu-347 to Ser-390, Ala-392 to Pro-404, Pro-425 to Gly-435, Pro-438 to Gly-443, Gly-467 to Pro-480, Pro-486 to Pro-499, Pro-506 to Met-512, Pro-572 to Glu-580, Arg-592 to Gly-597, Ala-601 to Ser-610, Ala-618 to Pro-623.
844685	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1003 as residues: Ser-14 to Ser-19, Pro-25 to Gly-32, Asn-98 to Lys-108.
844855	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1004 as residues: Ala-9 to Ser-15, Pro-21 to Arg-26.
845101	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1005 as residues: Ala-2 to Gly-13, Pro-31 to Pro-42, Gln-89 to Tyr-95, Gln-169 to Leu-189.
845141	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1006 as residues: Gly-13 to Met-26, Arg-34 to Gly-39, Ile-60 to Ser-80, Ala-85 to Thr-98.
845220	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1007 as residues: Pro-14 to Gly-24, Glu-33 to Ala-39, Asp-145 to Pro-168, Ala-238 to Arg-250, Pro-258 to Phe-269, Arg-285 to Pro-290, Ala-340 to Cys-364.
845434	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1008 as residues: Ala-1 to Glu-7, Gln-29 to Phe-34, Gly-67 to Ala-75, Gln-78 to Leu-83, Asn-96 to Ile-109, Thr-144 to Trp-151.
845510	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1009 as residues: Arg-79 to Leu-86, Met-114 to Asp-122, Leu-129 to Leu-134, Gln-145 to Arg-152.
845600	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1010 as residues: Ala-22 to Phe-28.
845882	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1011 as residues: Ala-1 to Gly-7, Arg-29 to Lys-35, Lys-72 to Ala-79, Leu-94 to Val-101, Gly-137 to Asn-142, Arg-145 to Leu-150, Gly-180 to Lys-187, Glu-194 to Gly-208, Arg-257 to Ser-267, Ser-278 to Asp-290, Gly-312 to Ser-319, Leu-338 to Lys-351, Tyr-358 to Ser-363.
846007	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1012 as residues: Tyr-16 to Ala-24, Arg-59 to Ser-66, Thr-78 to Glu-83, Glu-90 to Ser-103, Gln-108 to Thr-113, Ser-115 to Cys-124.
HCRNG17R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1016 as residues: Pro-16 to Asp-21.
HWMFG64R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1017 as residues: Ser-70 to Asp-76, Lys-87 to Leu-95.
HAGCZ94R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1018 as residues: Val-3 to Lys-9.
HBJEJ74R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1019 as residues: Pro-1 to Asp-8.
HUTHM43R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1021 as residues: Pro-7 to Arg-15.
HLTGU75R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1022 as residues: Ser-1 to Gly-11.
HWLKF77R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1023 as residues: Leu-10 to Asn-28.
HWLGX29R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1027 as residues: Val-3 to Ile-10, Pro-34 to Gln-40.
HWMFZ29R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1028 as residues: Leu-7 to Leu-13.
H6EEP19R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1030 as



	residues: Ala-1 to Trp-8, Lys-10 to Asp-27.
HJMAM83R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1031 as residues: Ser-1 to Val-11, Glu-19 to Ala-29, Asp-52 to Ala-68, Gly-78 to Lys-94.
HAGHF58R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1032 as residues: Lys-1 to Val-7.
HDPHG48R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1033 as residues: Gly-24 to Lys-34.
HCDMC32R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1038 as residues: Pro-2 to Arg-17, Lys-36 to Pro-47, Phe-61 to Trp-68, Gln-72 to Ala-86.
HTEQO80R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1040 as residues: Gly-1 to Val-15, Pro-17 to Pro-23, Leu-32 to Met-41, Lys-102 to His-109.
H2LAR08R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1043 as residues: Asn-58 to Gly-64.
HWMFN58R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1046 as residues: Glu-6 to Asn-14, Arg-22 to Asp-31, Gly-49 to Thr-56.
HUFBP63R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1049 as residues: Pro-1 to Gln-8, Thr-57 to Gly-64, Arg-69 to Arg-74, Gly-80 to Asp-91, Asp-105 to Gln-110, Arg-130 to Tyr-148.
HUFBN90R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1050 as residues: Glu-34 to Ala-40, Arg-111 to Ala-116.
HFKHD61R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1054 as residues: Arg-11 to Gly-38, Arg-44 to Glu-50, Gln-53 to Lys-67.
HTXNL13R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1057 as residues: Ser-48 to Arg-57, Glu-89 to Pro-95, Ser-102 to Asn-107.
H2LAK62R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1059 as residues: Pro-20 to Ser-25.
HATAR77R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1061 as residues: Gly-2 to Arg-16.
HWMEH18R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1066 as residues: Gln-61 to Ser-67.
HCNDP66R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1068 as residues: Leu-8 to Arg-15, Gln-46 to Pro-54.
HCRMK82R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1069 as residues: Ser-32 to Arg-38, Ala-72 to Lys-79, Arg-103 to Phe-111.
HSSGC52R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1075 as residues: Gly-1 to Pro-6, Arg-25 to Ile-30.
HCYBN49R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1076 as residues: Gly-16 to Gly-21, Ile-99 to Gln-109.
HWMGB90R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1077 as residues: Gly-1 to Ala-7, Asp-17 to Arg-27, Glu-32 to Leu-40.
HTEAW21R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1078 as residues: Glu-1 to Gly-6, Gln-19 to Leu-37.
H2LAQ68R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1082 as residues: Val-2 to Trp-10, Leu-25 to Lys-33.
HBAAD60R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1087 as residues: Pro-1 to Lys-32.
HCROA35R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1088 as residues: Gly-6 to Lys-12.
HCROM64R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1089 as residues: Asn-1 to Arg-7.
HKBAG82R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1091 as residues: Pro-9 to Gly-28.
HUTSB76R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1092 as residues: Lys-1 to Ser-17.
HWLJS67R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1093 as residues: Gln-3 to Lys-18, Gln-44 to Glu-49.

HTGAZ53R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1098 as residues: Ser-1 to Ala-16, Gln-36 to Thr-48.
HWLL51R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1100 as residues: Gln-6 to Glu-18.
HWLJZ72R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1103 as residues: Ile-1 to Ser-19.
HWMFG06R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1104 as residues: Arg-1 to Lys-14, Gln-40 to Glu-45, Arg-65 to Arg-80.
HPRT065R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1105 as residues: Thr-12 to Thr-17, Cys-35 to Ser-40.
HUFDC01R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1106 as residues: Pro-11 to Glu-26.
HWLHY44R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1107 as residues: Pro-14 to Gln-24, Cys-34 to Leu-39, Thr-72 to Val-77, Glu-94 to Thr-99, Asp-101 to Met-107, Lys-109 to Pro-116.
HWLGR92R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1108 as residues: Pro-17 to Gly-22.
HCNCQ71R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1109 as residues: Glu-22 to Leu-30.
HWLEN11R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1111 as residues: Pro-6 to Lys-21, Ala-26 to Val-34, Lys-37 to Ser-46.
HWLEH56R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1116 as residues: Thr-23 to Ala-28, Asn-88 to Trp-98, Cys-114 to Asp-131.
H2LAD26R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1117 as residues: Pro-20 to Gly-31.
H2LAK66R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1125 as residues: Pro-33 to Leu-39, Glu-54 to Val-59, Gly-69 to Ser-76.
HSDKC65R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1126 as residues: Asn-32 to Pro-39, Pro-41 to Pro-49.
H2LAK52R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1127 as residues: Pro-20 to Ala-28.
HKAEG12R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1128 as residues: Asp-47 to Lys-52.
HKADP43R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1129 as residues: Pro-7 to Pro-15, Arg-35 to Val-44.
HUSJE17R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1131 as residues: Pro-26 to Gln-32.
HHBEF06R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1133 as residues: Pro-1 to Gly-6.
HISCW28R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1134 as residues: Pro-26 to Gln-32.
HPIAK29R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1137 as residues: Thr-1 to Tyr-7.
HUFAR71R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1138 as residues: Pro-26 to Gln-32.
HOEC121R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1141 as residues: Asn-11 to Pro-20, Pro-22 to Thr-30, Glu-49 to Glu-70, Ser-84 to Thr-96, Thr-108 to Thr-113.
HMCAR63R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1143 as residues: Ala-1 to Gly-9, Lys-41 to Glu-47, Asn-65 to Gly-70, Glu-85 to Asp-93, Glu-103 to Tyr-109.
HAICY55R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1152 as residues: Glu-2 to His-9.
HWLIA38R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1153 as residues: Arg-60 to Gly-74, Ser-80 to Ile-88, Leu-92 to Ser-98.
HBXCL69R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1154 as

	residues: Ser-2 to Cys-8, Pro-10 to Leu-17.
H2LAP90R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1155 as residues: Thr-3 to Gln-9, Asn-11 to Pro-19, Gln-35 to Glu-42.
HTELE03R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1157 as residues: Asp-1 to Gln-9, Asn-11 to Arg-16, Cys-28 to Ser-44, Gln-50 to Gln-56.
HJMBN86R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1158 as residues: Ser-31 to Glu-47.
HSKJC32R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1159 as residues: Gln-151 to Glu-158, Glu-168 to Pro-173, Ser-188 to Ile-195.
HAOAG76R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1161 as residues: Gly-1 to Ala-14.
HCIAD45R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1162 as residues: Pro-1 to Lys-23, Pro-43 to Leu-49.
H2MAC82R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1163 as residues: Lys-54 to Lys-59.
H2LAJ41R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1164 as residues: Met-20 to Val-36, Ser-82 to Lys-93, Pro-101 to Arg-106.
HBJFH33R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1166 as residues: Gly-10 to Tyr-26, Asn-29 to Leu-37, Thr-52 to His-59.
HISDV92R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1167 as residues: Pro-3 to Ser-8, Asn-48 to Tyr-54.
HE9QB35R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1169 as residues: Gly-1 to Asp-6, Pro-20 to Gln-33, Tyr-46 to Arg-52, Asn-72 to Lys-85, Gln-91 to Ala-110.
HDABQ50R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1170 as residues: Ser-9 to Lys-17, Lys-41 to Arg-46.
HTPAC28R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1176 as residues: Lys-10 to Thr-15, Thr-17 to Leu-23.
HMCQN07R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1177 as residues: Asn-88 to Ser-98, Pro-123 to Val-129.
HBMVM66R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1180 as residues: Ser-2 to Gly-7, Arg-10 to Phe-24, Ala-36 to Arg-41.
HEPNA09R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1186 as residues: Ser-1 to Pro-6.
HCNDR62R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1190 as residues: Pro-14 to Ser-21.
HNJBF13R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1191 as residues: Asp-18 to Asp-28.
HLYCD69R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1192 as residues: Gly-90 to Thr-109.
HWCAAS3R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1194 as residues: Ser-22 to Gly-28, Glu-37 to Ile-45, Val-67 to Arg-85, Asn-91 to Trp-99.
HFVGP11R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1198 as residues: Ala-4 to Asn-13.
HWLQH07R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1199 as residues: Lys-1 to Lys-25.
HWLKH07R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1201 as residues: Pro-49 to Asp-58.
HAPQC14R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1202 as residues: Lys-1 to Met-8.
HSODB48R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1203 as residues: Ser-24 to Glu-31, Ala-37 to Ser-44, Pro-57 to Ser-64, Pro-97 to Gly-104.
HBEAC75R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1204 as residues: Pro-1 to Arg-9.
HBGMJ24R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1205 as residues: Tyr-11 to Val-17, Thr-30 to Phe-48, Gln-150 to Thr-155.

HBJEN94R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1206 as residues: Gln-1 to Asn-6.
HLQGB87R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1213 as residues: Lys-2 to Ser-7.
HAOAC69R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1215 as residues: Ser-2 to Arg-10.
HWLEQ08R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1216 as residues: Glu-21 to His-31.
HKAAY70R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1217 as residues: Gly-6 to Thr-93, Glu-95 to Glu-104, Asp-117 to Asp-125.
HNFJE41R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1221 as residues: Arg-15 to His-21, Pro-48 to Ala-58, Asn-61 to Leu-66, Val-92 to Thr-110, Pro-114 to Thr-120.
HCRMW41R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1224 as residues: Phe-14 to Asn-19.
HOVAX78R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1225 as residues: Gly-1 to Thr-8.
HWAEH57R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1226 as residues: Ser-54 to Tyr-60, Gln-65 to Pro-72, Thr-81 to Gly-92.
HAHEK76R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1230 as residues: Cys-20 to Cys-28.
HOSCG81R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1232 as residues: Thr-8 to Asn-13.
HTFMD43R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1233 as residues: Lys-44 to Ile-52, Arg-57 to Lys-77.
H2LAR73R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1235 as residues: Pro-20 to Arg-27, Asn-47 to Lys-53, Asp-116 to Asn-123, Glu-145 to Gly-154.
HWHPK71R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1238 as residues: Asp-15 to His-24, Pro-27 to Leu-39.
HWBBJ39R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1239 as residues: His-1 to Lys-6.
HSODD94R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1241 as residues: Gly-7 to Glu-15, Gly-29 to Lys-41, Pro-43 to Ser-52, Pro-68 to His-73.
HMIAG25R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1242 as residues: Arg-19 to Ser-41, Pro-43 to Glu-54, Ser-59 to Gly-74.
HCNDW17R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1244 as residues: Lys-7 to Lys-15, Thr-54 to Asn-59.
HWLEY08R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1245 as residues: Glu-9 to Arg-14, Thr-19 to Arg-27, Asp-48 to Ile-57, Gln-63 to Leu-75, Cys-89 to Thr-104, Gly-106 to Pro-113.
HULFN68R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1246 as residues: Ser-1 to Cys-16, Lys-18 to Gly-23, Pro-31 to Tyr-37, Gly-53 to Pro-58.
HTEJJ32R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1249 as residues: Ser-17 to Cys-23, Gln-42 to Leu-51, Ser-68 to Asp-73.
H2CBS58R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1251 as residues: Ser-82 to Phe-88, Lys-110 to Gly-118.
H2LAB77R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1252 as residues: Met-13 to Asp-18, Glu-23 to Ser-43, Glu-45 to Gly-54.
HWAFP88R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1254 as residues: Arg-8 to Lys-13, Gly-35 to Lys-42, Ala-48 to Lys-54.
HWMEB67R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1256 as residues: Arg-9 to Arg-16.
HKMAA52R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1261 as residues: Gly-2 to Lys-10, Asp-36 to Asn-42.
H2LAB37R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1262 as residues: Glu-52 to Thr-59.

H2LAP46R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1263 as residues: Pro-40 to Asn-46, Tyr-71 to Arg-79.
H6BSE61R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1264 as residues: Ile-36 to Asp-41, Ala-54 to Pro-63.
HACBS75R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1269 as residues: Arg-20 to Ser-27, Arg-45 to Trp-59.
HACCA48R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1270 as residues: Lys-12 to Lys-26.
HACCS19R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1271 as residues: Gly-1 to Gly-10.
HAGGL96R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1273 as residues: Ser-74 to Phe-88.
HAGGT37R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1274 as residues: Phe-17 to Pro-22.
HAHDR66R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1275 as residues: Gly-11 to Ala-18.
HAJCL80R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1277 as residues: Asn-22 to Phe-32.
HAQMH45R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1283 as residues: Pro-2 to Tyr-13, Leu-21 to Gly-47, Val-49 to Gly-55, Pro-63 to Glu-78.
HBGCA44R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1290 as residues: Thr-20 to Trp-25, Lys-32 to Leu-40.
HBGFX27R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1291 as residues: Ser-1 to Pro-6.
HBGMU38R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1292 as residues: Gln-1 to Phe-8, Thr-34 to Trp-53, Arg-56 to Gly-63, Arg-86 to Cys-102.
HBJED55R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1295 as residues: Arg-6 to Pro-14.
HBMTJ51R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1300 as residues: Cys-8 to Asp-13.
HBWBD78R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1302 as residues: Pro-51 to Ala-58.
HCDDQ63R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1307 as residues: Gln-1 to Lys-10.
HCFC01R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1310 as residues: Ser-1 to Thr-6.
HCFCR43R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1311 as residues: Arg-10 to Thr-20.
HCHAO92R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1313 as residues: Asn-19 to Arg-25.
HCHOH49R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1314 as residues: Asn-19 to Asp-30.
HCHPG05R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1315 as residues: Pro-6 to Ser-11.
HCIAD24R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1316 as residues: Lys-1 to Gly-7.
HCNCY51R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1319 as residues: Lys-10 to Arg-16.
HCNCY63R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1320 as residues: Gly-1 to Lys-9.
HCNDO71R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1321 as residues: Lys-33 to Ile-42, Arg-51 to Phe-64.
HCQBN22R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1324 as residues: Lys-1 to Asn-11.
HCQCL27R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1325 as residues: Gly-7 to His-27.

HCQCL48R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1326 as residues: Ala-1 to Thr-13.
HCQDJ42R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1330 as residues: Glu-8 to Asn-13, Arg-16 to Glu-24.
HCRMD77R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1331 as residues: Asn-4 to Asn-10.
HCROJ68R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1339 as residues: Ile-2 to His-8.
HCROM30R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1342 as residues: Glu-1 to Glu-7, Pro-26 to Leu-32, Gly-37 to Gln-44, Thr-84 to Thr-92.
HCROQ34R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1343 as residues: Asn-1 to Asp-11.
HCROZ66R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1345 as residues: Arg-7 to Lys-13.
HCRPC61R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1346 as residues: Ala-3 to Gly-8.
HCRPG28R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1347 as residues: Pro-26 to Ser-32.
HCRPN52R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1349 as residues: Ser-24 to Lys-30, Lys-54 to Ser-61.
HDCAA21R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1354 as residues: Phe-6 to Val-12, Ile-15 to Phe-20.
HDDAA85R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1355 as residues: Lys-18 to Lys-24.
HDPGO03R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1356 as residues: Ala-4 to Gln-17.
HDPLB08R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1357 as residues: Pro-2 to Tyr-13, Leu-21 to Ala-36.
HDQEX80R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1359 as residues: Arg-1 to Arg-6, Phe-27 to Arg-32, Pro-37 to Lys-42, Arg-47 to Trp-53, Arg-55 to Ser-61.
HDRMI91R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1360 as residues: Thr-1 to Lys-8.
HE6DJ45R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1364 as residues: Pro-1 to Asn-8.
HE9FH12R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1366 as residues: Asn-12 to Ser-20.
HEAAL59R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1370 as residues: Gln-20 to Asn-25.
HEGAR32R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1371 as residues: Lys-9 to Ser-19.
HEGAR85R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1372 as residues: Ser-16 to His-46, Arg-49 to Thr-58.
HELFE05R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1373 as residues: Tyr-8 to Leu-16.
HEMFI88R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1374 as residues: Pro-6 to Ala-13.
HEMFR18R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1375 as residues: Ala-1 to Ala-10, Pro-12 to Gly-17, Ala-22 to Cys-27, Glu-30 to Arg-35, Pro-43 to Ser-50.
HEONL43R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1376 as residues: Arg-1 to Val-10.
HFADM62R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1380 as residues: Lys-6 to Lys-14.
HFATE31R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1381 as residues: Asp-1 to Arg-9, Arg-20 to Arg-26, Glu-33 to Gly-40.

HFCEL77R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1383 as residues: Glu-33 to Ser-48, Ile-54 to Ile-63, Leu-79 to Asp-84.
HFTBI57R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1392 as residues: Pro-18 to Ser-23.
HFXGX46R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1394 as residues: Pro-11 to Gln-28.
HHBEW72R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1400 as residues: Pro-20 to Thr-27.
HHERT59R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1401 as residues: Arg-1 to Trp-9.
HJMAH76R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1405 as residues: Cys-10 to Ala-15.
HJMAN56R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1406 as residues: Ala-45 to Asp-60.
HJMAO54R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1407 as residues: Pro-28 to Gln-39, Pro-65 to Cys-80.
HKLSD93R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1409 as residues: Gly-11 to Gly-17.
HLMFH16R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1410 as residues: Gly-1 to Asp-8.
HLQCQ73R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1412 as residues: Glu-1 to Gly-6, Arg-8 to Phe-13.
HLQEF47R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1413 as residues: Leu-8 to Leu-13.
HLQFM50R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1414 as residues: Gly-29 to Asp-34.
HLQGA76R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1416 as residues: Ser-16 to Ser-33.
HLTEV09R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1418 as residues: Arg-9 to Asn-17.
HMACF85R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1421 as residues: Glu-29 to Lys-34, Leu-113 to Gln-120.
HMAIA15R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1422 as residues: Lys-15 to Gln-21, Ile-51 to Gly-57, Lys-72 to Gly-83.
HMCIS54R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1424 as residues: Lys-3 to His-24.
HNHMR05R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1427 as residues: Pro-9 to Gly-20, Thr-26 to Arg-42, Ala-48 to Ser-54.
HNJBB78R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1428 as residues: Thr-6 to Lys-13, Leu-48 to Asn-54.
HOCND06R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1433 as residues: Pro-2 to Tyr-13, Leu-21 to Ala-35.
HOCND49R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1434 as residues: Asn-2 to Gly-12, Ile-14 to Ala-30.
HODFA26R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1436 as residues: Glu-1 to His-6, Gly-19 to Asp-29, Leu-44 to Leu-49.
HODHL89R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1437 as residues: Ser-16 to His-46, Arg-49 to Thr-58.
HOEJM67R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1438 as residues: Ser-19 to Lys-25, Asp-29 to Glu-55, Ser-102 to Thr-107.
HGOBN48R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1439 as residues: Lys-14 to Arg-19, Asp-25 to Phe-32.
HOUHN53R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1442 as residues: Glu-1 to His-6, Gly-19 to Trp-31.
HPBEE63R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1444 as residues: Pro-14 to Gly-20, His-28 to Arg-35.

HPJBE91R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1446 as residues: Ser-15 to Asn-20, Ala-22 to Ile-49, Lys-52 to Val-57, Tyr-71 to Cys-83, Thr-90 to Tyr-95.
HSDZG83R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1454 as residues: Val-17 to Lys-22.
HSICQ60R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1455 as residues: Val-12 to Gly-17.
HSIFA64R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1456 as residues: His-17 to Ile-22, Leu-33 to Pro-40.
HSKYE52R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1458 as residues: Pro-2 to Ser-7.
HSODA95R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1460 as residues: Ser-14 to His-44, Arg-47 to Thr-56.
HSSGK43R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1462 as residues: Ser-24 to Leu-35, Pro-38 to Ser-45.
HTXFA64R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1470 as residues: Thr-1 to Glu-8.
HUSJF91R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1471 as residues: Glu-1 to Gly-6.
HUSJN48R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1472 as residues: Ser-16 to Tyr-24.
HUSZN23R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1474 as residues: Ser-16 to Lys-24.
HUTSD20R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1475 as residues: Arg-10 to Asn-20.
HWAFI63R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1477 as residues: Pro-15 to Gly-24, Pro-26 to Arg-45.
HWAGZ89R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1478 as residues: Ser-47 to Lys-52.
HWHHM83R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1480 as residues: Leu-1 to Gly-6.
HWLBS90R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1484 as residues: Lys-37 to Asn-44.
HWLEH13R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1486 as residues: Gln-22 to Glu-29.
HWLEJ67R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1487 as residues: Asn-5 to Trp-13.
HWLEM49R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1488 as residues: Glu-1 to His-6, Gly-19 to Trp-31.
HWLGM21R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1492 as residues: Glu-1 to His-6, Gly-19 to Trp-31.
HWLGS46R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1494 as residues: Glu-17 to Asn-23, Glu-38 to Gly-49.
HWLGU40R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1495 as residues: His-10 to Pro-15.
HWLGX63R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1496 as residues: Glu-1 to Asn-7.
HWLHD09R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1497 as residues: Pro-6 to Ala-37, Arg-40 to Ser-49.
HWLHW89R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1500 as residues: Asn-1 to Lys-16, Glu-32 to Ser-41, Leu-57 to Gly-71.
HWLJL19R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1506 as residues: Arg-46 to Phe-58.
HWLKG82R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1508 as residues: Pro-5 to Gly-25, Ser-29 to Leu-36, Arg-49 to Phe-55.
HWLKM86R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1512 as



	residues: Arg-10 to Lys-23.
HWLQS83R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1515 as residues: Ala-1 to Arg-6.
HWLRP86R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1518 as residues: Tyr-3 to Gly-10.
HWLRQ49R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1519 as residues: Pro-19 to Ser-26, Gln-44 to Lys-52.
HWLUF60R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1520 as residues: Gln-7 to Lys-31.
HWLUR41R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1522 as residues: Ser-24 to Trp-30.
HWLVD60R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1523 as residues: Cys-15 to Lys-51.
HWMAN61R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1525 as residues: Ser-21 to Asp-26.
HWMEH26R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1528 as residues: Ser-16 to His-46, Arg-49 to Thr-58.
HWMEL50R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1529 as residues: Pro-24 to Thr-40, Phe-63 to Arg-69.
HWMFB31R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1530 as residues: Asn-2 to Lys-10, Cys-16 to Pro-28, Ser-36 to Glu-41.
HWMFO93R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1532 as residues: Ser-8 to Gln-14.
HMAFE48R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1537 as residues: Glu-9 to Gly-17.
HRODJ88R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1538 as residues: Gly-6 to Tyr-14.
HWLAR31R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1539 as residues: Glu-9 to Gly-17.
H2LAU24R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1541 as residues: Glu-11 to Gly-19.
HATDR94R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1542 as residues: Glu-14 to Lys-19, Asn-21 to Gly-27.
HWLLI85R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1543 as residues: Val-19 to Asn-32.
HSYCH41R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1545 as residues: Thr-71 to Ile-79.

The present invention encompasses polypeptides comprising, or alternatively consisting of, an epitope of the polypeptide sequence shown in SEQ ID NO:Y, or an epitope of the polypeptide sequence encoded by the cDNA in the related cDNA clone contained in a deposited library or encoded by a polynucleotide that hybridizes to the complement of an epitope encoding sequence of SEQ ID NO:X, or an epitope encoding sequence contained in the deposited cDNA clone under stringent hybridization conditions, or alternatively, under lower stringency hybridization conditions, as defined supra. The present invention further encompasses polynucleotide sequences encoding an epitope of a polypeptide sequence of the invention (such as, for example, the sequence disclosed in SEQ ID NO:X), polynucleotide sequences of the complementary strand of a polynucleotide sequence encoding an epitope of the invention, and polynucleotide sequences which hybridize to this complementary strand under stringent hybridization conditions or alternatively, under lower stringency hybridization conditions, as defined supra.

The term "epitopes," as used herein, refers to portions of a polypeptide having antigenic or immunogenic activity in an animal, preferably a mammal, and most preferably in a human. In a preferred embodiment, the present invention encompasses a polypeptide comprising an epitope, as well as the polynucleotide encoding this polypeptide. An "immunogenic epitope," as used herein, is defined as a portion of a protein that elicits an antibody response in an animal, as determined by any method known in the art, for example, by the methods for generating antibodies described infra. (See, for example, Geysen et al., Proc. Natl. Acad. Sci. USA 81:3998- 4002 (1983)). The term "antigenic epitope," as used herein, is defined as a portion of a protein to which an antibody can immunospecifically bind its antigen as determined by any method well known in the art, for example, by the immunoassays described herein. Immunospecific binding excludes non-specific binding but does not necessarily exclude cross- reactivity with other antigens. Antigenic epitopes need not necessarily be immunogenic.

Fragments which function as epitopes may be produced by any conventional means. (See, e.g., Houghten, R. A., Proc. Natl. Acad. Sci. USA 82:5131-5135 (1985) further described in U.S. Patent No. 4,631,211.)

In the present invention, antigenic epitopes preferably contain a sequence of at least 4, at least 5, at least 6, at least 7, more preferably at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 20, at least 25, at least 30, at least 40, at

least 50, and, most preferably, between about 15 to about 30 amino acids. Preferred polypeptides comprising immunogenic or antigenic epitopes are at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, or 100 amino acid residues in length. Additional non-exclusive preferred antigenic epitopes include the antigenic epitopes disclosed herein, as well as portions thereof. Antigenic epitopes are useful, for example, to raise antibodies, including monoclonal antibodies, that specifically bind the epitope. Preferred antigenic epitopes include the antigenic epitopes disclosed herein, as well as any combination of two, three, four, five or more of these antigenic epitopes. Antigenic epitopes can be used as the target molecules in immunoassays. (See, for instance, Wilson et al., Cell 5 37:767-778 (1984); Sutcliffe et al., Science 219:660-666 (1983)).

Similarly, immunogenic epitopes can be used, for example, to induce antibodies according to methods well known in the art. (See, for instance, Sutcliffe et al., supra; Wilson et al., supra; Chow et al., Proc. Natl. Acad. Sci. USA 82:910-914; and Bittle et al., J. Gen. Virol. 66:2347-2354 (1985). Preferred immunogenic epitopes include the immunogenic epitopes disclosed herein, as well as any combination of two, three, four, five or more of these immunogenic epitopes. The polypeptides comprising one or more immunogenic epitopes may be presented for eliciting an antibody response together with a carrier protein, such as an albumin, to an animal system (such as rabbit or mouse), or, if the polypeptide is of sufficient length (at least about 25 amino acids), the polypeptide may be presented without a carrier. However, immunogenic epitopes comprising as few as 8 to 10 amino acids have 15 been shown to be sufficient to raise antibodies capable of binding to, at the very least, linear epitopes in a denatured polypeptide (e.g., in Western blotting).

Epitope-bearing polypeptides of the present invention may be used to induce antibodies according to methods well known in the art including, but not limited to, in vivo immunization, in vitro immunization, and phage display methods. See, e.g., Sutcliffe et al., 25 supra; Wilson et al., supra, and Bittle et al., J. Gen. Virol., 66:2347-2354 (1985). If in vivo immunization is used, animals may be immunized with free peptide; however, anti-peptide antibody titer may be boosted by coupling the peptide to a macromolecular carrier, such as keyhole limpet hemacyanin (KLH) or tetanus toxoid. For instance, peptides containing cysteine residues may be coupled to a carrier using a linker such as maleimidobenzoyl- N- 30 hydroxysuccinimide ester (MBS), while other peptides may be coupled to carriers using a more general linking agent such as glutaraldehyde. Animals such as rabbits, rats and mice

are immunized with either free or carrier- coupled peptides, for instance, by intraperitoneal and/or intradermal injection of emulsions containing about 100 µg of peptide or carrier protein and Freund's adjuvant or any other adjuvant known for stimulating an immune response. Several booster injections may be needed, for instance, at intervals of about two weeks, to provide a useful titer of anti-peptide antibody which can be detected, for example, by ELISA assay using free peptide adsorbed to a solid surface. The titer of anti-peptide antibodies in serum from an immunized animal may be increased by selection of anti-peptide antibodies, for instance, by adsorption to the peptide on a solid support and elution of the selected antibodies according to methods well known in the art.

As one of skill in the art will appreciate, and as discussed above, the polypeptides of the present invention, and immunogenic and/or antigenic epitope fragments thereof can be fused to other polypeptide sequences. For example, the polypeptides of the present invention may be fused with the constant domain of immunoglobulins (IgA, IgE, IgG, IgM), or portions thereof (CH1, CH2, CH3, or any combination thereof and portions thereof) resulting in chimeric polypeptides. Such fusion proteins may facilitate purification and may increase half-life in vivo. This has been shown for chimeric proteins consisting of the first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light chains of mammalian immunoglobulins. See, e.g., EP 394,827; Traunecker et al., *Nature*, 331:84-86 (1988). Enhanced delivery of an antigen across the epithelial barrier to the immune system has been demonstrated for antigens (e.g., insulin) conjugated to an FcRn binding partner such as IgG or Fc fragments (see, e.g., PCT Publications WO 96/22024 and WO 99/04813). IgG Fusion proteins that have a disulfide-linked dimeric structure due to the IgG portion disulfide bonds have also been found to be more efficient in binding and neutralizing other molecules than monomeric polypeptides or fragments thereof alone. See, e.g., Fountoulakis et al., *J. Biochem.*, 270:3958-3964 (1995).

Similarly, EP-A-O 464 533 (Canadian counterpart 2045869) discloses fusion proteins comprising various portions of constant region of immunoglobulin molecules together with another human protein or part thereof. In many cases, the Fc part in a fusion protein is beneficial in therapy and diagnosis, and thus can result in, for example, improved pharmacokinetic properties. (EP-A 0232 262.) Alternatively, deleting the Fc part after the fusion protein has been expressed, detected, and purified, may be desired. For example, the Fc portion may hinder therapy and diagnosis if the fusion protein is used as an antigen for

immunizations. In drug discovery, for example, human proteins, such as hIL-5, have been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists of hIL-5. (See, D. Bennett et al., *J. Molecular Recognition* 8:52-58 (1995); K. Johanson et al., *J. Biol. Chem.* 270:9459-9471 (1995).)

5        Moreover, the polypeptides of the present invention can be fused to marker sequences, such as a peptide which facilitates purification of the fused polypeptide. In preferred embodiments, the marker amino acid sequence is a hexa-histidine peptide, such as the tag provided in a pQE vector (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311), among others, many of which are commercially available. As described in Gentz et al., *Proc. Natl. Acad. Sci. USA* 86:821-824 (1989), for instance, hexa-histidine provides for  
10        convenient purification of the fusion protein. Another peptide tag useful for purification, the "HA" tag, corresponds to an epitope derived from the influenza hemagglutinin protein. (Wilson et al., *Cell* 37:767 (1984).)

15        Thus, any of these above fusions can be engineered using the polynucleotides or the polypeptides of the present invention.

20        Nucleic acids encoding the above epitopes can also be recombined with a gene of interest as an epitope tag (e.g., the hemagglutinin ("HA") tag or flag tag) to aid in detection and purification of the expressed polypeptide. For example, a system described by Janknecht et al. allows for the ready purification of non-denatured fusion proteins expressed in human cell lines (Janknecht et al., *Proc. Natl. Acad. Sci. USA* 88:8972- 897 (1991)). In this system, the gene of interest is subcloned into a vaccinia recombination plasmid such that the open reading frame of the gene is translationally fused to an amino-terminal tag consisting of six histidine residues. The tag serves as a matrix binding domain for the fusion protein. Extracts from cells infected with the recombinant vaccinia virus are loaded onto  
25        Ni<sup>2+</sup> nitriloacetic acid-agarose column and histidine-tagged proteins can be selectively eluted with imidazole-containing buffers.

30        Additional fusion proteins of the invention may be generated through the techniques of gene-shuffling, motif-shuffling, exon-shuffling, and/or codon-shuffling (collectively referred to as "DNA shuffling"). DNA shuffling may be employed to modulate the activities of polypeptides of the invention, such methods can be used to generate polypeptides with altered activity, as well as agonists and antagonists of the polypeptides. See, generally, U.S. Patent Nos. 5,605,793; 5,811,238; 5,830,721; 5,834,252; and 5,837,458, and Patten et al.,

Curr. Opin. Biotechnol. 8:724-33 (1997); Harayama, Trends Biotechnol. 16(2):76-82 (1998); Hansson, et al., J. Mol. Biol. 287:265-76 (1999); and Lorenzo and Blasco, Biotechniques 24(2):308-13 (1998) (each of these patents and publications are hereby incorporated by reference in its entirety). In one embodiment, alteration of polynucleotides  
5 corresponding to SEQ ID NO:X and the polypeptides encoded by these polynucleotides may be achieved by DNA shuffling. DNA shuffling involves the assembly of two or more DNA segments by homologous or site-specific recombination to generate variation in the polynucleotide sequence. In another embodiment, polynucleotides of the invention, or the encoded polypeptides, may be altered by being subjected to random mutagenesis by error-prone  
10 PCR, random nucleotide insertion or other methods prior to recombination. In another embodiment, one or more components, motifs, sections, parts, domains, fragments, etc., of a polynucleotide encoding a polypeptide of the invention may be recombined with one or more components, motifs, sections, parts, domains, fragments, etc. of one or more heterologous molecules.

15 As discussed herein, any polypeptide of the present invention can be used to generate fusion proteins. For example, the polypeptide of the present invention, when fused to a second protein, can be used as an antigenic tag. Antibodies raised against the polypeptide of the present invention can be used to indirectly detect the second protein by binding to the polypeptide. Moreover, because secreted proteins target cellular locations based on  
20 trafficking signals, polypeptides of the present invention which are shown to be secreted can be used as targeting molecules once fused to other proteins.

Examples of domains that can be fused to polypeptides of the present invention include not only heterologous signal sequences, but also other heterologous functional regions. The fusion does not necessarily need to be direct, but may occur through linker  
25 sequences.

In certain preferred embodiments, proteins of the invention comprise fusion proteins wherein the polypeptides are N and/or C-terminal deletion mutants. In preferred embodiments, the application is directed to nucleic acid molecules at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to the nucleic acid sequences encoding polypeptides  
30 having the amino acid sequence of the specific N- and C-terminal deletions mutants. Polynucleotides encoding these polypeptides are also encompassed by the invention.

Moreover, fusion proteins may also be engineered to improve characteristics of the polypeptide of the present invention. For instance, a region of additional amino acids, particularly charged amino acids, may be added to the N-terminus of the polypeptide to improve stability and persistence during purification from the host cell or subsequent handling and storage. Also, peptide moieties may be added to the polypeptide to facilitate purification. Such regions may be removed prior to final preparation of the polypeptide. The addition of peptide moieties to facilitate handling of polypeptides are familiar and routine techniques in the art.

#### 10 **Vectors, Host Cells, and Protein Production**

The present invention also relates to vectors containing the polynucleotide of the present invention, host cells, and the production of polypeptides by recombinant techniques. The vector may be, for example, a phage, plasmid, viral, or retroviral vector. Retroviral vectors may be replication competent or replication defective. In the latter case, viral propagation generally will occur only in complementing host cells.

The polynucleotides of the invention may be joined to a vector containing a selectable marker for propagation in a host. Generally, a plasmid vector is introduced in a precipitate, such as a calcium phosphate precipitate, or in a complex with a charged lipid. If the vector is a virus, it may be packaged in vitro using an appropriate packaging cell line and then transduced into host cells.

The polynucleotide insert should be operatively linked to an appropriate promoter, such as the phage lambda PL promoter, the E. coli lac, trp, phoA and tac promoters, the SV40 early and late promoters and promoters of retroviral LTRs, to name a few. Other suitable promoters will be known to the skilled artisan. The expression constructs will further contain sites for transcription initiation, termination, and, in the transcribed region, a ribosome binding site for translation. The coding portion of the transcripts expressed by the constructs will preferably include a translation initiating codon at the beginning and a termination codon (UAA, UGA or UAG) appropriately positioned at the end of the polypeptide to be translated.

As indicated, the expression vectors will preferably include at least one selectable marker. Such markers include dihydrofolate reductase, G418 or neomycin resistance for eukaryotic cell culture and tetracycline, kanamycin or ampicillin resistance genes for culturing in E. coli and other bacteria. Representative examples of appropriate hosts include,

but are not limited to, bacterial cells, such as *E. coli*, *Streptomyces* and *Salmonella typhimurium* cells; fungal cells, such as yeast cells (e.g., *Saccharomyces cerevisiae* or *Pichia pastoris* (ATCC Accession No. 201178)); insect cells such as *Drosophila* S2 and *Spodoptera Sf9* cells; animal cells such as CHO, COS, 293, and Bowes melanoma cells; and plant cells.

5 Appropriate culture mediums and conditions for the above-described host cells are known in the art.

Among vectors preferred for use in bacteria include pQE70, pQE60 and pQE-9, available from QIAGEN, Inc.; pBluescript vectors, Phagescript vectors, pNH8A, pNH16a, pNH18A, pNH46A, available from Stratagene Cloning Systems, Inc.; and ptrc99a, pKK223-  
10 3, pKK233-3, pDR540, pRIT5 available from Pharmacia Biotech, Inc. Among preferred eukaryotic vectors are pWLNEO, pSV2CAT, pOG44, pXT1 and pSG available from Stratagene; and pSVK3, pBPV, pMSG and pSVL available from Pharmacia. Preferred expression vectors for use in yeast systems include, but are not limited to pYES2, pYD1, pTEF1/Zeo, pYES2/GS, pPICZ, pGAPZ, pGAPZalph, pPIC9, pPIC3.5, pHIL-D2, pHIL-S1,  
15 pPIC3.5K, pPIC9K, and PAO815 (all available from Invitrogen, Carlsbad, CA). Other suitable vectors will be readily apparent to the skilled artisan.

Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-dextran mediated transfection, cationic lipid-mediated transfection, electroporation, transduction, infection, or other methods. Such methods are described in  
20 many standard laboratory manuals, such as Davis et al., Basic Methods In Molecular Biology (1986). It is specifically contemplated that the polypeptides of the present invention may in fact be expressed by a host cell lacking a recombinant vector.

A polypeptide of this invention can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid  
25 extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Most preferably, high performance liquid chromatography ("HPLC") is employed for purification.

Polypeptides of the present invention can also be recovered from: products purified  
30 from natural sources, including bodily fluids, tissues and cells, whether directly isolated or cultured; products of chemical synthetic procedures; and products produced by recombinant techniques from a prokaryotic or eukaryotic host, including, for example, bacterial, yeast,



higher plant, insect, and mammalian cells. Depending upon the host employed in a recombinant production procedure, the polypeptides of the present invention may be glycosylated or may be non-glycosylated. In addition, polypeptides of the invention may also include an initial modified methionine residue, in some cases as a result of host-mediated processes. Thus, it is well known in the art that the N-terminal methionine encoded by the translation initiation codon generally is removed with high efficiency from any protein after translation in all eukaryotic cells. While the N-terminal methionine on most proteins also is efficiently removed in most prokaryotes, for some proteins, this prokaryotic removal process is inefficient, depending on the nature of the amino acid to which the N-terminal methionine is covalently linked.

In one embodiment, the yeast *Pichia pastoris* is used to express polypeptides of the invention in a eukaryotic system. *Pichia pastoris* is a methylotrophic yeast which can metabolize methanol as its sole carbon source. A main step in the methanol metabolism pathway is the oxidation of methanol to formaldehyde using  $O_2$ . This reaction is catalyzed by the enzyme alcohol oxidase. In order to metabolize methanol as its sole carbon source, *Pichia pastoris* must generate high levels of alcohol oxidase due, in part, to the relatively low affinity of alcohol oxidase for  $O_2$ . Consequently, in a growth medium depending on methanol as a main carbon source, the promoter region of one of the two alcohol oxidase genes (*AOX1*) is highly active. In the presence of methanol, alcohol oxidase produced from the *AOX1* gene comprises up to approximately 30% of the total soluble protein in *Pichia pastoris*. See, Ellis, S.B., et al., *Mol. Cell. Biol.* 5:1111-21 (1985); Koutz, P.J., et al., *Yeast* 5:167-77 (1989); Tschopp, J.F., et al., *Nucl. Acids Res.* 15:3859-76 (1987). Thus, a heterologous coding sequence, such as, for example, a polynucleotide of the present invention, under the transcriptional regulation of all or part of the *AOX1* regulatory sequence is expressed at exceptionally high levels in *Pichia* yeast grown in the presence of methanol.

In one example, the plasmid vector pPIC9K is used to express DNA encoding a polypeptide of the invention, as set forth herein, in a *Pichea* yeast system essentially as described in "*Pichia* Protocols: Methods in Molecular Biology," D.R. Higgins and J. Cregg, eds. The Humana Press. Totowa, NJ, 1998. This expression vector allows expression and secretion of a polypeptide of the invention by virtue of the strong *AOX1* promoter linked to

the *Pichia pastoris* alkaline phosphatase (PHO) secretory signal peptide (i.e., leader) located upstream of a multiple cloning site.

Many other yeast vectors could be used in place of pPIC9K, such as, pYES2, pYD1, pTEF1/Zeo, pYES2/GS, pPICZ, pGAPZ, pGAPZalpha, pPIC9, pPIC3.5, pHIL-D2, pHIL-S1, pPIC3.5K, and PAO815. as one skilled in the art would readily appreciate, as long as the proposed expression construct provides appropriately located signals for transcription, translation, secretion (if desired), and the like, including an in-frame AUG as required.

In another embodiment, high-level expression of a heterologous coding sequence, such as, for example, a polynucleotide of the present invention, may be achieved by cloning the heterologous polynucleotide of the invention into an expression vector such as, for example, pGAPZ or pGAPZalpha, and growing the yeast culture in the absence of methanol.

In addition to encompassing host cells containing the vector constructs discussed herein, the invention also encompasses primary, secondary, and immortalized host cells of vertebrate origin, particularly mammalian origin, that have been engineered to delete or replace endogenous genetic material (e.g., coding sequence), and/or to include genetic material (e.g., heterologous polynucleotide sequences) that is operably associated with polynucleotides of the invention, and which activates, alters, and/or amplifies endogenous polynucleotides. For example, techniques known in the art may be used to operably associate heterologous control regions (e.g., promoter and/or enhancer) and endogenous polynucleotide sequences via homologous recombination (see, e.g., U.S. Patent No. 5,641,670, issued June 24, 1997; International Publication No. WO 96/29411, published September 26, 1996; International Publication No. WO 94/12650, published August 4, 1994; Koller et al., Proc. Natl. Acad. Sci. USA 86:8932-8935 (1989); and Zijlstra et al., Nature 342:435-438 (1989), the disclosures of each of which are incorporated by reference in their entireties).

In addition, polypeptides of the invention can be chemically synthesized using techniques known in the art (e.g., see Creighton, 1983, Proteins: Structures and Molecular Principles, W.H. Freeman & Co., N.Y., and Hunkapiller et al., Nature, 310:105-111 (1984)). For example, a polypeptide corresponding to a fragment of a polypeptide can be synthesized by use of a peptide synthesizer. Furthermore, if desired, nonclassical amino acids or chemical amino acid analogs can be introduced as a substitution or addition into the

polypeptide sequence. Non-classical amino acids include, but are not limited to, to the D-isomers of the common amino acids, 2,4-diaminobutyric acid,  $\alpha$ -amino isobutyric acid, 4-aminobutyric acid, Abu, 2-amino butyric acid,  $\gamma$ -Abu, e-Ahx, 6-amino hexanoic acid, Aib, 2-amino isobutyric acid, 3-amino propionic acid, ornithine, norleucine, norvaline, 5 hydroxyproline, sarcosine, citrulline, homocitrulline, cysteic acid, t-butylglycine, t-butylalanine, phenylglycine, cyclohexylalanine, b-alanine, fluoro-amino acids, designer amino acids such as b-methyl amino acids, Ca-methyl amino acids, Na-methyl amino acids, and amino acid analogs in general. Furthermore, the amino acid can be D (dextrorotary) or L (levorotary).

10 Non-naturally occurring variants may be produced using art-known mutagenesis techniques, which include, but are not limited to oligonucleotide mediated mutagenesis, alanine scanning, PCR mutagenesis, site directed mutagenesis (*see, e.g., Carter et al., Nucl. Acids Res. 13:4331 (1986); and Zoller et al., Nucl. Acids Res. 10:6487 (1982)*), cassette mutagenesis (*see, e.g., Wells et al., Gene 34:315 (1985)*), restriction selection mutagenesis 15 (*see, e.g., Wells et al., Philos. Trans. R. Soc. London SerA 317:415 (1986)*).

The invention additionally, encompasses polypeptides of the present invention which are differentially modified during or after translation, e.g., by glycosylation, acetylation, phosphorylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, linkage to an antibody molecule or other cellular ligand, etc. Any of numerous 20 chemical modifications may be carried out by known techniques, including but not limited, to specific chemical cleavage by cyanogen bromide, trypsin, chymotrypsin, papain, V8 protease, NaBH<sub>4</sub>; acetylation, formylation, oxidation, reduction; metabolic synthesis in the presence of tunicamycin; etc.

Additional post-translational modifications encompassed by the invention include, for 25 example, e.g., N-linked or O-linked carbohydrate chains, processing of N-terminal or C-terminal ends), attachment of chemical moieties to the amino acid backbone, chemical modifications of N-linked or O-linked carbohydrate chains, and addition or deletion of an N-terminal methionine residue as a result of procaryotic host cell expression. The polypeptides may also be modified with a detectable label, such as an enzymatic, fluorescent, 30 isotopic or affinity label to allow for detection and isolation of the protein.

Also provided by the invention are chemically modified derivatives of the polypeptides of the invention which may provide additional advantages such as increased

solubility, stability and circulating time of the polypeptide, or decreased immunogenicity (see U.S. Patent No. 4,179,337). The chemical moieties for derivitization may be selected from water soluble polymers such as polyethylene glycol, ethylene glycol/propylene glycol copolymers, carboxymethylcellulose, dextran, polyvinyl alcohol and the like. The polypeptides may be modified at random positions within the molecule, or at predetermined positions within the molecule and may include one, two, three or more attached chemical moieties.

The polymer may be of any molecular weight, and may be branched or unbranched. For polyethylene glycol, the preferred molecular weight is between about 1 kDa and about 100 kDa (the term "about" indicating that in preparations of polyethylene glycol, some molecules will weigh more, some less, than the stated molecular weight) for ease in handling and manufacturing. Other sizes may be used, depending on the desired therapeutic profile (e.g., the duration of sustained release desired, the effects, if any on biological activity, the ease in handling, the degree or lack of antigenicity and other known effects of the polyethylene glycol to a therapeutic protein or analog). For example, the polyethylene glycol may have an average molecular weight of about 200; 500; 1000; 1500; 2000; 2500; 3000; 3500; 4000; 4500; 5000; 5500; 6000; 6500; 7000; 7500; 8000; 8500; 9000; 9500; 10,000; 10,500; 11,000; 11,500; 12,000; 12,500; 13,000; 13,500; 14,000; 14,500; 15,000; 15,500; 16,000; 16,500; 17,000; 17,500; 18,000; 18,500; 19,000; 19,500; 20,000; 25,000; 30,000; 35,000; 40,000; 50,000; 55,000; 60,000; 65,000; 70,000; 75,000; 80,000; 85,000; 90,000; 95,000; or 100,000 kDa.

As noted above, the polyethylene glycol may have a branched structure. Branched polyethylene glycols are described, for example, in U.S. Patent No. 5,643,575; Morpurgo *et al.*, *Appl. Biochem. Biotechnol.* 56:59-72 (1996); Vorobjev *et al.*, *Nucleosides Nucleotides* 18:2745-2750 (1999); and Caliceti *et al.*, *Bioconjug. Chem.* 10:638-646 (1999), the disclosures of each of which are incorporated herein by reference.

The polyethylene glycol molecules (or other chemical moieties) should be attached to the protein with consideration of effects on functional or antigenic domains of the protein. There are a number of attachment methods available to those skilled in the art, e.g., EP 0 401 384, herein incorporated by reference (coupling PEG to G-CSF), see also Malik *et al.*, *Exp. Hematol.* 20:1028-1035 (1992) (reporting pegylation of GM-CSF using tresyl chloride). For example, polyethylene glycol may be covalently bound through amino acid residues via a

reactive group, such as, a free amino or carboxyl group. Reactive groups are those to which an activated polyethylene glycol molecule may be bound. The amino acid residues having a free amino group may include lysine residues and the N-terminal amino acid residues; those having a free carboxyl group may include aspartic acid residues glutamic acid residues and the C-terminal amino acid residue. Sulfhydryl groups may also be used as a reactive group for attaching the polyethylene glycol molecules. Preferred for therapeutic purposes is attachment at an amino group, such as attachment at the N-terminus or lysine group.

As suggested above, polyethylene glycol may be attached to proteins via linkage to any of a number of amino acid residues. For example, polyethylene glycol can be linked to a proteins via covalent bonds to lysine, histidine, aspartic acid, glutamic acid, or cysteine residues. One or more reaction chemistries may be employed to attach polyethylene glycol to specific amino acid residues (e.g., lysine, histidine, aspartic acid, glutamic acid, or cysteine) of the protein or to more than one type of amino acid residue (e.g., lysine, histidine, aspartic acid, glutamic acid, cysteine and combinations thereof) of the protein.

One may specifically desire proteins chemically modified at the N-terminus. Using polyethylene glycol as an illustration of the present composition, one may select from a variety of polyethylene glycol molecules (by molecular weight, branching, etc.), the proportion of polyethylene glycol molecules to protein (polypeptide) molecules in the reaction mix, the type of pegylation reaction to be performed, and the method of obtaining the selected N-terminally pegylated protein. The method of obtaining the N-terminally pegylated preparation (i.e., separating this moiety from other monopegylated moieties if necessary) may be by purification of the N-terminally pegylated material from a population of pegylated protein molecules. Selective proteins chemically modified at the N-terminus modification may be accomplished by reductive alkylation which exploits differential reactivity of different types of primary amino groups (lysine versus the N-terminal) available for derivatization in a particular protein. Under the appropriate reaction conditions, substantially selective derivatization of the protein at the N-terminus with a carbonyl group containing polymer is achieved.

As indicated above, pegylation of the proteins of the invention may be accomplished by any number of means. For example, polyethylene glycol may be attached to the protein either directly or by an intervening linker. Linkerless systems for attaching polyethylene glycol to proteins are described in Delgado *et al.*, *Crit. Rev. Thera. Drug Carrier Sys.* 9:249-

304 (1992); Francis *et al.*, *Intern. J. of Hematol.* 68:1-18 (1998); U.S. Patent No. 4,002,531; U.S. Patent No. 5,349,052; WO 95/06058; and WO 98/32466, the disclosures of each of which are incorporated herein by reference.

One system for attaching polyethylene glycol directly to amino acid residues of proteins without an intervening linker employs tresylated MPEG, which is produced by the modification of monmethoxy polyethylene glycol (MPEG) using tresylchloride ( $\text{ClSO}_2\text{CH}_2\text{CF}_3$ ). Upon reaction of protein with tresylated MPEG, polyethylene glycol is directly attached to amine groups of the protein. Thus, the invention includes protein-polyethylene glycol conjugates produced by reacting proteins of the invention with a polyethylene glycol molecule having a 2,2,2-trifluoroethane sulphonyl group.

Polyethylene glycol can also be attached to proteins using a number of different intervening linkers. For example, U.S. Patent No. 5,612,460, the entire disclosure of which is incorporated herein by reference, discloses urethane linkers for connecting polyethylene glycol to proteins. Protein-polyethylene glycol conjugates wherein the polyethylene glycol is attached to the protein by a linker can also be produced by reaction of proteins with compounds such as MPEG-succinimidylsuccinate, MPEG activated with 1,1'-carbonyldiimidazole, MPEG-2,4,5-trichloropenylcarbonate, MPEG-p-nitrophenolcarbonate, and various MPEG-succinate derivatives. A number additional polyethylene glycol derivatives and reaction chemistries for attaching polyethylene glycol to proteins are described in WO 98/32466, the entire disclosure of which is incorporated herein by reference. Pegylated protein products produced using the reaction chemistries set out herein are included within the scope of the invention.

The number of polyethylene glycol moieties attached to each protein of the invention (*i.e.*, the degree of substitution) may also vary. For example, the pegylated proteins of the invention may be linked, on average, to 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 17, 20, or more polyethylene glycol molecules. Similarly, the average degree of substitution within ranges such as 1-3, 2-4, 3-5, 4-6, 5-7, 6-8, 7-9, 8-10, 9-11, 10-12, 11-13, 12-14, 13-15, 14-16, 15-17, 16-18, 17-19, or 18-20 polyethylene glycol moieties per protein molecule. Methods for determining the degree of substitution are discussed, for example, in Delgado *et al.*, *Crit. Rev. Thera. Drug Carrier Sys.* 9:249-304 (1992).

The colon cancer antigen polypeptides of the invention may be in monomers or multimers (*i.e.*, dimers, trimers, tetramers and higher multimers). Accordingly, the present

invention relates to monomers and multimers of the polypeptides of the invention, their preparation, and compositions (preferably, Therapeutics) containing them. In specific embodiments, the polypeptides of the invention are monomers, dimers, trimers or tetramers. In additional embodiments, the multimers of the invention are at least dimers, at least trimers, or at least tetramers.

Multimers encompassed by the invention may be homomers or heteromers. As used herein, the term homomer, refers to a multimer containing only polypeptides corresponding to the amino acid sequence of SEQ ID NO:Y or an amino acid sequence encoded by SEQ ID NO:X, and/or an amino acid sequence encoded by the cDNA in a related cDNA clone contained in a deposited library (including fragments, variants, splice variants, and fusion proteins, corresponding to any one of these as described herein). These homomers may contain polypeptides having identical or different amino acid sequences. In a specific embodiment, a homomer of the invention is a multimer containing only polypeptides having an identical amino acid sequence. In another specific embodiment, a homomer of the invention is a multimer containing polypeptides having different amino acid sequences. In specific embodiments, the multimer of the invention is a homodimer (e.g., containing polypeptides having identical or different amino acid sequences) or a homotrimer (e.g., containing polypeptides having identical and/or different amino acid sequences). In additional embodiments, the homomeric multimer of the invention is at least a homodimer, at least a homotrimer, or at least a homotetramer.

As used herein, the term heteromer refers to a multimer containing one or more heterologous polypeptides (i.e., polypeptides of different proteins) in addition to the polypeptides of the invention. In a specific embodiment, the multimer of the invention is a heterodimer, a heterotrimer, or a heterotetramer. In additional embodiments, the heteromeric multimer of the invention is at least a heterodimer, at least a heterotrimer, or at least a heterotetramer.

Multimers of the invention may be the result of hydrophobic, hydrophilic, ionic and/or covalent associations and/or may be indirectly linked, by for example, liposome formation. Thus, in one embodiment, multimers of the invention, such as, for example, homodimers or homotrimers, are formed when polypeptides of the invention contact one another in solution. In another embodiment, heteromultimers of the invention, such as, for example, heterotrimers or heterotetramers, are formed when polypeptides of the invention

contact antibodies to the polypeptides of the invention (including antibodies to the heterologous polypeptide sequence in a fusion protein of the invention) in solution. In other embodiments, multimers of the invention are formed by covalent associations with and/or between the polypeptides of the invention. Such covalent associations may involve one or more amino acid residues contained in the polypeptide sequence (e.g., that recited in SEQ ID NO:Y, or contained in a polypeptide encoded by SEQ ID NO:X, and/or by the cDNA in the related cDNA clone contained in a deposited library). In one instance, the covalent associations are cross-linking between cysteine residues located within the polypeptide sequences which interact in the native (i.e., naturally occurring) polypeptide. In another instance, the covalent associations are the consequence of chemical or recombinant manipulation. Alternatively, such covalent associations may involve one or more amino acid residues contained in the heterologous polypeptide sequence in a fusion protein. In one example, covalent associations are between the heterologous sequence contained in a fusion protein of the invention (see, e.g., US Patent Number 5,478,925). In a specific example, the covalent associations are between the heterologous sequence contained in a Fc fusion protein of the invention (as described herein). In another specific example, covalent associations of fusion proteins of the invention are between heterologous polypeptide sequence from another protein that is capable of forming covalently associated multimers, such as for example, oseteoprotegerin (see, e.g., International Publication NO: WO 98/49305, the contents of which are herein incorporated by reference in its entirety). In another embodiment, two or more polypeptides of the invention are joined through peptide linkers. Examples include those peptide linkers described in U.S. Pat. No. 5,073,627 (hereby incorporated by reference). Proteins comprising multiple polypeptides of the invention separated by peptide linkers may be produced using conventional recombinant DNA technology.

Another method for preparing multimer polypeptides of the invention involves use of polypeptides of the invention fused to a leucine zipper or isoleucine zipper polypeptide sequence. Leucine zipper and isoleucine zipper domains are polypeptides that promote multimerization of the proteins in which they are found. Leucine zippers were originally identified in several DNA-binding proteins (Landschulz et al., Science 240:1759, (1988)), and have since been found in a variety of different proteins. Among the known leucine zippers are naturally occurring peptides and derivatives thereof that dimerize or trimerize. Examples of leucine zipper domains suitable for producing soluble multimeric proteins of the



invention are those described in PCT application WO 94/10308, hereby incorporated by reference. Recombinant fusion proteins comprising a polypeptide of the invention fused to a polypeptide sequence that dimerizes or trimerizes in solution are expressed in suitable host cells, and the resulting soluble multimeric fusion protein is recovered from the culture supernatant using techniques known in the art.

Trimeric polypeptides of the invention may offer the advantage of enhanced biological activity. Preferred leucine zipper moieties and isoleucine moieties are those that preferentially form trimers. One example is a leucine zipper derived from lung surfactant protein D (SPD), as described in Hoppe et al. (FEBS Letters 344:191, (1994)) and in U.S. patent application Ser. No. 08/446,922, hereby incorporated by reference. Other peptides derived from naturally occurring trimeric proteins may be employed in preparing trimeric polypeptides of the invention.

In another example, proteins of the invention are associated by interactions between Flag® polypeptide sequence contained in fusion proteins of the invention containing Flag® polypeptide sequence. In a further embodiment, associations proteins of the invention are associated by interactions between heterologous polypeptide sequence contained in Flag® fusion proteins of the invention and anti-Flag® antibody.

The multimers of the invention may be generated using chemical techniques known in the art. For example, polypeptides desired to be contained in the multimers of the invention may be chemically cross-linked using linker molecules and linker molecule length optimization techniques known in the art (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety). Additionally, multimers of the invention may be generated using techniques known in the art to form one or more inter-molecule cross-links between the cysteine residues located within the sequence of the polypeptides desired to be contained in the multimer (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety). Further, polypeptides of the invention may be routinely modified by the addition of cysteine or biotin to the C-terminus or N-terminus of the polypeptide and techniques known in the art may be applied to generate multimers containing one or more of these modified polypeptides (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety). Additionally, techniques known in the art may be applied to generate liposomes containing the polypeptide

components desired to be contained in the multimer of the invention (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety).

Alternatively, multimers of the invention may be generated using genetic engineering techniques known in the art. In one embodiment, polypeptides contained in multimers of the invention are produced recombinantly using fusion protein technology described herein or otherwise known in the art (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety). In a specific embodiment, polynucleotides coding for a homodimer of the invention are generated by ligating a polynucleotide sequence encoding a polypeptide of the invention to a sequence encoding a linker polypeptide and then further to a synthetic polynucleotide encoding the translated product of the polypeptide in the reverse orientation from the original C-terminus to the N-terminus (lacking the leader sequence) (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety). In another embodiment, recombinant techniques described herein or otherwise known in the art are applied to generate recombinant polypeptides of the invention which contain a transmembrane domain (or hydrophobic or signal peptide) and which can be incorporated by membrane reconstitution techniques into liposomes (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety).

#### Antibodies

Further polypeptides of the invention relate to antibodies and T-cell antigen receptors (TCR) which immunospecifically bind a polypeptide, polypeptide fragment, or variant of SEQ ID NO:Y, and/or an epitope, of the present invention (as determined by immunoassays well known in the art for assaying specific antibody-antigen binding). Antibodies of the invention include, but are not limited to, polyclonal, monoclonal, multispecific, human, humanized or chimeric antibodies, single chain antibodies, Fab fragments, F(ab') fragments, fragments produced by a Fab expression library, anti-idiotypic (anti-Id) antibodies (including, e.g., anti-Id antibodies to antibodies of the invention), and epitope-binding fragments of any of the above. The term "antibody," as used herein, refers to immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, i.e., molecules that contain an antigen binding site that immunospecifically binds an antigen. The immunoglobulin molecules of the invention can be of any type (e.g., IgG,

IgE, IgM, IgD, IgA and IgY), class (e.g., IgG1, IgG2, IgG3, IgG4, IgA1 and IgA2) or subclass of immunoglobulin molecule.

Most preferably the antibodies are human antigen-binding antibody fragments of the present invention and include, but are not limited to, Fab, Fab' and F(ab')<sub>2</sub>, Fd, single-chain Fvs (scFv), single-chain antibodies, disulfide-linked Fvs (sdFv) and fragments comprising either a VL or VH domain. Antigen-binding antibody fragments, including single-chain antibodies, may comprise the variable region(s) alone or in combination with the entirety or a portion of the following: hinge region, CH1, CH2, and CH3 domains. Also included in the invention are antigen-binding fragments also comprising any combination of variable region(s) with a hinge region, CH1, CH2, and CH3 domains. The antibodies of the invention may be from any animal origin including birds and mammals. Preferably, the antibodies are human, murine (e.g., mouse and rat), donkey, ship rabbit, goat, guinea pig, camel, horse, or chicken. As used herein, "human" antibodies include antibodies having the amino acid sequence of a human immunoglobulin and include antibodies isolated from human immunoglobulin libraries or from animals transgenic for one or more human immunoglobulin and that do not express endogenous immunoglobulins, as described infra and, for example in, U.S. Patent No. 5,939,598 by Kucherlapati et al.

The antibodies of the present invention may be monospecific, bispecific, trispecific or of greater multispecificity. Multispecific antibodies may be specific for different epitopes of a polypeptide of the present invention or may be specific for both a polypeptide of the present invention as well as for a heterologous epitope, such as a heterologous polypeptide or solid support material. See, e.g., PCT publications WO 93/17715; WO 92/08802; WO 91/00360; WO 92/05793; Tutt, et al., J. Immunol. 147:60-69 (1991); U.S. Patent Nos. 4,474,893; 4,714,681; 4,925,648; 5,573,920; 5,601,819; Kostelny et al., J. Immunol. 148:1547-1553 (1992).

Antibodies of the present invention may be described or specified in terms of the epitope(s) or portion(s) of a polypeptide of the present invention which they recognize or specifically bind. The epitope(s) or polypeptide portion(s) may be specified as described herein, e.g., by N-terminal and C-terminal positions, or by size in contiguous amino acid residues. Antibodies which specifically bind any epitope or polypeptide of the present invention may also be excluded. Therefore, the present invention includes antibodies that

specifically bind polypeptides of the present invention, and allows for the exclusion of the same.

Antibodies of the present invention may also be described or specified in terms of their cross-reactivity. Antibodies that do not bind any other analog, ortholog, or homolog of a polypeptide of the present invention are included. Antibodies that bind polypeptides with at least 95%, at least 90%, at least 85%, at least 80%, at least 75%, at least 70%, at least 65%, at least 60%, at least 55%, and at least 50% identity (as calculated using methods known in the art and described herein) to a polypeptide of the present invention are also included in the present invention. In specific embodiments, antibodies of the present invention cross-react with murine, rat and/or rabbit homologs of human proteins and the corresponding epitopes thereof. Antibodies that do not bind polypeptides with less than 95%, less than 90%, less than 85%, less than 80%, less than 75%, less than 70%, less than 65%, less than 60%, less than 55%, and less than 50% identity (as calculated using methods known in the art and described herein) to a polypeptide of the present invention are also included in the present invention. In a specific embodiment, the above-described cross-reactivity is with respect to any single specific antigenic or immunogenic polypeptide, or combination(s) of 2, 3, 4, 5, or more of the specific antigenic and/or immunogenic polypeptides disclosed herein. Further included in the present invention are antibodies which bind polypeptides encoded by polynucleotides which hybridize to a polynucleotide of the present invention under stringent hybridization conditions (as described herein). Antibodies of the present invention may also be described or specified in terms of their binding affinity to a polypeptide of the invention. Preferred binding affinities include those with a dissociation constant or  $K_d$  less than  $5 \times 10^{-2}$  M,  $10^{-2}$  M,  $5 \times 10^{-3}$  M,  $10^{-3}$  M,  $5 \times 10^{-4}$  M,  $10^{-4}$  M,  $5 \times 10^{-5}$  M,  $10^{-5}$  M,  $5 \times 10^{-6}$  M,  $10^{-6}$  M,  $5 \times 10^{-7}$  M,  $10^{-7}$  M,  $5 \times 10^{-8}$  M,  $10^{-8}$  M,  $5 \times 10^{-9}$  M,  $10^{-9}$  M,  $5 \times 10^{-10}$  M,  $10^{-10}$  M,  $5 \times 10^{-11}$  M,  $10^{-11}$  M,  $5 \times 10^{-12}$  M,  $10^{-12}$  M,  $5 \times 10^{-13}$  M,  $10^{-13}$  M,  $5 \times 10^{-14}$  M,  $10^{-14}$  M,  $5 \times 10^{-15}$  M, or  $10^{-15}$  M.

The invention also provides antibodies that competitively inhibit binding of an antibody to an epitope of the invention as determined by any method known in the art for determining competitive binding, for example, the immunoassays described herein. In preferred embodiments, the antibody competitively inhibits binding to the epitope by at least 95%, at least 90%, at least 85 %, at least 80%, at least 75%, at least 70%, at least 60%, or at least 50%.

Antibodies of the present invention may act as agonists or antagonists of the polypeptides of the present invention. For example, the present invention includes antibodies which disrupt the receptor/ligand interactions with the polypeptides of the invention either partially or fully. Preferably, antibodies of the present invention bind an antigenic epitope disclosed herein, or a portion thereof. The invention features both receptor-specific antibodies and ligand-specific antibodies. The invention also features receptor-specific antibodies which do not prevent ligand binding but prevent receptor activation. Receptor activation (i.e., signaling) may be determined by techniques described herein or otherwise known in the art. For example, receptor activation can be determined by detecting the phosphorylation (e.g., tyrosine or serine/threonine) of the receptor or its substrate by immunoprecipitation followed by western blot analysis (for example, as described supra). In specific embodiments, antibodies are provided that inhibit ligand activity or receptor activity by at least 95%, at least 90%, at least 85%, at least 80%, at least 75%, at least 70%, at least 60%, or at least 50% of the activity in absence of the antibody.

The invention also features receptor-specific antibodies which both prevent ligand binding and receptor activation as well as antibodies that recognize the receptor-ligand complex, and, preferably, do not specifically recognize the unbound receptor or the unbound ligand. Likewise, included in the invention are neutralizing antibodies which bind the ligand and prevent binding of the ligand to the receptor, as well as antibodies which bind the ligand, thereby preventing receptor activation, but do not prevent the ligand from binding the receptor. Further included in the invention are antibodies which activate the receptor. These antibodies may act as receptor agonists, i.e., potentiate or activate either all or a subset of the biological activities of the ligand-mediated receptor activation, for example, by inducing dimerization of the receptor. The antibodies may be specified as agonists, antagonists or inverse agonists for biological activities comprising the specific biological activities of the peptides of the invention disclosed herein. The above antibody agonists can be made using methods known in the art. See, e.g., PCT publication WO 96/40281; U.S. Patent No. 5,811,097; Deng et al., *Blood* 92(6):1981-1988 (1998); Chen et al., *Cancer Res.* 58(16):3668-3678 (1998); Harrop et al., *J. Immunol.* 161(4):1786-1794 (1998); Zhu et al., *Cancer Res.* 58(15):3209-3214 (1998); Yoon et al., *J. Immunol.* 160(7):3170-3179 (1998); Prat et al., *J. Cell. Sci.* 111(Pt2):237-247 (1998); Pitard et al., *J. Immunol. Methods* 205(2):177-190 (1997); Liautard et al., *Cytokine* 9(4):233-241 (1997); Carlson et al., *J. Biol.*

Chem. 272(17):11295-11301 (1997); Taryman et al., Neuron 14(4):755-762 (1995); Muller et al., Structure 6(9):1153-1167 (1998); Bartunek et al., Cytokine 8(1):14-20 (1996) (which are all incorporated by reference herein in their entireties).

Antibodies of the present invention may be used, for example, but not limited to, to  
5 purify, detect, and target the polypeptides of the present invention, including both in vitro and  
in vivo diagnostic and therapeutic methods. For example, the antibodies have use in  
immunoassays for qualitatively and quantitatively measuring levels of the polypeptides of the  
present invention in biological samples. See, e.g., Harlow et al., Antibodies: A Laboratory  
Manual. (Cold Spring Harbor Laboratory Press, 2nd ed. 1988) (incorporated by reference  
10 herein in its entirety).

As discussed in more detail below, the antibodies of the present invention may be  
used either alone or in combination with other compositions. The antibodies may further be  
recombinantly fused to a heterologous polypeptide at the N- or C-terminus or chemically  
conjugated (including covalently and non-covalently conjugations) to polypeptides or other  
15 compositions. For example, antibodies of the present invention may be recombinantly fused  
or conjugated to molecules useful as labels in detection assays and effector molecules such as  
heterologous polypeptides, drugs, radionuclides, or toxins. See, e.g., PCT publications WO  
92/08495; WO 91/14438; WO 89/12624; U.S. Patent No. 5,314,995; and EP 396,387.

The antibodies of the invention include derivatives that are modified, i.e., by the  
20 covalent attachment of any type of molecule to the antibody such that covalent attachment  
does not prevent the antibody from generating an anti-idiotypic response. For example, but  
not by way of limitation, the antibody derivatives include antibodies that have been modified,  
e.g., by glycosylation, acetylation, pegylation, phosphorylation, amidation, derivatization by  
known protecting/blocking groups, proteolytic cleavage, linkage to a cellular ligand or other  
25 protein, etc. Any of numerous chemical modifications may be carried out by known  
techniques, including, but not limited to specific chemical cleavage, acetylation, formylation,  
metabolic synthesis of tunicamycin, etc. Additionally, the derivative may contain one or  
more non-classical amino acids.

The antibodies of the present invention may be generated by any suitable method  
30 known in the art. Polyclonal antibodies to an antigen-of-interest can be produced by various  
procedures well known in the art. For example, a polypeptide of the invention can be  
administered to various host animals including, but not limited to, rabbits, mice, rats, etc. to

induce the production of sera containing polyclonal antibodies specific for the antigen. Various adjuvants may be used to increase the immunological response, depending on the host species, and include but are not limited to, Freund's (complete and incomplete), mineral gels such as aluminum hydroxide, surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanins, dinitrophenol, and potentially useful human adjuvants such as BCG (bacille Calmette-Guerin) and corynebacterium parvum. Such adjuvants are also well known in the art.

Monoclonal antibodies can be prepared using a wide variety of techniques known in the art including the use of hybridoma, recombinant, and phage display technologies, or a combination thereof. For example, monoclonal antibodies can be produced using hybridoma techniques including those known in the art and taught, for example, in Harlow et al., *Antibodies: A Laboratory Manual*, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988); Hammerling, et al., in: *Monoclonal Antibodies and T-Cell Hybridomas* 563-681 (Elsevier, N.Y., 1981) (said references incorporated by reference in their entireties). The term "monoclonal antibody" as used herein is not limited to antibodies produced through hybridoma technology. The term "monoclonal antibody" refers to an antibody that is derived from a single clone, including any eukaryotic, prokaryotic, or phage clone, and not the method by which it is produced.

Methods for producing and screening for specific antibodies using hybridoma technology are routine and well known in the art and are discussed in detail in the Examples. In a non-limiting example, mice can be immunized with a polypeptide of the invention or a cell expressing such peptide. Once an immune response is detected, e.g., antibodies specific for the antigen are detected in the mouse serum, the mouse spleen is harvested and splenocytes isolated. The splenocytes are then fused by well known techniques to any suitable myeloma cells, for example cells from cell line SP20 available from the ATCC. Hybridomas are selected and cloned by limited dilution. The hybridoma clones are then assayed by methods known in the art for cells that secrete antibodies capable of binding a polypeptide of the invention. Ascites fluid, which generally contains high levels of antibodies, can be generated by immunizing mice with positive hybridoma clones.

Accordingly, the present invention provides methods of generating monoclonal antibodies as well as antibodies produced by the method comprising culturing a hybridoma cell secreting an antibody of the invention wherein, preferably, the hybridoma is generated by

fusing splenocytes isolated from a mouse immunized with an antigen of the invention with myeloma cells and then screening the hybridomas resulting from the fusion for hybridoma clones that secrete an antibody able to bind a polypeptide of the invention.

Antibody fragments which recognize specific epitopes may be generated by known techniques. For example, Fab and F(ab')<sub>2</sub> fragments of the invention may be produced by proteolytic cleavage of immunoglobulin molecules, using enzymes such as papain (to produce Fab fragments) or pepsin (to produce F(ab')<sub>2</sub> fragments). F(ab')<sub>2</sub> fragments contain the variable region, the light chain constant region and the CH1 domain of the heavy chain.

For example, the antibodies of the present invention can also be generated using various phage display methods known in the art. In phage display methods, functional antibody domains are displayed on the surface of phage particles which carry the polynucleotide sequences encoding them. In a particular embodiment, such phage can be utilized to display antigen binding domains expressed from a repertoire or combinatorial antibody library (e.g., human or murine). Phage expressing an antigen binding domain that binds the antigen of interest can be selected or identified with antigen, e.g., using labeled antigen or antigen bound or captured to a solid surface or bead. Phage used in these methods are typically filamentous phage including fd and M13 binding domains expressed from phage with Fab, Fv or disulfide stabilized Fv antibody domains recombinantly fused to either the phage gene III or gene VIII protein. Examples of phage display methods that can be used to make the antibodies of the present invention include those disclosed in Brinkman et al., J. Immunol. Methods 182:41-50 (1995); Ames et al., J. Immunol. Methods 184:177-186 (1995); Kettleborough et al., Eur. J. Immunol. 24:952-958 (1994); Persic et al., Gene 187 9-18 (1997); Burton et al., Advances in Immunology 57:191-280 (1994); PCT application No. PCT/GB91/01134; PCT publications WO 90/02809; WO 91/10737; WO 92/01047; WO 92/18619; WO 93/11236; WO 95/15982; WO 95/20401; and U.S. Patent Nos. 5,698,426; 5,223,409; 5,403,484; 5,580,717; 5,427,908; 5,750,753; 5,821,047; 5,571,698; 5,427,908; 5,516,637; 5,780,225; 5,658,727; 5,733,743 and 5,969,108; each of which is incorporated herein by reference in its entirety.

As described in the above references, after phage selection, the antibody coding regions from the phage can be isolated and used to generate whole antibodies, including human antibodies, or any other desired antigen binding fragment, and expressed in any desired host, including mammalian cells, insect cells, plant cells, yeast, and bacteria, e.g., as



described in detail below. For example, techniques to recombinantly produce Fab, Fab' and F(ab')<sub>2</sub> fragments can also be employed using methods known in the art such as those disclosed in PCT publication WO 92/22324; Mullinax et al., *BioTechniques* 12(6):864-869 (1992); and Sawai et al., *AJRI* 34:26-34 (1995); and Better et al., *Science* 240:1041-1043  
5 (1988) (said references incorporated by reference in their entireties).

Examples of techniques which can be used to produce single-chain Fvs and antibodies include those described in U.S. Patents 4,946,778 and 5,258,498; Huston et al., *Methods in Enzymology* 203:46-88 (1991); Shu et al., *PNAS* 90:7995-7999 (1993); and Skerra et al., *Science* 240:1038-1040 (1988). For some uses, including in vivo use of antibodies in  
10 humans and in vitro detection assays, it may be preferable to use chimeric, humanized, or human antibodies. A chimeric antibody is a molecule in which different portions of the antibody are derived from different animal species, such as antibodies having a variable region derived from a murine monoclonal antibody and a human immunoglobulin constant region. Methods for producing chimeric antibodies are known in the art. See e.g., Morrison,  
15 *Science* 229:1202 (1985); Oi et al., *BioTechniques* 4:214 (1986); Gillies et al., (1989) *J. Immunol. Methods* 125:191-202; U.S. Patent Nos. 5,807,715; 4,816,567; and 4,816,397, which are incorporated herein by reference in their entirety. Humanized antibodies are antibody molecules from non-human species antibody that binds the desired antigen having one or more complementarity determining regions (CDRs) from the non-human species and  
20 a framework regions from a human immunoglobulin molecule. Often, framework residues in the human framework regions will be substituted with the corresponding residue from the CDR donor antibody to alter, preferably improve, antigen binding. These framework substitutions are identified by methods well known in the art, e.g., by modeling of the interactions of the CDR and framework residues to identify framework residues important  
25 for antigen binding and sequence comparison to identify unusual framework residues at particular positions. (See, e.g., Queen et al., U.S. Patent No. 5,585,089; Riechmann et al., *Nature* 332:323 (1988), which are incorporated herein by reference in their entireties.) Antibodies can be humanized using a variety of techniques known in the art including, for example, CDR-grafting (EP 239,400; PCT publication WO 91/09967; U.S. Patent Nos.  
30 5,225,539; 5,530,101; and 5,585,089), veneering or resurfacing (EP 592,106; EP 519,596; Padlan, *Molecular Immunology* 28(4/5):489-498 (1991); Studnicka et al., *Protein*

Engineering 7(6):805-814 (1994); Roguska. et al., PNAS 91:969-973 (1994)), and chain shuffling (U.S. Patent No. 5,565,332).

Completely human antibodies are particularly desirable for therapeutic treatment of human patients. Human antibodies can be made by a variety of methods known in the art including phage display methods described above using antibody libraries derived from human immunoglobulin sequences. See also, U.S. Patent Nos. 4,444,887 and 4,716,111; and PCT publications WO 98/46645, WO 98/50433, WO 98/24893, WO 98/16654, WO 96/34096, WO 96/33735, and WO 91/10741; each of which is incorporated herein by reference in its entirety.

Human antibodies can also be produced using transgenic mice which are incapable of expressing functional endogenous immunoglobulins, but which can express human immunoglobulin genes. For example, the human heavy and light chain immunoglobulin gene complexes may be introduced randomly or by homologous recombination into mouse embryonic stem cells. Alternatively, the human variable region, constant region, and diversity region may be introduced into mouse embryonic stem cells in addition to the human heavy and light chain genes. The mouse heavy and light chain immunoglobulin genes may be rendered non-functional separately or simultaneously with the introduction of human immunoglobulin loci by homologous recombination. In particular, homozygous deletion of the JH region prevents endogenous antibody production. The modified embryonic stem cells are expanded and microinjected into blastocysts to produce chimeric mice. The chimeric mice are then bred to produce homozygous offspring which express human antibodies. The transgenic mice are immunized in the normal fashion with a selected antigen, e.g., all or a portion of a polypeptide of the invention. Monoclonal antibodies directed against the antigen can be obtained from the immunized, transgenic mice using conventional hybridoma technology. The human immunoglobulin transgenes harbored by the transgenic mice rearrange during B cell differentiation, and subsequently undergo class switching and somatic mutation. Thus, using such a technique, it is possible to produce therapeutically useful IgG, IgA, IgM and IgE antibodies. For an overview of this technology for producing human antibodies, see Lonberg and Huszar, *Int. Rev. Immunol.* 13:65-93 (1995). For a detailed discussion of this technology for producing human antibodies and human monoclonal antibodies and protocols for producing such antibodies, see, e.g., PCT publications WO 98/24893; WO 92/01047; WO 96/34096; WO 96/33735; European Patent

No. 0 598 877; U.S. Patent Nos. 5,413,923; 5,625,126; 5,633,425; 5,569,825; 5,661,016; 5,545,806; 5,814,318; 5,885,793; 5,916,771; and 5,939,598, which are incorporated by reference herein in their entirety. In addition, companies such as Abgenix, Inc. (Freemont, CA) and Genpharm (San Jose, CA) can be engaged to provide human antibodies directed  
5 against a selected antigen using technology similar to that described above.

Completely human antibodies which recognize a selected epitope can be generated using a technique referred to as "guided selection." In this approach a selected non-human monoclonal antibody, e.g., a mouse antibody, is used to guide the selection of a completely human antibody recognizing the same epitope. (Jespers et al., Bio/technology 12:899-903  
10 (1988)).

Further, antibodies to the polypeptides of the invention can, in turn, be utilized to generate anti-idiotypic antibodies that "mimic" polypeptides of the invention using techniques well known to those skilled in the art. (See, e.g., Greenspan & Bona, FASEB J. 7(5):437-444; (1989) and Nissinoff, J. Immunol. 147(8):2429-2438 (1991)). For example, antibodies  
15 which bind to and competitively inhibit polypeptide multimerization and/or binding of a polypeptide of the invention to a ligand can be used to generate anti-idiotypes that "mimic" the polypeptide multimerization and/or binding domain and, as a consequence, bind to and neutralize polypeptide and/or its ligand. Such neutralizing anti-idiotypes or Fab fragments of such anti-idiotypes can be used in therapeutic regimens to neutralize polypeptide ligand. For  
20 example, such anti-idiotypic antibodies can be used to bind a polypeptide of the invention and/or to bind its ligands/receptors, and thereby block its biological activity.

#### ***Polynucleotides Encoding Antibodies***

The invention further provides polynucleotides comprising a nucleotide sequence  
25 encoding an antibody of the invention and fragments thereof. The invention also encompasses polynucleotides that hybridize under stringent or alternatively, under lower stringency hybridization conditions, e.g., as defined supra, to polynucleotides that encode an antibody, preferably, that specifically binds to a polypeptide of the invention, preferably, an antibody that binds to a polypeptide having the amino acid sequence of SEQ ID NO:Y.

30 The polynucleotides may be obtained, and the nucleotide sequence of the polynucleotides determined, by any method known in the art. For example, if the nucleotide sequence of the antibody is known, a polynucleotide encoding the antibody may be

assembled from chemically synthesized oligonucleotides (e.g., as described in Kutmeier et al., *BioTechniques* 17:242 (1994)), which, briefly, involves the synthesis of overlapping oligonucleotides containing portions of the sequence encoding the antibody, annealing and ligating of those oligonucleotides, and then amplification of the ligated oligonucleotides by PCR.

Alternatively, a polynucleotide encoding an antibody may be generated from nucleic acid from a suitable source. If a clone containing a nucleic acid encoding a particular antibody is not available, but the sequence of the antibody molecule is known, a nucleic acid encoding the immunoglobulin may be chemically synthesized or obtained from a suitable source (e.g., an antibody cDNA library, or a cDNA library generated from, or nucleic acid, preferably poly A+ RNA, isolated from, any tissue or cells expressing the antibody, such as hybridoma cells selected to express an antibody of the invention) by PCR amplification using synthetic primers hybridizable to the 3' and 5' ends of the sequence or by cloning using an oligonucleotide probe specific for the particular gene sequence to identify, e.g., a cDNA clone from a cDNA library that encodes the antibody. Amplified nucleic acids generated by PCR may then be cloned into replicable cloning vectors using any method well known in the art.

Once the nucleotide sequence and corresponding amino acid sequence of the antibody is determined, the nucleotide sequence of the antibody may be manipulated using methods well known in the art for the manipulation of nucleotide sequences, e.g., recombinant DNA techniques, site directed mutagenesis, PCR, etc. (see, for example, the techniques described in Sambrook et al., 1990, *Molecular Cloning, A Laboratory Manual*, 2d Ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, NY and Ausubel et al., eds., 1998, *Current Protocols in Molecular Biology*, John Wiley & Sons, NY, which are both incorporated by reference herein in their entireties ), to generate antibodies having a different amino acid sequence, for example to create amino acid substitutions, deletions, and/or insertions.

In a specific embodiment, the amino acid sequence of the heavy and/or light chain variable domains may be inspected to identify the sequences of the complementarity determining regions (CDRs) by methods that are well known in the art. e.g., by comparison to known amino acid sequences of other heavy and light chain variable regions to determine the regions of sequence hypervariability. Using routine recombinant DNA techniques, one or more of the CDRs may be inserted within framework regions, e.g., into human framework

regions to humanize a non-human antibody, as described supra. The framework regions may be naturally occurring or consensus framework regions, and preferably human framework regions (see, e.g., Chothia et al., J. Mol. Biol. 278: 457-479 (1998) for a listing of human framework regions). Preferably, the polynucleotide generated by the combination of the framework regions and CDRs encodes an antibody that specifically binds a polypeptide of the invention. Preferably, as discussed supra, one or more amino acid substitutions may be made within the framework regions, and, preferably, the amino acid substitutions improve binding of the antibody to its antigen. Additionally, such methods may be used to make amino acid substitutions or deletions of one or more variable region cysteine residues participating in an intrachain disulfide bond to generate antibody molecules lacking one or more intrachain disulfide bonds. Other alterations to the polynucleotide are encompassed by the present invention and within the skill of the art.

In addition, techniques developed for the production of "chimeric antibodies" (Morrison et al., Proc. Natl. Acad. Sci. 81:851-855 (1984); Neuberger et al., Nature 312:604-608 (1984); Takeda et al., Nature 314:452-454 (1985)) by splicing genes from a mouse antibody molecule of appropriate antigen specificity together with genes from a human antibody molecule of appropriate biological activity can be used. As described supra, a chimeric antibody is a molecule in which different portions are derived from different animal species, such as those having a variable region derived from a murine mAb and a human immunoglobulin constant region, e.g., humanized antibodies.

Alternatively, techniques described for the production of single chain antibodies (U.S. Patent No. 4,946,778; Bird, Science 242:423-42 (1988); Huston et al., Proc. Natl. Acad. Sci. USA 85:5879-5883 (1988); and Ward et al., Nature 334:544-54 (1989)) can be adapted to produce single chain antibodies. Single chain antibodies are formed by linking the heavy and light chain fragments of the Fv region via an amino acid bridge, resulting in a single chain polypeptide. Techniques for the assembly of functional Fv fragments in E. coli may also be used (Skerra et al., Science 242:1038-1041 (1988)).

#### ***Methods of Producing Antibodies***

The antibodies of the invention can be produced by any method known in the art for the synthesis of antibodies, in particular, by chemical synthesis or preferably, by recombinant expression techniques.

Recombinant expression of an antibody of the invention, or fragment, derivative or analog thereof, (e.g., a heavy or light chain of an antibody of the invention or a single chain antibody of the invention), requires construction of an expression vector containing a polynucleotide that encodes the antibody. Once a polynucleotide encoding an antibody molecule or a heavy or light chain of an antibody, or portion thereof (preferably containing the heavy or light chain variable domain), of the invention has been obtained, the vector for the production of the antibody molecule may be produced by recombinant DNA technology using techniques well known in the art. Thus, methods for preparing a protein by expressing a polynucleotide containing an antibody encoding nucleotide sequence are described herein.

Methods which are well known to those skilled in the art can be used to construct expression vectors containing antibody coding sequences and appropriate transcriptional and translational control signals. These methods include, for example, in vitro recombinant DNA techniques, synthetic techniques, and in vivo genetic recombination. The invention, thus, provides replicable vectors comprising a nucleotide sequence encoding an antibody molecule of the invention, or a heavy or light chain thereof, or a heavy or light chain variable domain, operably linked to a promoter. Such vectors may include the nucleotide sequence encoding the constant region of the antibody molecule (see, e.g., PCT Publication WO 86/05807; PCT Publication WO 89/01036; and U.S. Patent No. 5,122,464) and the variable domain of the antibody may be cloned into such a vector for expression of the entire heavy or light chain.

The expression vector is transferred to a host cell by conventional techniques and the transfected cells are then cultured by conventional techniques to produce an antibody of the invention. Thus, the invention includes host cells containing a polynucleotide encoding an antibody of the invention, or a heavy or light chain thereof, or a single chain antibody of the invention, operably linked to a heterologous promoter. In preferred embodiments for the expression of double-chained antibodies, vectors encoding both the heavy and light chains may be co-expressed in the host cell for expression of the entire immunoglobulin molecule, as detailed below.

A variety of host-expression vector systems may be utilized to express the antibody molecules of the invention. Such host-expression systems represent vehicles by which the coding sequences of interest may be produced and subsequently purified, but also represent cells which may, when transformed or transfected with the appropriate nucleotide coding sequences, express an antibody molecule of the invention in situ. These include but are not

limited to microorganisms such as bacteria (e.g., *E. coli*, *B. subtilis*) transformed with recombinant bacteriophage DNA, plasmid DNA or cosmid DNA expression vectors containing antibody coding sequences; yeast (e.g., *Saccharomyces*, *Pichia*) transformed with recombinant yeast expression vectors containing antibody coding sequences; insect cell  
5 systems infected with recombinant virus expression vectors (e.g., baculovirus) containing antibody coding sequences; plant cell systems infected with recombinant virus expression vectors (e.g., cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or transformed with recombinant plasmid expression vectors (e.g., Ti plasmid) containing antibody coding sequences; or mammalian cell systems (e.g., COS, CHO, BHK, 293, 3T3 cells) harboring  
10 recombinant expression constructs containing promoters derived from the genome of mammalian cells (e.g., metallothionein promoter) or from mammalian viruses (e.g., the adenovirus late promoter; the vaccinia virus 7.5K promoter). Preferably, bacterial cells such as *Escherichia coli*, and more preferably, eukaryotic cells, especially for the expression of whole recombinant antibody molecule, are used for the expression of a recombinant antibody  
15 molecule. For example, mammalian cells such as Chinese hamster ovary cells (CHO), in conjunction with a vector such as the major intermediate early gene promoter element from human cytomegalovirus is an effective expression system for antibodies (Foecking et al., *Gene* 45:101 (1986); Cockett et al., *Bio/Technology* 8:2 (1990)).

In bacterial systems, a number of expression vectors may be advantageously selected  
20 depending upon the use intended for the antibody molecule being expressed. For example, when a large quantity of such a protein is to be produced, for the generation of pharmaceutical compositions of an antibody molecule, vectors which direct the expression of high levels of fusion protein products that are readily purified may be desirable. Such vectors include, but are not limited, to the *E. coli* expression vector pUR278 (Ruther et al., *EMBO J.*  
25 2:1791 (1983)), in which the antibody coding sequence may be ligated individually into the vector in frame with the lac Z coding region so that a fusion protein is produced; pIN vectors (Inouye & Inouye, *Nucleic Acids Res.* 13:3101-3109 (1985); Van Heeke & Schuster, *J. Biol. Chem.* 24:5503-5509 (1989)); and the like. pGEX vectors may also be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general,  
30 such fusion proteins are soluble and can easily be purified from lysed cells by adsorption and binding to matrix glutathione-agarose beads followed by elution in the presence of free

glutathione. The pGEX vectors are designed to include thrombin or factor Xa protease cleavage sites so that the cloned target gene product can be released from the GST moiety.

In an insect system, Autographa californica nuclear polyhedrosis virus (AcNPV) is used as a vector to express foreign genes. The virus grows in *Spodoptera frugiperda* cells.

- 5 The antibody coding sequence may be cloned individually into non-essential regions (for example the polyhedrin gene) of the virus and placed under control of an AcNPV promoter (for example the polyhedrin promoter).

- In mammalian host cells, a number of viral-based expression systems may be utilized. In cases where an adenovirus is used as an expression vector, the antibody coding sequence  
10 of interest may be ligated to an adenovirus transcription/translation control complex, e.g., the late promoter and tripartite leader sequence. This chimeric gene may then be inserted in the adenovirus genome by in vitro or in vivo recombination. Insertion in a non-essential region of the viral genome (e.g., region E1 or E3) will result in a recombinant virus that is viable and capable of expressing the antibody molecule in infected hosts. (e.g., see Logan & Shenk,  
15 Proc. Natl. Acad. Sci. USA 81:355-359 (1984)). Specific initiation signals may also be required for efficient translation of inserted antibody coding sequences. These signals include the ATG initiation codon and adjacent sequences. Furthermore, the initiation codon must be in phase with the reading frame of the desired coding sequence to ensure translation of the entire insert. These exogenous translational control signals and initiation codons can  
20 be of a variety of origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of appropriate transcription enhancer elements, transcription terminators, etc. (see Bittner et al., Methods in Enzymol. 153:51-544 (1987)).

- In addition, a host cell strain may be chosen which modulates the expression of the inserted sequences, or modifies and processes the gene product in the specific fashion  
25 desired. Such modifications (e.g., glycosylation) and processing (e.g., cleavage) of protein products may be important for the function of the protein. Different host cells have characteristic and specific mechanisms for the post-translational processing and modification of proteins and gene products. Appropriate cell lines or host systems can be chosen to ensure the correct modification and processing of the foreign protein expressed. To this end,  
30 eukaryotic host cells which possess the cellular machinery for proper processing of the primary transcript, glycosylation, and phosphorylation of the gene product may be used. Such mammalian host cells include but are not limited to CHO, VERY, BHK, HeLa, COS,



MDCK, 293, 3T3, WI38, and in particular, breast cancer cell lines such as, for example, BT483, Hs578T, HTB2, BT20 and T47D, and normal mammary gland cell line such as, for example, CRL7030 and Hs578Bst.

For long-term, high-yield production of recombinant proteins, stable expression is preferred. For example, cell lines which stably express the antibody molecule may be engineered. Rather than using expression vectors which contain viral origins of replication, host cells can be transformed with DNA controlled by appropriate expression control elements (e.g., promoter, enhancer, sequences, transcription terminators, polyadenylation sites, etc.), and a selectable marker. Following the introduction of the foreign DNA, engineered cells may be allowed to grow for 1-2 days in an enriched media, and then are switched to a selective media. The selectable marker in the recombinant plasmid confers resistance to the selection and allows cells to stably integrate the plasmid into their chromosomes and grow to form foci which in turn can be cloned and expanded into cell lines. This method may advantageously be used to engineer cell lines which express the antibody molecule. Such engineered cell lines may be particularly useful in screening and evaluation of compounds that interact directly or indirectly with the antibody molecule.

A number of selection systems may be used, including but not limited to the herpes simplex virus thymidine kinase (Wigler et al., Cell 11:223 (1977)), hypoxanthine-guanine phosphoribosyltransferase (Szybalska & Szybalski, Proc. Natl. Acad. Sci. USA 48:202 (1992)), and adenine phosphoribosyltransferase (Lowy et al., Cell 22:817 (1980)) genes can be employed in tk-, hgp<sup>r</sup>t- or ap<sup>r</sup>t- cells, respectively. Also, antimetabolite resistance can be used as the basis of selection for the following genes: dhfr, which confers resistance to methotrexate (Wigler et al., Natl. Acad. Sci. USA 77:357 (1980); O'Hare et al., Proc. Natl. Acad. Sci. USA 78:1527 (1981)); gpt, which confers resistance to mycophenolic acid (Mulligan & Berg, Proc. Natl. Acad. Sci. USA 78:2072 (1981)); neo, which confers resistance to the aminoglycoside G-418 Clinical Pharmacy 12:488-505; Wu and Wu, Biotherapy 3:87-95 (1991); Tolstoshev, Ann. Rev. Pharmacol. Toxicol. 32:573-596 (1993); Mulligan, Science 260:926-932 (1993); and Morgan and Anderson, Ann. Rev. Biochem. 62:191-217 (1993); May, 1993, TIB TECH 11(5):155-215; and hyg<sup>r</sup>, which confers resistance to hygromycin (Santerre et al., Gene 30:147 (1984)). Methods commonly known in the art of recombinant DNA technology may be routinely applied to select the desired recombinant clone, and such methods are described, for example, in Ausubel et al. (eds.),

Current Protocols in Molecular Biology, John Wiley & Sons, NY (1993); Kriegler, Gene Transfer and Expression, A Laboratory Manual, Stockton Press, NY (1990); and in Chapters 12 and 13, Dracopoli et al. (eds), Current Protocols in Human Genetics, John Wiley & Sons, NY (1994); Colberre-Garapin et al., J. Mol. Biol. 150:1 (1981), which are incorporated by  
5 reference herein in their entirety.

The expression levels of an antibody molecule can be increased by vector amplification (for a review, see Bebbington and Hentschel, The use of vectors based on gene amplification for the expression of cloned genes in mammalian cells in DNA cloning, Vol.3. (Academic Press, New York, 1987)). When a marker in the vector system expressing  
10 antibody is amplifiable, increase in the level of inhibitor present in culture of host cell will increase the number of copies of the marker gene. Since the amplified region is associated with the antibody gene, production of the antibody will also increase (Crouse et al., Mol. Cell. Biol. 3:257 (1983)).

The host cell may be co-transfected with two expression vectors of the invention, the  
15 first vector encoding a heavy chain derived polypeptide and the second vector encoding a light chain derived polypeptide. The two vectors may contain identical selectable markers which enable equal expression of heavy and light chain polypeptides. Alternatively, a single vector may be used which encodes, and is capable of expressing, both heavy and light chain polypeptides. In such situations, the light chain should be placed before the heavy chain to  
20 avoid an excess of toxic free heavy chain (Proudfoot, Nature 322:52 (1986); Kohler, Proc. Natl. Acad. Sci. USA 77:2197 (1980)). The coding sequences for the heavy and light chains may comprise cDNA or genomic DNA.

Once an antibody molecule of the invention has been produced by an animal, chemically synthesized, or recombinantly expressed, it may be purified by any method  
25 known in the art for purification of an immunoglobulin molecule, for example, by chromatography (e.g., ion exchange, affinity, particularly by affinity for the specific antigen after Protein A, and sizing column chromatography), centrifugation, differential solubility, or by any other standard technique for the purification of proteins. In addition, the antibodies of the present invention or fragments thereof can be fused to heterologous polypeptide  
30 sequences described herein or otherwise known in the art, to facilitate purification.

The present invention encompasses antibodies recombinantly fused or chemically conjugated (including both covalently and non-covalently conjugations) to a polypeptide (or

portion thereof, preferably at least 10, 20, 30, 40, 50, 60, 70, 80, 90 or 100 amino acids of the polypeptide) of the present invention to generate fusion proteins. The fusion does not necessarily need to be direct, but may occur through linker sequences. The antibodies may be specific for antigens other than polypeptides (or portion thereof, preferably at least 10, 20, 30, 40, 50, 60, 70, 80, 90 or 100 amino acids of the polypeptide) of the present invention. For example, antibodies may be used to target the polypeptides of the present invention to particular cell types, either in vitro or in vivo, by fusing or conjugating the polypeptides of the present invention to antibodies specific for particular cell surface receptors. Antibodies fused or conjugated to the polypeptides of the present invention may also be used in in vitro immunoassays and purification methods using methods known in the art. See e.g., Harbor et al., supra, and PCT publication WO 93/21232; EP 439,095; Naramura et al., Immunol. Lett. 39:91-99 (1994); U.S. Patent 5,474,981; Gillies et al., PNAS 89:1428-1432 (1992); Fell et al., J. Immunol. 146:2446-2452(1991), which are incorporated by reference in their entireties.

The present invention further includes compositions comprising the polypeptides of the present invention fused or conjugated to antibody domains other than the variable regions. For example, the polypeptides of the present invention may be fused or conjugated to an antibody Fc region, or portion thereof. The antibody portion fused to a polypeptide of the present invention may comprise the constant region, hinge region, CH1 domain, CH2 domain, and CH3 domain or any combination of whole domains or portions thereof. The polypeptides may also be fused or conjugated to the above antibody portions to form multimers. For example, Fc portions fused to the polypeptides of the present invention can form dimers through disulfide bonding between the Fc portions. Higher multimeric forms can be made by fusing the polypeptides to portions of IgA and IgM. Methods for fusing or conjugating the polypeptides of the present invention to antibody portions are known in the art. See, e.g., U.S. Patent Nos. 5,336,603; 5,622,929; 5,359,046; 5,349,053; 5,447,851; 5,112,946; EP 307,434; EP 367,166; PCT publications WO 96/04388; WO 91/06570; Ashkenazi et al., Proc. Natl. Acad. Sci. USA 88:10535-10539 (1991); Zheng et al., J. Immunol. 154:5590-5600 (1995); and Vil et al., Proc. Natl. Acad. Sci. USA 89:11337-11341(1992) (said references incorporated by reference in their entireties).

As discussed, supra, the polypeptides corresponding to a polypeptide, polypeptide fragment, or a variant of SEQ ID NO:Y may be fused or conjugated to the above antibody portions to increase the in vivo half life of the polypeptides or for use in immunoassays using

methods known in the art. Further, the polypeptides corresponding to SEQ ID NO:Y may be fused or conjugated to the above antibody portions to facilitate purification. One reported example describes chimeric proteins consisting of the first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light chains of mammalian immunoglobulins. (EP 394,827; Traunecker et al., *Nature* 331:84-86 (1988)). The polypeptides of the present invention fused or conjugated to an antibody having disulfide-linked dimeric structures (due to the IgG) may also be more efficient in binding and neutralizing other molecules, than the monomeric secreted protein or protein fragment alone. (Fountoulakis et al., *J. Biochem.* 270:3958-3964 (1995)). In many cases, the Fc part in a fusion protein is beneficial in therapy and diagnosis, and thus can result in, for example, improved pharmacokinetic properties. (EP A 232,262). Alternatively, deleting the Fc part after the fusion protein has been expressed, detected, and purified, would be desired. For example, the Fc portion may hinder therapy and diagnosis if the fusion protein is used as an antigen for immunizations. In drug discovery, for example, human proteins, such as hIL-5, have been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists of hIL-5. (See, Bennett et al., *J. Molecular Recognition* 8:52-58 (1995); Johanson et al., *J. Biol. Chem.* 270:9459-9471 (1995)).

Moreover, the antibodies or fragments thereof of the present invention can be fused to marker sequences, such as a peptide to facilitate purification. In preferred embodiments, the marker amino acid sequence is a hexa-histidine peptide, such as the tag provided in a pQE vector (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311), among others, many of which are commercially available. As described in Gentz et al., *Proc. Natl. Acad. Sci. USA* 86:821-824 (1989), for instance, hexa-histidine provides for convenient purification of the fusion protein. Other peptide tags useful for purification include, but are not limited to, the "HA" tag, which corresponds to an epitope derived from the influenza hemagglutinin protein (Wilson et al., *Cell* 37:767 (1984)) and the "flag" tag.

The present invention further encompasses antibodies or fragments thereof conjugated to a diagnostic or therapeutic agent. The antibodies can be used diagnostically to, for example, monitor the development or progression of a tumor as part of a clinical testing procedure to, e.g., determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent

materials, bioluminescent materials, radioactive materials, positron emitting metals using various positron emission tomographies, and nonradioactive paramagnetic metal ions. The detectable substance may be coupled or conjugated either directly to the antibody (or fragment thereof) or indirectly, through an intermediate (such as, for example, a linker known in the art) using techniques known in the art. See, for example, U.S. Patent No. 4,741,900 for metal ions which can be conjugated to antibodies for use as diagnostics according to the present invention. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, beta-galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin; and examples of suitable radioactive material include <sup>125</sup>I, <sup>131</sup>I, <sup>111</sup>In or <sup>99</sup>Tc.

Further, an antibody or fragment thereof may be conjugated to a therapeutic moiety such as a cytotoxin, e.g., a cytostatic or cytotoxic agent, a therapeutic agent or a radioactive metal ion, e.g., alpha-emitters such as, for example, <sup>213</sup>Bi. A cytotoxin or cytotoxic agent includes any agent that is detrimental to cells. Examples include paclitaxol, cytochalasin B, gramicidin D, ethidium bromide, emetine, mitomycin, etoposide, teniposide, vincristine, vinblastine, colchicin, doxorubicin, daunorubicin, dihydroxy anthracin dione, mitoxantrone, mithramycin, actinomycin D, 1-dehydrotestosterone, glucocorticoids, procaine, tetracaine, lidocaine, propranolol, and puromycin and analogs or homologs thereof. Therapeutic agents include, but are not limited to, antimetabolites (e.g., methotrexate, 6-mercaptopurine, 6-thioguanine, cytarabine, 5-fluorouracil decarbazine), alkylating agents (e.g., mechlorethamine, thioepa chlorambucil, melphalan, carmustine (BSNU) and lomustine (CCNU), cyclophosphamide, busulfan, dibromomannitol, streptozotocin, mitomycin C, and cis-dichlorodiamine platinum (II) (DDP) cisplatin), anthracyclines (e.g., daunorubicin (formerly daunomycin) and doxorubicin), antibiotics (e.g., dactinomycin (formerly actinomycin), bleomycin, mithramycin, and anthramycin (AMC)), and anti-mitotic agents (e.g., vincristine and vinblastine).

The conjugates of the invention can be used for modifying a given biological response, the therapeutic agent or drug moiety is not to be construed as limited to classical

chemical therapeutic agents. For example, the drug moiety may be a protein or polypeptide possessing a desired biological activity. Such proteins may include, for example, a toxin such as abrin, ricin A, pseudomonas exotoxin, or diphtheria toxin; a protein such as tumor necrosis factor,  $\alpha$ -interferon,  $\beta$ -interferon, nerve growth factor, platelet derived growth factor, 5 tissue plasminogen activator, an apoptotic agent, e.g., TNF- $\alpha$ , TNF- $\beta$ , AIM I (See, International Publication No. WO 97/33899), AIM II (See, International Publication No. WO 97/34911), Fas Ligand (Takahashi *et al.*, *Int. Immunol.*, 6:1567-1574 (1994)), VEGF (See, International Publication No. WO 99/23105), a thrombotic agent or an anti-angiogenic agent, e.g., angiostatin or endostatin; or, biological response modifiers such as, for example, 10 lymphokines, interleukin-1 ("IL-1"), interleukin-2 ("IL-2"), interleukin-6 ("IL-6"), granulocyte macrophage colony stimulating factor ("GM-CSF"), granulocyte colony stimulating factor ("G-CSF"), or other growth factors.

Antibodies may also be attached to solid supports, which are particularly useful for immunoassays or purification of the target antigen. Such solid supports include, but are not 15 limited to, glass, cellulose, polyacrylamide, nylon, polystyrene, polyvinyl chloride or polypropylene.

Techniques for conjugating such therapeutic moiety to antibodies are well known, see, e.g., Amon *et al.*, "Monoclonal Antibodies For Immunotargeting Of Drugs In Cancer Therapy", in *Monoclonal Antibodies And Cancer Therapy*, Reisfeld *et al.* (eds.), pp. 243-56 20 (Alan R. Liss, Inc. 1985); Hellstrom *et al.*, "Antibodies For Drug Delivery", in *Controlled Drug Delivery* (2nd Ed.), Robinson *et al.* (eds.), pp. 623-53 (Marcel Dekker, Inc. 1987); Thorpe, "Antibody Carriers Of Cytotoxic Agents In Cancer Therapy: A Review", in *Monoclonal Antibodies '84: Biological And Clinical Applications*, Pinchera *et al.* (eds.), pp. 475-506 (1985); "Analysis, Results, And Future Prospective Of The Therapeutic Use Of 25 Radiolabeled Antibody In Cancer Therapy", in *Monoclonal Antibodies For Cancer Detection And Therapy*, Baldwin *et al.* (eds.), pp. 303-16 (Academic Press 1985), and Thorpe *et al.*, "The Preparation And Cytotoxic Properties Of Antibody-Toxin Conjugates", *Immunol. Rev.* 62:119-58 (1982).

Alternatively, an antibody can be conjugated to a second antibody to form an antibody 30 heteroconjugate as described by Segal in U.S. Patent No. 4,676,980, which is incorporated herein by reference in its entirety.

An antibody, with or without a therapeutic moiety conjugated to it, administered alone or in combination with cytotoxic factor(s) and/or cytokine(s) can be used as a therapeutic.

### ***Immunophenotyping***

5       The antibodies of the invention may be utilized for immunophenotyping of cell lines and biological samples. The translation product of the gene of the present invention may be useful as a cell specific marker, or more specifically as a cellular marker that is differentially expressed at various stages of differentiation and/or maturation of particular cell types. Monoclonal antibodies directed against a specific epitope, or combination of epitopes, will  
10       allow for the screening of cellular populations expressing the marker. Various techniques can be utilized using monoclonal antibodies to screen for cellular populations expressing the marker(s), and include magnetic separation using antibody-coated magnetic beads, "panning" with antibody attached to a solid matrix (i.e., plate), and flow cytometry (See, e.g., U.S. Patent 5,985,660; and Morrison *et al.*, *Cell*, 96:737-49 (1999)).

15       These techniques allow for the screening of particular populations of cells, such as might be found with hematological malignancies (i.e. minimal residual disease (MRD) in acute leukemic patients) and "non-self" cells in transplantations to prevent Graft-versus-Host Disease (GVHD). Alternatively, these techniques allow for the screening of hematopoietic stem and progenitor cells capable of undergoing proliferation and/or differentiation, as might  
20       be found in human umbilical cord blood.

### ***Assays For Antibody Binding***

      The antibodies of the invention may be assayed for immunospecific binding by any method known in the art. The immunoassays which can be used include but are not limited  
25       to competitive and non-competitive assay systems using techniques such as western blots, radioimmunoassays, ELISA (enzyme linked immunosorbent assay), "sandwich" immunoassays, immunoprecipitation assays, precipitin reactions, gel diffusion precipitin reactions, immunodiffusion assays, agglutination assays, complement-fixation assays, immunoradiometric assays, fluorescent immunoassays, protein A immunoassays, to name  
30       but a few. Such assays are routine and well known in the art (see, e.g., Ausubel *et al.*, eds. 1994, *Current Protocols in Molecular Biology*, Vol. 1, John Wiley & Sons, Inc., New York,

which is incorporated by reference herein in its entirety). Exemplary immunoassays are described briefly below (but are not intended by way of limitation).

Immunoprecipitation protocols generally comprise lysing a population of cells in a lysis buffer such as RIPA buffer (1% NP-40 or Triton X- 100, 1% sodium deoxycholate, 0.1% SDS, 0.15 M NaCl, 0.01 M sodium phosphate at pH 7.2, 1% Trasylol) supplemented with protein phosphatase and/or protease inhibitors (e.g., EDTA, PMSF, aprotinin, sodium vanadate), adding the antibody of interest to the cell lysate, incubating for a period of time (e.g., 1-4 hours) at 4° C. adding protein A and/or protein G sepharose beads to the cell lysate, incubating for about an hour or more at 4° C, washing the beads in lysis buffer and resuspending the beads in SDS/sample buffer. The ability of the antibody of interest to immunoprecipitate a particular antigen can be assessed by, e.g., western blot analysis. One of skill in the art would be knowledgeable as to the parameters that can be modified to increase the binding of the antibody to an antigen and decrease the background (e.g., pre-clearing the cell lysate with sepharose beads). For further discussion regarding immunoprecipitation protocols see, e.g., Ausubel et al, eds, 1994, Current Protocols in Molecular Biology, Vol. 1, John Wiley & Sons, Inc., New York at 10.16.1.

Western blot analysis generally comprises preparing protein samples, electrophoresis of the protein samples in a polyacrylamide gel (e.g., 8%- 20% SDS-PAGE depending on the molecular weight of the antigen), transferring the protein sample from the polyacrylamide gel to a membrane such as nitrocellulose, PVDF or nylon, blocking the membrane in blocking solution (e.g., PBS with 3% BSA or non-fat milk), washing the membrane in washing buffer (e.g., PBS-Tween 20), blocking the membrane with primary antibody (the antibody of interest) diluted in blocking buffer, washing the membrane in washing buffer, blocking the membrane with a secondary antibody (which recognizes the primary antibody, e.g., an anti-human antibody) conjugated to an enzymatic substrate (e.g., horseradish peroxidase or alkaline phosphatase) or radioactive molecule (e.g., <sup>32</sup>P or <sup>125</sup>I) diluted in blocking buffer, washing the membrane in wash buffer, and detecting the presence of the antigen. One of skill in the art would be knowledgeable as to the parameters that can be modified to increase the signal detected and to reduce the background noise. For further discussion regarding western blot protocols see, e.g., Ausubel et al, eds, 1994, Current Protocols in Molecular Biology, Vol. 1, John Wiley & Sons, Inc., New York at 10.8.1.



ELISAs comprise preparing antigen, coating the well of a 96 well microtiter plate with the antigen, adding the antibody of interest conjugated to a detectable compound such as an enzymatic substrate (e.g., horseradish peroxidase or alkaline phosphatase) to the well and incubating for a period of time, and detecting the presence of the antigen. In ELISAs the antibody of interest does not have to be conjugated to a detectable compound: instead, a second antibody (which recognizes the antibody of interest) conjugated to a detectable compound may be added to the well. Further, instead of coating the well with the antigen, the antibody may be coated to the well. In this case, a second antibody conjugated to a detectable compound may be added following the addition of the antigen of interest to the coated well. One of skill in the art would be knowledgeable as to the parameters that can be modified to increase the signal detected as well as other variations of ELISAs known in the art. For further discussion regarding ELISAs see, e.g., Ausubel et al, eds. 1994, Current Protocols in Molecular Biology, Vol. 1, John Wiley & Sons, Inc., New York at 11.2.1.

The binding affinity of an antibody to an antigen and the off-rate of an antibody-antigen interaction can be determined by competitive binding assays. One example of a competitive binding assay is a radioimmunoassay comprising the incubation of labeled antigen (e.g., <sup>3</sup>H or <sup>125</sup>I) with the antibody of interest in the presence of increasing amounts of unlabeled antigen, and the detection of the antibody bound to the labeled antigen. The affinity of the antibody of interest for a particular antigen and the binding off-rates can be determined from the data by scatchard plot analysis. Competition with a second antibody can also be determined using radioimmunoassays. In this case, the antigen is incubated with antibody of interest conjugated to a labeled compound (e.g., <sup>3</sup>H or <sup>125</sup>I) in the presence of increasing amounts of an unlabeled second antibody.

## 25 *Therapeutic Uses*

The present invention is further directed to antibody-based therapies which involve administering antibodies of the invention to an animal, preferably a mammal, and most preferably a human, patient for treating one or more of the disclosed diseases, disorders, or conditions. Therapeutic compounds of the invention include, but are not limited to, antibodies of the invention (including fragments, analogs and derivatives thereof as described herein) and nucleic acids encoding antibodies of the invention (including fragments, analogs and derivatives thereof and anti-idiotypic antibodies as described herein). The antibodies of

the invention can be used to treat, inhibit or prevent diseases, disorders or conditions associated with aberrant expression and/or activity of a polypeptide of the invention, including, but not limited to, any one or more of the diseases, disorders, or conditions described herein. The treatment and/or prevention of diseases, disorders, or conditions associated with aberrant expression and/or activity of a polypeptide of the invention includes, but is not limited to, alleviating symptoms associated with those diseases, disorders or conditions. Antibodies of the invention may be provided in pharmaceutically acceptable compositions as known in the art or as described herein.

A summary of the ways in which the antibodies of the present invention may be used therapeutically includes binding polynucleotides or polypeptides of the present invention locally or systemically in the body or by direct cytotoxicity of the antibody, e.g. as mediated by complement (CDC) or by effector cells (ADCC). Some of these approaches are described in more detail below. Armed with the teachings provided herein, one of ordinary skill in the art will know how to use the antibodies of the present invention for diagnostic, monitoring or therapeutic purposes without undue experimentation.

The antibodies of this invention may be advantageously utilized in combination with other monoclonal or chimeric antibodies, or with lymphokines or hematopoietic growth factors (such as, e.g., IL-2, IL-3 and IL-7), for example, which serve to increase the number or activity of effector cells which interact with the antibodies.

The antibodies of the invention may be administered alone or in combination with other types of treatments (e.g., radiation therapy, chemotherapy, hormonal therapy, immunotherapy and anti-tumor agents). Generally, administration of products of a species origin or species reactivity (in the case of antibodies) that is the same species as that of the patient is preferred. Thus, in a preferred embodiment, human antibodies, fragments derivatives, analogs, or nucleic acids, are administered to a human patient for therapy or prophylaxis.

It is preferred to use high affinity and/or potent in vivo inhibiting and/or neutralizing antibodies against polypeptides or polynucleotides of the present invention, fragments or regions thereof, for both immunoassays directed to and therapy of disorders related to polynucleotides or polypeptides, including fragments thereof, of the present invention. Such antibodies, fragments, or regions, will preferably have an affinity for polynucleotides or polypeptides of the invention, including fragments thereof. Preferred binding affinities

include those with a dissociation constant or  $K_d$  less than  $5 \times 10^{-2}$  M,  $10^{-2}$  M,  $5 \times 10^{-3}$  M,  $10^{-3}$  M,  $5 \times 10^{-4}$  M,  $10^{-4}$  M,  $5 \times 10^{-5}$  M,  $10^{-5}$  M,  $5 \times 10^{-6}$  M,  $10^{-6}$  M,  $5 \times 10^{-7}$  M,  $10^{-7}$  M,  $5 \times 10^{-8}$  M,  $10^{-8}$  M,  $5 \times 10^{-9}$  M,  $10^{-9}$  M,  $5 \times 10^{-10}$  M,  $10^{-10}$  M,  $5 \times 10^{-11}$  M,  $10^{-11}$  M,  $5 \times 10^{-12}$  M,  $10^{-12}$  M,  $5 \times 10^{-13}$  M,  $10^{-13}$  M,  $5 \times 10^{-14}$  M,  $10^{-14}$  M,  $5 \times 10^{-15}$  M, and  $10^{-15}$  M.

5

### *Gene Therapy*

In a specific embodiment, nucleic acids comprising sequences encoding antibodies or functional derivatives thereof, are administered to treat, inhibit or prevent a disease or disorder associated with aberrant expression and/or activity of a polypeptide of the invention, by way of gene therapy. Gene therapy refers to therapy performed by the administration to a subject of an expressed or expressible nucleic acid. In this embodiment of the invention, the nucleic acids produce their encoded protein that mediates a therapeutic effect.

Any of the methods for gene therapy available in the art can be used according to the present invention. Exemplary methods are described below.

For general reviews of the methods of gene therapy, see Goldspiel et al., *Clinical Pharmacy* 12:488-505 (1993); Wu and Wu, *Biotherapy* 3:87-95 (1991); Tolstoshev, *Ann. Rev. Pharmacol. Toxicol.* 32:573-596 (1993); Mulligan, *Science* 260:926-932 (1993); and Morgan and Anderson, *Ann. Rev. Biochem.* 62:191-217 (1993); May, *TIBTECH* 11(5):155-215 (1993). Methods commonly known in the art of recombinant DNA technology which can be used are described in Ausubel et al. (eds.), *Current Protocols in Molecular Biology*, John Wiley & Sons, NY (1993); and Kriegler, *Gene Transfer and Expression, A Laboratory Manual*, Stockton Press, NY (1990).

In a preferred aspect, the compound comprises nucleic acid sequences encoding an antibody, said nucleic acid sequences being part of expression vectors that express the antibody or fragments or chimeric proteins or heavy or light chains thereof in a suitable host. In particular, such nucleic acid sequences have promoters operably linked to the antibody coding region, said promoter being inducible or constitutive, and, optionally, tissue-specific. In another particular embodiment, nucleic acid molecules are used in which the antibody coding sequences and any other desired sequences are flanked by regions that promote homologous recombination at a desired site in the genome, thus providing for intrachromosomal expression of the antibody encoding nucleic acids (Koller and Smithies, *Proc. Natl. Acad. Sci. USA* 86:8932-8935 (1989); Zijlstra et al., *Nature* 342:435-438 (1989).

In specific embodiments, the expressed antibody molecule is a single chain antibody; alternatively, the nucleic acid sequences include sequences encoding both the heavy and light chains, or fragments thereof, of the antibody.

Delivery of the nucleic acids into a patient may be either direct, in which case the patient is directly exposed to the nucleic acid or nucleic acid-carrying vectors, or indirect, in which case, cells are first transformed with the nucleic acids in vitro, then transplanted into the patient. These two approaches are known, respectively, as in vivo or ex vivo gene therapy.

In a specific embodiment, the nucleic acid sequences are directly administered in vivo, where it is expressed to produce the encoded product. This can be accomplished by any of numerous methods known in the art, e.g., by constructing them as part of an appropriate nucleic acid expression vector and administering it so that they become intracellular, e.g., by infection using defective or attenuated retrovirals or other viral vectors (see U.S. Patent No. 4,980,286), or by direct injection of naked DNA, or by use of microparticle bombardment (e.g., a gene gun; Biolistic, Dupont), or coating with lipids or cell-surface receptors or transfecting agents, encapsulation in liposomes, microparticles, or microcapsules, or by administering them in linkage to a peptide which is known to enter the nucleus, by administering it in linkage to a ligand subject to receptor-mediated endocytosis (see, e.g., Wu and Wu, J. Biol. Chem. 262:4429-4432 (1987)) (which can be used to target cell types specifically expressing the receptors), etc. In another embodiment, nucleic acid-ligand complexes can be formed in which the ligand comprises a fusogenic viral peptide to disrupt endosomes, allowing the nucleic acid to avoid lysosomal degradation. In yet another embodiment, the nucleic acid can be targeted in vivo for cell specific uptake and expression, by targeting a specific receptor (see, e.g., PCT Publications WO 92/06180; WO 92/22635; WO92/20316; WO93/14188, WO 93/20221). Alternatively, the nucleic acid can be introduced intracellularly and incorporated within host cell DNA for expression, by homologous recombination (Koller and Smithies, Proc. Natl. Acad. Sci. USA 86:8932-8935 (1989); Zijlstra et al., Nature 342:435-438 (1989)).

In a specific embodiment, viral vectors that contains nucleic acid sequences encoding an antibody of the invention are used. For example, a retroviral vector can be used (see Miller et al., Meth. Enzymol. 217:581-599 (1993)). These retroviral vectors contain the components necessary for the correct packaging of the viral genome and integration into the

host cell DNA. The nucleic acid sequences encoding the antibody to be used in gene therapy are cloned into one or more vectors, which facilitates delivery of the gene into a patient. More detail about retroviral vectors can be found in Boesen et al., *Biotherapy* 6:291-302 (1994), which describes the use of a retroviral vector to deliver the *mdr1* gene to hematopoietic stem cells in order to make the stem cells more resistant to chemotherapy. Other references illustrating the use of retroviral vectors in gene therapy are: Clowes et al., *J. Clin. Invest.* 93:644-651 (1994); Kiem et al., *Blood* 83:1467-1473 (1994); Salmons and Gunzberg, *Human Gene Therapy* 4:129-141 (1993); and Grossman and Wilson, *Curr. Opin. in Genetics and Devel.* 3:110-114 (1993).

10 Adenoviruses are other viral vectors that can be used in gene therapy. Adenoviruses are especially attractive vehicles for delivering genes to respiratory epithelia. Adenoviruses naturally infect respiratory epithelia where they cause a mild disease. Other targets for adenovirus-based delivery systems are liver, the central nervous system, endothelial cells, and muscle. Adenoviruses have the advantage of being capable of infecting non-dividing  
15 cells. Kozarsky and Wilson, *Current Opinion in Genetics and Development* 3:499-503 (1993) present a review of adenovirus-based gene therapy. Bout et al., *Human Gene Therapy* 5:3-10 (1994) demonstrated the use of adenovirus vectors to transfer genes to the respiratory epithelia of rhesus monkeys. Other instances of the use of adenoviruses in gene therapy can be found in Rosenfeld et al., *Science* 252:431-434 (1991); Rosenfeld et al., *Cell*  
20 68:143-155 (1992); Mastrangeli et al., *J. Clin. Invest.* 91:225-234 (1993); PCT Publication WO94/12649; and Wang, et al., *Gene Therapy* 2:775-783 (1995). In a preferred embodiment, adenovirus vectors are used.

Adeno-associated virus (AAV) has also been proposed for use in gene therapy (Walsh et al., *Proc. Soc. Exp. Biol. Med.* 204:289-300 (1993); U.S. Patent No. 5,436,146).

25 Another approach to gene therapy involves transferring a gene to cells in tissue culture by such methods as electroporation, lipofection, calcium phosphate mediated transfection, or viral infection. Usually, the method of transfer includes the transfer of a selectable marker to the cells. The cells are then placed under selection to isolate those cells that have taken up and are expressing the transferred gene. Those cells are then delivered to a  
30 patient.

In this embodiment, the nucleic acid is introduced into a cell prior to administration in vivo of the resulting recombinant cell. Such introduction can be carried out by any method

known in the art, including but not limited to transfection, electroporation, microinjection, infection with a viral or bacteriophage vector containing the nucleic acid sequences, cell fusion, chromosome-mediated gene transfer, microcell-mediated gene transfer, spheroplast fusion, etc. Numerous techniques are known in the art for the introduction of foreign genes  
5 into cells (see, e.g., Loeffler and Behr, *Meth. Enzymol.* 217:599-618 (1993); Cohen et al., *Meth. Enzymol.* 217:618-644 (1993); Cline, *Pharmac. Ther.* 29:69-92m (1985) and may be used in accordance with the present invention, provided that the necessary developmental and physiological functions of the recipient cells are not disrupted. The technique should provide for the stable transfer of the nucleic acid to the cell, so that the nucleic acid is  
10 expressible by the cell and preferably heritable and expressible by its cell progeny.

The resulting recombinant cells can be delivered to a patient by various methods known in the art. Recombinant blood cells (e.g., hematopoietic stem or progenitor cells) are preferably administered intravenously. The amount of cells envisioned for use depends on the desired effect, patient state, etc., and can be determined by one skilled in the art.

15 Cells into which a nucleic acid can be introduced for purposes of gene therapy encompass any desired, available cell type, and include but are not limited to epithelial cells, endothelial cells, keratinocytes, fibroblasts, muscle cells, hepatocytes; blood cells such as Tlymphocytes, Blymphocytes, monocytes, macrophages, neutrophils, eosinophils, megakaryocytes, granulocytes; various stem or progenitor cells, in particular hematopoietic  
20 stem or progenitor cells, e.g., as obtained from bone marrow, umbilical cord blood, peripheral blood, fetal liver, etc.

In a preferred embodiment, the cell used for gene therapy is autologous to the patient.

In an embodiment in which recombinant cells are used in gene therapy, nucleic acid sequences encoding an antibody are introduced into the cells such that they are expressible  
25 by the cells or their progeny, and the recombinant cells are then administered in vivo for therapeutic effect. In a specific embodiment, stem or progenitor cells are used. Any stem and/or progenitor cells which can be isolated and maintained in vitro can potentially be used in accordance with this embodiment of the present invention (see e.g. PCT Publication WO 94/08598; Stemple and Anderson, *Cell* 71:973-985 (1992); Rheinwald, *Meth. Cell Bio.*  
30 21A:229 (1980); and Pittelkow and Scott, *Mayo Clinic Proc.* 61:771 (1986)).

In a specific embodiment, the nucleic acid to be introduced for purposes of gene therapy comprises an inducible promoter operably linked to the coding region, such that

expression of the nucleic acid is controllable by controlling the presence or absence of the appropriate inducer of transcription. **Demonstration of Therapeutic or Prophylactic Activity**

The compounds or pharmaceutical compositions of the invention are preferably tested in vitro, and then in vivo for the desired therapeutic or prophylactic activity, prior to use in  
5 humans. For example, in vitro assays to demonstrate the therapeutic or prophylactic utility of a compound or pharmaceutical composition include, the effect of a compound on a cell line or a patient tissue sample. The effect of the compound or composition on the cell line and/or tissue sample can be determined utilizing techniques known to those of skill in the art including, but not limited to, rosette formation assays and cell lysis assays. In accordance  
10 with the invention, in vitro assays which can be used to determine whether administration of a specific compound is indicated, include in vitro cell culture assays in which a patient tissue sample is grown in culture, and exposed to or otherwise administered a compound, and the effect of such compound upon the tissue sample is observed.

15 ***Therapeutic/Prophylactic Administration and Composition***

The invention provides methods of treatment, inhibition and prophylaxis by administration to a subject of an effective amount of a compound or pharmaceutical composition of the invention, preferably a polypeptide or antibody of the invention. In a preferred aspect, the compound is substantially purified (e.g., substantially free from  
20 substances that limit its effect or produce undesired side-effects). The subject is preferably an animal, including but not limited to animals such as cows, pigs, horses, chickens, cats, dogs, etc., and is preferably a mammal, and most preferably human.

Formulations and methods of administration that can be employed when the compound comprises a nucleic acid or an immunoglobulin are described above; additional  
25 appropriate formulations and routes of administration can be selected from among those described herein below.

Various delivery systems are known and can be used to administer a compound of the invention, e.g., encapsulation in liposomes, microparticles, microcapsules, recombinant cells capable of expressing the compound, receptor-mediated endocytosis (see, e.g., Wu and Wu,  
30 J. Biol. Chem. 262:4429-4432 (1987)), construction of a nucleic acid as part of a retroviral or other vector, etc. Methods of introduction include but are not limited to intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, intranasal, epidural, and oral

routes. The compounds or compositions may be administered by any convenient route, for example by infusion or bolus injection, by absorption through epithelial or mucocutaneous linings (e.g., oral mucosa, rectal and intestinal mucosa, etc.) and may be administered together with other biologically active agents. Administration can be systemic or local. In addition, it may be desirable to introduce the pharmaceutical compounds or compositions of the invention into the central nervous system by any suitable route, including intraventricular and intrathecal injection; intraventricular injection may be facilitated by an intraventricular catheter, for example, attached to a reservoir, such as an Ommaya reservoir. Pulmonary administration can also be employed, e.g., by use of an inhaler or nebulizer, and formulation with an aerosolizing agent.

In a specific embodiment, it may be desirable to administer the pharmaceutical compounds or compositions of the invention locally to the area in need of treatment; this may be achieved by, for example, and not by way of limitation, local infusion during surgery, topical application, e.g., in conjunction with a wound dressing after surgery, by injection, by means of a catheter, by means of a suppository, or by means of an implant, said implant being of a porous, non-porous, or gelatinous material, including membranes, such as sialastic membranes, or fibers. Preferably, when administering a protein, including an antibody, of the invention, care must be taken to use materials to which the protein does not absorb.

In another embodiment, the compound or composition can be delivered in a vesicle, in particular a liposome (see Langer, *Science* 249:1527-1533 (1990); Treat et al., in *Liposomes in the Therapy of Infectious Disease and Cancer*, Lopez-Berestein and Fidler (eds.), Liss, New York, pp. 353- 365 (1989); Lopez-Berestein, *ibid.*, pp. 317-327; see generally *ibid.*)

In yet another embodiment, the compound or composition can be delivered in a controlled release system. In one embodiment, a pump may be used (see Langer, *supra*; Sefton, *CRC Crit. Ref. Biomed. Eng.* 14:201 (1987); Buchwald et al., *Surgery* 88:507 (1980); Saudek et al., *N. Engl. J. Med.* 321:574 (1989)). In another embodiment, polymeric materials can be used (see *Medical Applications of Controlled Release*, Langer and Wise (eds.), CRC Pres., Boca Raton, Florida (1974); *Controlled Drug Bioavailability, Drug Product Design and Performance*, Smolen and Ball (eds.), Wiley, New York (1984); Ranger and Peppas, J., *Macromol. Sci. Rev. Macromol. Chem.* 23:61 (1983); see also Levy et al., *Science* 228:190 (1985); During et al., *Ann. Neurol.* 25:351 (1989); Howard et al.,



J.Neurosurg. 71:105 (1989)). In yet another embodiment, a controlled release system can be placed in proximity of the therapeutic target, i.e., the brain, thus requiring only a fraction of the systemic dose (see, e.g., Goodson, in Medical Applications of Controlled Release, *supra*, vol. 2, pp. 115-138 (1984)).

5 Other controlled release systems are discussed in the review by Langer (Science 249:1527-1533 (1990)).

In a specific embodiment where the compound of the invention is a nucleic acid encoding a protein, the nucleic acid can be administered in vivo to promote expression of its encoded protein, by constructing it as part of an appropriate nucleic acid expression vector and administering it so that it becomes intracellular, e.g., by use of a retroviral vector (see 10 U.S. Patent No. 4,980,286), or by direct injection, or by use of microparticle bombardment (e.g., a gene gun; Biolistic, Dupont), or coating with lipids or cell-surface receptors or transfecting agents, or by administering it in linkage to a homeobox-like peptide which is known to enter the nucleus (see e.g., Joliot et al., Proc. Natl. Acad. Sci. USA 88:1864-1868 15 (1991)), etc. Alternatively, a nucleic acid can be introduced intracellularly and incorporated within host cell DNA for expression, by homologous recombination.

The present invention also provides pharmaceutical compositions. Such compositions comprise a therapeutically effective amount of a compound, and a pharmaceutically acceptable carrier. In a specific embodiment, the term "pharmaceutically acceptable" means 20 approved by a regulatory agency of the Federal or a state government or listed in the U.S. Pharmacopeia or other generally recognized pharmacopeia for use in animals, and more particularly in humans. The term "carrier" refers to a diluent, adjuvant, excipient, or vehicle with which the therapeutic is administered. Such pharmaceutical carriers can be sterile liquids, such as water and oils, including those of petroleum, animal, vegetable or synthetic origin, such as peanut oil, soybean oil, mineral oil, sesame oil and the like. Water is a 25 preferred carrier when the pharmaceutical composition is administered intravenously. Saline solutions and aqueous dextrose and glycerol solutions can also be employed as liquid carriers, particularly for injectable solutions. Suitable pharmaceutical excipients include starch, glucose, lactose, sucrose, gelatin, malt, rice, flour, chalk, silica gel, sodium stearate, glycerol monostearate, talc, sodium chloride, dried skim milk, glycerol, propylene glycol, water, 30 ethanol and the like. The composition, if desired, can also contain minor amounts of wetting or emulsifying agents, or pH buffering agents. These compositions can take the form of

solutions, suspensions, emulsion, tablets, pills, capsules, powders, sustained-release formulations and the like. The composition can be formulated as a suppository, with traditional binders and carriers such as triglycerides. Oral formulation can include standard carriers such as pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, magnesium carbonate, etc. Examples of suitable pharmaceutical carriers are described in "Remington's Pharmaceutical Sciences" by E.W. Martin. Such compositions will contain a therapeutically effective amount of the compound, preferably in purified form, together with a suitable amount of carrier so as to provide the form for proper administration to the patient. The formulation should suit the mode of administration.

In a preferred embodiment, the composition is formulated in accordance with routine procedures as a pharmaceutical composition adapted for intravenous administration to human beings. Typically, compositions for intravenous administration are solutions in sterile isotonic aqueous buffer. Where necessary, the composition may also include a solubilizing agent and a local anesthetic such as lignocaine to ease pain at the site of the injection. Generally, the ingredients are supplied either separately or mixed together in unit dosage form, for example, as a dry lyophilized powder or water free concentrate in a hermetically sealed container such as an ampoule or sachette indicating the quantity of active agent. Where the composition is to be administered by infusion, it can be dispensed with an infusion bottle containing sterile pharmaceutical grade water or saline. Where the composition is administered by injection, an ampoule of sterile water for injection or saline can be provided so that the ingredients may be mixed prior to administration.

The compounds of the invention can be formulated as neutral or salt forms. Pharmaceutically acceptable salts include those formed with anions such as those derived from hydrochloric, phosphoric, acetic, oxalic, tartaric acids, etc., and those formed with cations such as those derived from sodium, potassium, ammonium, calcium, ferric hydroxides, isopropylamine, triethylamine, 2-ethylamino ethanol, histidine, procaine, etc.

The amount of the compound of the invention which will be effective in the treatment, inhibition and prevention of a disease or disorder associated with aberrant expression and/or activity of a polypeptide of the invention can be determined by standard clinical techniques. In addition, in vitro assays may optionally be employed to help identify optimal dosage ranges. The precise dose to be employed in the formulation will also depend

on the route of administration, and the seriousness of the disease or disorder, and should be decided according to the judgment of the practitioner and each patient's circumstances. Effective doses may be extrapolated from dose-response curves derived from in vitro or animal model test systems.

5 For antibodies, the dosage administered to a patient is typically 0.1 mg/kg to 100 mg/kg of the patient's body weight. Preferably, the dosage administered to a patient is between 0.1 mg/kg and 20 mg/kg of the patient's body weight, more preferably 1 mg/kg to 10 mg/kg of the patient's body weight. Generally, human antibodies have a longer half-life  
10 foreign polypeptides. Thus, lower dosages of human antibodies and less frequent administration is often possible. Further, the dosage and frequency of administration of antibodies of the invention may be reduced by enhancing uptake and tissue penetration (e.g., into the brain) of the antibodies by modifications such as, for example, lipidation.

The invention also provides a pharmaceutical pack or kit comprising one or more  
15 containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Optionally associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration.

20

### *Diagnosis and Imaging*

Labeled antibodies, and derivatives and analogs thereof, which specifically bind to a polypeptide of interest can be used for diagnostic purposes to detect, diagnose, or monitor  
25 of a polypeptide of the invention. The invention provides for the detection of aberrant expression of a polypeptide of interest, comprising (a) assaying the expression of the polypeptide of interest in cells or body fluid of an individual using one or more antibodies specific to the polypeptide interest and (b) comparing the level of gene expression with a standard gene expression level, whereby an increase or decrease in the assayed polypeptide  
30 gene expression level compared to the standard expression level is indicative of aberrant expression.

The invention provides a diagnostic assay for diagnosing a disorder, comprising (a) assaying the expression of the polypeptide of interest in cells or body fluid of an individual using one or more antibodies specific to the polypeptide of interest and (b) comparing the level of gene expression with a standard gene expression level, whereby an increase or decrease in the assayed polypeptide gene expression level compared to the standard expression level is indicative of a particular disorder. With respect to cancer, the presence of a relatively high amount of transcript in biopsied tissue from an individual may indicate a predisposition for the development of the disease, or may provide a means for detecting the disease prior to the appearance of actual clinical symptoms. A more definitive diagnosis of this type may allow health professionals to employ preventative measures or aggressive treatment earlier thereby preventing the development or further progression of the cancer.

Antibodies of the invention can be used to assay protein levels in a biological sample using classical immunohistological methods known to those of skill in the art (e.g., see Jalkanen, et al., J. Cell. Biol. 101:976-985 (1985); Jalkanen, et al., J. Cell. Biol. 105:3087-3096 (1987)). Other antibody-based methods useful for detecting protein gene expression include immunoassays, such as the enzyme linked immunosorbent assay (ELISA) and the radioimmunoassay (RIA). Suitable antibody assay labels are known in the art and include enzyme labels, such as, glucose oxidase; radioisotopes, such as iodine ( $^{125}\text{I}$ ,  $^{121}\text{I}$ ), carbon ( $^{14}\text{C}$ ), sulfur ( $^{35}\text{S}$ ), tritium ( $^3\text{H}$ ), indium ( $^{112}\text{In}$ ), and technetium ( $^{99}\text{Tc}$ ); luminescent labels, such as luminol; and fluorescent labels, such as fluorescein and rhodamine, and biotin.

One aspect of the invention is the detection and diagnosis of a disease or disorder associated with aberrant expression of a polypeptide of interest in an animal, preferably a mammal and most preferably a human. In one embodiment, diagnosis comprises: a) administering (for example, parenterally, subcutaneously, or intraperitoneally) to a subject an effective amount of a labeled molecule which specifically binds to the polypeptide of interest; b) waiting for a time interval following the administering for permitting the labeled molecule to preferentially concentrate at sites in the subject where the polypeptide is expressed (and for unbound labeled molecule to be cleared to background level); c) determining background level; and d) detecting the labeled molecule in the subject, such that detection of labeled molecule above the background level indicates that the subject has a particular disease or disorder associated with aberrant expression of the polypeptide of interest. Background level can be determined by various methods including, comparing the

amount of labeled molecule detected to a standard value previously determined for a particular system.

It will be understood in the art that the size of the subject and the imaging system used will determine the quantity of imaging moiety needed to produce diagnostic images. In the case of a radioisotope moiety, for a human subject, the quantity of radioactivity injected will normally range from about 5 to 20 millicuries of <sup>99m</sup>Tc. The labeled antibody or antibody fragment will then preferentially accumulate at the location of cells which contain the specific protein. In vivo tumor imaging is described in S.W. Burchiel et al., "Immunopharmacokinetics of Radiolabeled Antibodies and Their Fragments." (Chapter 13 in Tumor Imaging: The Radiochemical Detection of Cancer, S.W. Burchiel and B. A. Rhodes, eds., Masson Publishing Inc. (1982).

Depending on several variables, including the type of label used and the mode of administration, the time interval following the administration for permitting the labeled molecule to preferentially concentrate at sites in the subject and for unbound labeled molecule to be cleared to background level is 6 to 48 hours or 6 to 24 hours or 6 to 12 hours. In another embodiment the time interval following administration is 5 to 20 days or 5 to 10 days.

In an embodiment, monitoring of the disease or disorder is carried out by repeating the method for diagnosing the disease or disease, for example, one month after initial diagnosis, six months after initial diagnosis, one year after initial diagnosis, etc.

Presence of the labeled molecule can be detected in the patient using methods known in the art for in vivo scanning. These methods depend upon the type of label used. Skilled artisans will be able to determine the appropriate method for detecting a particular label. Methods and devices that may be used in the diagnostic methods of the invention include, but are not limited to, computed tomography (CT), whole body scan such as position emission tomography (PET), magnetic resonance imaging (MRI), and sonography.

In a specific embodiment, the molecule is labeled with a radioisotope and is detected in the patient using a radiation responsive surgical instrument (Thurston et al., U.S. Patent No. 5,441,050). In another embodiment, the molecule is labeled with a fluorescent compound and is detected in the patient using a fluorescence responsive scanning instrument. In another embodiment, the molecule is labeled with a positron emitting metal and is detected in the patient using positron emission-tomography. In yet another embodiment, the molecule

is labeled with a paramagnetic label and is detected in a patient using magnetic resonance imaging (MRI).

### *Kits*

5           The present invention provides kits that can be used in the above methods. In one embodiment, a kit comprises an antibody of the invention, preferably a purified antibody, in one or more containers. In a specific embodiment, the kits of the present invention contain a substantially isolated polypeptide comprising an epitope which is specifically immunoreactive with an antibody included in the kit. Preferably, the kits of the present  
10           invention further comprise a control antibody which does not react with the polypeptide of interest. In another specific embodiment, the kits of the present invention contain a means for detecting the binding of an antibody to a polypeptide of interest (e.g., the antibody may be conjugated to a detectable substrate such as a fluorescent compound, an enzymatic substrate, a radioactive compound or a luminescent compound, or a second antibody which recognizes  
15           the first antibody may be conjugated to a detectable substrate).

          In another specific embodiment of the present invention, the kit is a diagnostic kit for use in screening serum containing antibodies specific against proliferative and/or cancerous polynucleotides and polypeptides. Such a kit may include a control antibody that does not react with the polypeptide of interest. Such a kit may include a substantially isolated  
20           polypeptide antigen comprising an epitope which is specifically immunoreactive with at least one anti-polypeptide antigen antibody. Further, such a kit includes means for detecting the binding of said antibody to the antigen (e.g., the antibody may be conjugated to a fluorescent compound such as fluorescein or rhodamine which can be detected by flow cytometry). In specific embodiments, the kit may include a recombinantly produced or chemically  
25           synthesized polypeptide antigen. The polypeptide antigen of the kit may also be attached to a solid support.

          In a more specific embodiment the detecting means of the above-described kit includes a solid support to which said polypeptide antigen is attached. Such a kit may also include a non-attached reporter-labeled anti-human antibody. In this embodiment, binding of  
30           the antibody to the polypeptide antigen can be detected by binding of the said reporter-labeled antibody.

In an additional embodiment, the invention includes a diagnostic kit for use in screening serum containing antigens of the polypeptide of the invention. The diagnostic kit includes a substantially isolated antibody specifically immunoreactive with polypeptide or polynucleotide antigens, and means for detecting the binding of the polynucleotide or polypeptide antigen to the antibody. In one embodiment, the antibody is attached to a solid support. In a specific embodiment, the antibody may be a monoclonal antibody. The detecting means of the kit may include a second, labeled monoclonal antibody. Alternatively, or in addition, the detecting means may include a labeled, competing antigen.

In one diagnostic configuration, test serum is reacted with a solid phase reagent having a surface-bound antigen obtained by the methods of the present invention. After binding with specific antigen antibody to the reagent and removing unbound serum components by washing, the reagent is reacted with reporter-labeled anti-human antibody to bind reporter to the reagent in proportion to the amount of bound anti-antigen antibody on the solid support. The reagent is again washed to remove unbound labeled antibody, and the amount of reporter associated with the reagent is determined. Typically, the reporter is an enzyme which is detected by incubating the solid phase in the presence of a suitable fluorometric, luminescent or colorimetric substrate (Sigma, St. Louis, MO).

The solid surface reagent in the above assay is prepared by known techniques for attaching protein material to solid support material, such as polymeric beads, dip sticks, 96-well plate or filter material. These attachment methods generally include non-specific adsorption of the protein to the support or covalent attachment of the protein, typically through a free amine group, to a chemically reactive group on the solid support, such as an activated carboxyl, hydroxyl, or aldehyde group. Alternatively, streptavidin coated plates can be used in conjunction with biotinylated antigen(s).

Thus, the invention provides an assay system or kit for carrying out this diagnostic method. The kit generally includes a support with surface-bound recombinant antigens, and a reporter-labeled anti-human antibody for detecting surface-bound anti-antigen antibody.

#### **Uses of the Polynucleotides**

Each of the polynucleotides identified herein can be used in numerous ways as reagents. The following description should be considered exemplary and utilizes known techniques.

The colon cancer antigen polynucleotides of the present invention are useful for chromosome identification. There exists an ongoing need to identify new chromosome markers, since few chromosome marking reagents, based on actual sequence data (repeat polymorphisms), are presently available. Each sequence is specifically targeted to and can  
5 hybridize with a particular location on an individual human chromosome, thus each polynucleotide of the present invention can routinely be used as a chromosome marker using techniques known in the art.

Briefly, sequences can be mapped to chromosomes by preparing PCR primers (preferably at least 15 bp (e.g., 15-25 bp) from the sequences shown in SEQ ID NO:X, or the  
10 complement thereto. Primers can optionally be selected using computer analysis so that primers do not span more than one predicted exon in the genomic DNA. These primers are then used for PCR screening of somatic cell hybrids containing individual human chromosomes. Only those hybrids containing the human gene corresponding to SEQ ID NO:X will yield an amplified fragment.

15 Similarly, somatic hybrids provide a rapid method of PCR mapping the polynucleotides to particular chromosomes. Three or more clones can be assigned per day using a single thermal cycler. Moreover, sublocalization of the polynucleotides can be achieved with panels of specific chromosome fragments. Other gene mapping strategies that can be used include in situ hybridization, prescreening with labeled flow-sorted  
20 chromosomes, preselection by hybridization to construct chromosome specific-cDNA libraries, and computer mapping techniques (See, e.g., Shuler, Trends Biotechnol 16:456-459 (1998) which is hereby incorporated by reference in its entirety).

Precise chromosomal location of the polynucleotides can also be achieved using fluorescence in situ hybridization (FISH) of a metaphase chromosomal spread. This  
25 technique uses polynucleotides as short as 500 or 600 bases; however, polynucleotides 2,000-4,000 bp are preferred. For a review of this technique, see Verma et al., "Human Chromosomes: a Manual of Basic Techniques," Pergamon Press, New York (1988).

For chromosome mapping, the polynucleotides can be used individually (to mark a single chromosome or a single site on that chromosome) or in panels (for marking multiple  
30 sites and/or multiple chromosomes).



Thus, the present invention also provides a method for chromosomal localization which involves (a) preparing PCR primers from the polynucleotide sequences in Table 3 and SEQ ID NO:X and (b) screening somatic cell hybrids containing individual chromosomes.

The polynucleotides of the present invention would likewise be useful for radiation  
5 hybrid mapping, HAPPY mapping, and long range restriction mapping. For a review of these techniques and others known in the art, see, e.g. Dear, "Genome Mapping: A Practical Approach," IRL Press at Oxford University Press, London (1997); Aydin. J. Mol. Med. 77:691-694 (1999); Hacia et al., Mol. Psychiatry 3:483-492 (1998); Herrick et al., Chromosome Res. 7:409-423 (1999); Hamilton et al., Methods Cell Biol. 62:265-280 (2000);  
10 and/or Ott, J. Hered. 90:68-70 (1999) each of which is hereby incorporated by reference in its entirety.

Once a polynucleotide has been mapped to a precise chromosomal location, the physical position of the polynucleotide can be used in linkage analysis. Linkage analysis establishes coinheritance between a chromosomal location and presentation of a particular  
15 disease. (Disease mapping data are found, for example, in V. McKusick, Mendelian Inheritance in Man (available on line through Johns Hopkins University Welch Medical Library).) Assuming 1 megabase mapping resolution and one gene per 20 kb, a cDNA precisely localized to a chromosomal region associated with the disease could be one of 50-500 potential causative genes.

20 Thus, once coinheritance is established, differences in a polynucleotide of the invention and the corresponding gene between affected and unaffected individuals can be examined. First, visible structural alterations in the chromosomes, such as deletions or translocations, are examined in chromosome spreads or by PCR. If no structural alterations exist, the presence of point mutations are ascertained. Mutations observed in some or all  
25 affected individuals, but not in normal individuals, indicates that the mutation may cause the disease. However, complete sequencing of the polypeptide and the corresponding gene from several normal individuals is required to distinguish the mutation from a polymorphism. If a new polymorphism is identified, this polymorphic polypeptide can be used for further linkage analysis.

30 Furthermore, increased or decreased expression of the gene in affected individuals as compared to unaffected individuals can be assessed using the polynucleotides of the

invention. Any of these alterations (altered expression, chromosomal rearrangement, or mutation) can be used as a diagnostic or prognostic marker.

Thus, the invention provides a method of detecting increased or decreased expression levels of the colon cancer polynucleotides in affected individuals as compared to unaffected  
5 individuals using polynucleotides of the present invention and techniques known in the art, including but not limited to the method described in Example 11. Any of these alterations (altered expression, chromosomal rearrangement, or mutation) can be used as a diagnostic or prognostic marker.

Thus, the invention also provides a diagnostic method useful during diagnosis of a  
10 colon related disorder, including colon cancer, involving measuring the expression level of colon cancer polynucleotides in colon tissue or other cells or body fluid from an individual and comparing the measured gene expression level with a standard colon cancer polynucleotide expression level, whereby an increase or decrease in the gene expression level compared to the standard is indicative of a colon related disorder.

15 In still another embodiment, the invention includes a kit for analyzing samples for the presence of proliferative and/or cancerous polynucleotides derived from a test subject. In a general embodiment, the kit includes at least one polynucleotide probe containing a nucleotide sequence that will specifically hybridize with a polynucleotide of the invention and a suitable container. In a specific embodiment, the kit includes two polynucleotide probes  
20 defining an internal region of the polynucleotide of the invention, where each probe has one strand containing a 31'-mer-end internal to the region. In a further embodiment, the probes may be useful as primers for polymerase chain reaction amplification.

Where a diagnosis of a colon related disorder, including, for example, diagnosis of a tumor, has already been made according to conventional methods, the present invention is  
25 useful as a prognostic indicator, whereby patients exhibiting enhanced or depressed colon cancer polynucleotide expression will experience a worse clinical outcome relative to patients expressing the gene at a level nearer the standard level.

By "measuring the expression level of colon cancer polynucleotides" is intended qualitatively or quantitatively measuring or estimating the level of the colon cancer  
30 polypeptide or the level of the mRNA encoding the colon cancer polypeptide in a first biological sample either directly (e.g., by determining or estimating absolute protein level or mRNA level) or relatively (e.g., by comparing to the colon cancer polypeptide level or

mRNA level in a second biological sample). Preferably, the colon cancer polypeptide level or mRNA level in the first biological sample is measured or estimated and compared to a standard colon cancer polypeptide level or mRNA level, the standard being taken from a second biological sample obtained from an individual not having the colon related disorder or being determined by averaging levels from a population of individuals not having a colon related disorder. As will be appreciated in the art, once a standard colon cancer polypeptide level or mRNA level is known, it can be used repeatedly as a standard for comparison.

By "biological sample" is intended any biological sample obtained from an individual, body fluid, cell line, tissue culture, or other source which contains colon cancer polypeptide or the corresponding mRNA. As indicated, biological samples include body fluids (such as lymph, sera, plasma, urine, bile, synovial fluid and spinal fluid) which contain the colon cancer polypeptide, colon tissue, and other tissue sources found to express the colon cancer polypeptide. Methods for obtaining tissue biopsies and body fluids from mammals are well known in the art. Where the biological sample is to include mRNA, a tissue biopsy is the preferred source.

The method(s) provided above may preferably be applied in a diagnostic method and/or kits in which polynucleotides and/or polypeptides of the invention are attached to a solid support. In one exemplary method, the support may be a "gene chip" or a "biological chip" as described in US Patents 5,837,832, 5,874,219, and 5,856,174. Further, such a gene chip with colon cancer polynucleotides attached may be used to identify polymorphisms between the colon cancer polynucleotide sequences, with polynucleotides isolated from a test subject. The knowledge of such polymorphisms (i.e. their location, as well as, their existence) would be beneficial in identifying disease loci for many disorders, such as for example, in neural disorders, immune system disorders, muscular disorders, reproductive disorders, gastrointestinal disorders, pulmonary disorders, cardiovascular disorders, renal disorders, proliferative disorders, and/or cancerous diseases and conditions, though most preferably in colon related proliferative, and/or cancerous diseases and conditions. Such a method is described in US Patents 5,858,659 and 5,856,104. The US Patents referenced supra are hereby incorporated by reference in their entirety herein.

The present invention encompasses colon cancer polynucleotides that are chemically synthesized, or reproduced as peptide nucleic acids (PNA), or according to other methods known in the art. The use of PNAs would serve as the preferred form if the polynucleotides

of the invention are incorporated onto a solid support, or gene chip. For the purposes of the present invention, a peptide nucleic acid (PNA) is a polyamide type of DNA analog and the monomeric units for adenine, guanine, thymine and cytosine are available commercially (Perceptive Biosystems). Certain components of DNA, such as phosphorus, phosphorus  
5 oxides, or deoxyribose derivatives, are not present in PNAs. As disclosed by P. E. Nielsen, M. Egholm, R. H. Berg and O. Buchardt, *Science* 254, 1497 (1991); and M. Egholm, O. Buchardt, L. Christensen, C. Behrens, S. M. Freier, D. A. Driver, R. H. Berg, S. K. Kim, B. Norden, and P. E. Nielsen, *Nature* 365, 666 (1993), PNAs bind specifically and tightly to complementary DNA strands and are not degraded by nucleases. In fact, PNA binds more  
10 strongly to DNA than DNA itself does. This is probably because there is no electrostatic repulsion between the two strands, and also the polyamide backbone is more flexible. Because of this, PNA/DNA duplexes bind under a wider range of stringency conditions than DNA/DNA duplexes, making it easier to perform multiplex hybridization. Smaller probes can be used than with DNA due to the strong binding. In addition, it is more likely that single  
15 base mismatches can be determined with PNA/DNA hybridization because a single mismatch in a PNA/DNA 15-mer lowers the melting point ( $T_{sub.m}$ ) by 8°-20° C, vs. 4°-16° C for the DNA/DNA 15-mer duplex. Also, the absence of charge groups in PNA means that hybridization can be done at low ionic strengths and reduce possible interference by salt during the analysis.

20 The present invention have uses which include, but are not limited to, detecting cancer in mammals. In particular the invention is useful during diagnosis of pathological cell proliferative neoplasias which include, but are not limited to: acute myelogenous leukemias including acute monocytic leukemia, acute myeloblastic leukemia, acute promyelocytic leukemia, acute myelomonocytic leukemia, acute erythroleukemia, acute megakaryocytic  
25 leukemia, and acute undifferentiated leukemia, etc.; and chronic myelogenous leukemias including chronic myelomonocytic leukemia, chronic granulocytic leukemia, etc. Preferred mammals include monkeys, apes, cats, dogs, cows, pigs, horses, rabbits and humans. Particularly preferred are humans.

Pathological cell proliferative disorders are often associated with inappropriate  
30 activation of proto-oncogenes. (Germann, E. P. et al., "The Etiology of Acute Leukemia: Molecular Genetics and Viral Oncology," in *Neoplastic Diseases of the Blood*, Vol 1., Wiernik, P. H. et al. eds., 161-182 (1985)). Neoplasias are now believed to result from the

qualitative alteration of a normal cellular gene product, or from the quantitative modification of gene expression by insertion into the chromosome of a viral sequence, by chromosomal translocation of a gene to a more actively transcribed region, or by some other mechanism. (Gelmann et al., supra) It is likely that mutated or altered expression of specific genes is involved in the pathogenesis of some leukemias, among other tissues and cell types. (Gelmann et al., supra) Indeed, the human counterparts of the oncogenes involved in some animal neoplasias have been amplified or translocated in some cases of human leukemia and carcinoma. (Gelmann et al., supra)

For example, c-myc expression is highly amplified in the non-lymphocytic leukemia cell line HL-60. When HL-60 cells are chemically induced to stop proliferation, the level of c-myc is found to be downregulated. (International Publication Number WO 91/15580). However, it has been shown that exposure of HL-60 cells to a DNA construct that is complementary to the 5' end of c-myc or c-myb blocks translation of the corresponding mRNAs which downregulates expression of the c-myc or c-myb proteins and causes arrest of cell proliferation and differentiation of the treated cells. (International Publication Number WO 91/15580; Wickstrom et al., Proc. Natl. Acad. Sci. 85:1028 (1988); Anfossi et al., Proc. Natl. Acad. Sci. 86:3379 (1989)). However, the skilled artisan would appreciate the present invention's usefulness is not limited to treatment of proliferative disorders of hematopoietic cells and tissues, in light of the numerous cells and cell types of varying origins which are known to exhibit proliferative phenotypes.

In addition to the foregoing, a colon cancer antigen polynucleotide can be used to control gene expression through triple helix formation or through antisense DNA or RNA. Antisense techniques are discussed, for example, in Okano, J. Neurochem. 56: 560 (1991); "Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988). Triple helix formation is discussed in, for instance Lee et al., Nucleic Acids Research 6: 3073 (1979); Cooney et al., Science 241: 456 (1988); and Dervan et al., Science 251: 1360 (1991). Both methods rely on binding of the polynucleotide to a complementary DNA or RNA. For these techniques, preferred polynucleotides are usually oligonucleotides 20 to 40 bases in length and complementary to either the region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991) ) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxy-nucleotides as Antisense

Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988).) Triple helix formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. The oligonucleotide described above can also be delivered to cells such that the antisense RNA or DNA may be  
5 expressed in vivo to inhibit production of polypeptide of the present invention antigens. Both techniques are effective in model systems, and the information disclosed herein can be used to design antisense or triple helix polynucleotides in an effort to treat disease, and in particular, for the treatment of proliferative diseases and/or conditions.

Polynucleotides of the present invention are also useful in gene therapy. One goal of  
10 gene therapy is to insert a normal gene into an organism having a defective gene, in an effort to correct the genetic defect. The polynucleotides disclosed in the present invention offer a means of targeting such genetic defects in a highly accurate manner. Another goal is to insert a new gene that was not present in the host genome, thereby producing a new trait in the host cell.

15 The polynucleotides are also useful for identifying individuals from minute biological samples. The United States military, for example, is considering the use of restriction fragment length polymorphism (RFLP) for identification of its personnel. In this technique, an individual's genomic DNA is digested with one or more restriction enzymes, and probed on a Southern blot to yield unique bands for identifying personnel. This method does not  
20 suffer from the current limitations of "Dog Tags" which can be lost, switched, or stolen, making positive identification difficult. The polynucleotides of the present invention can be used as additional DNA markers for RFLP.

The polynucleotides of the present invention can also be used as an alternative to RFLP, by determining the actual base-by-base DNA sequence of selected portions of an  
25 individual's genome. These sequences can be used to prepare PCR primers for amplifying and isolating such selected DNA, which can then be sequenced. Using this technique, individuals can be identified because each individual will have a unique set of DNA sequences. Once an unique ID database is established for an individual, positive identification of that individual, living or dead, can be made from extremely small tissue  
30 samples.

Forensic biology also benefits from using DNA-based identification techniques as disclosed herein. DNA sequences taken from very small biological samples such as tissues,

e.g., hair or skin, or body fluids, e.g., blood, saliva, semen, synovial fluid, amniotic fluid, breast milk, lymph, pulmonary sputum or surfactant, urine, fecal matter, etc., can be amplified using PCR. In one prior art technique, gene sequences amplified from polymorphic loci, such as DQa class II HLA gene, are used in forensic biology to identify individuals. (Erlich, H., PCR Technology, Freeman and Co. (1992).) Once these specific polymorphic loci are amplified, they are digested with one or more restriction enzymes, yielding an identifying set of bands on a Southern blot probed with DNA corresponding to the DQa class II HLA gene. Similarly, polynucleotides of the present invention can be used as polymorphic markers for forensic purposes.

10        There is also a need for reagents capable of identifying the source of a particular tissue. Such need arises, for example, in forensics when presented with tissue of unknown origin. Appropriate reagents can comprise, for example, DNA probes or primers specific to colon or colon cancer polynucleotides prepared from the sequences of the present invention. Panels of such reagents can identify tissue by species and/or by organ type. In a similar  
15        fashion, these reagents can be used to screen tissue cultures for contamination.

      The polynucleotides of the present invention are also useful as hybridization probes for differential identification of the tissue(s) or cell type(s) present in a biological sample. Similarly, polypeptides and antibodies directed to polypeptides of the present invention are useful to provide immunological probes for differential identification of the tissue(s) (e.g.,  
20        immunohistochemistry assays) or cell type(s) (e.g., immunocytochemistry assays). In addition, for a number of disorders of the above tissues or cells, significantly higher or lower levels of gene expression of the polynucleotides/polypeptides of the present invention may be detected in certain tissues (e.g., tissues expressing polypeptides and/or polynucleotides of the present invention, colon and colon cancer tissues and/or cancerous and/or wounded tissues)  
25        or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) taken from an individual having such a disorder, relative to a "standard" gene expression level, i.e., the expression level in healthy tissue from an individual not having the disorder.

      Thus, the invention provides a diagnostic method of a disorder, which involves: (a) assaying gene expression level in cells or body fluid of an individual; (b) comparing the gene  
30        expression level with a standard gene expression level, whereby an increase or decrease in the assayed gene expression level compared to the standard expression level is indicative of a disorder.

In the very least, the polynucleotides of the present invention can be used as molecular weight markers on Southern gels, as diagnostic probes for the presence of a specific mRNA in a particular cell type, as a probe to "subtract-out" known sequences in the process of discovering novel polynucleotides, for selecting and making oligomers for attachment to a "gene chip" or other support, to raise anti-DNA antibodies using DNA immunization techniques, and as an antigen to elicit an immune response.

#### Uses of the Polypeptides

Each of the polypeptides identified herein can be used in numerous ways. The following description should be considered exemplary and utilizes known techniques.

Polypeptides and antibodies directed to polypeptides of the present invention are useful to provide immunological probes for differential identification of the tissue(s) (e.g., immunohistochemistry assays such as, for example, ABC immunoperoxidase (Hsu et al., J. Histochem. Cytochem. 29:577-580 (1981)) or cell type(s) (e.g., immunocytochemistry assays).

Antibodies can be used to assay levels of polypeptides encoded by polynucleotides of the invention in a biological sample using classical immunohistological methods known to those of skill in the art (e.g., see Jalkanen, et al., J. Cell. Biol. 101:976-985 (1985); Jalkanen, et al., J. Cell. Biol. 105:3087-3096 (1987)). Other antibody-based methods useful for detecting protein gene expression include immunoassays, such as the enzyme linked immunosorbent assay (ELISA) and the radioimmunoassay (RIA). Suitable antibody assay labels are known in the art and include enzyme labels, such as, glucose oxidase; radioisotopes, such as iodine ( $^{131}\text{I}$ ,  $^{125}\text{I}$ ,  $^{123}\text{I}$ ,  $^{121}\text{I}$ ), carbon ( $^{14}\text{C}$ ), sulfur ( $^{35}\text{S}$ ), tritium ( $^3\text{H}$ ), indium ( $^{115\text{m}}\text{In}$ ,  $^{113\text{m}}\text{In}$ ,  $^{112}\text{In}$ ,  $^{111}\text{In}$ ), and technetium ( $^{99}\text{Tc}$ ,  $^{99\text{m}}\text{Tc}$ ), thallium ( $^{201}\text{Tl}$ ), gallium ( $^{68}\text{Ga}$ ,  $^{67}\text{Ga}$ ), palladium ( $^{103}\text{Pd}$ ), molybdenum ( $^{99}\text{Mo}$ ), xenon ( $^{133}\text{Xe}$ ), fluorine ( $^{18}\text{F}$ ),  $^{153}\text{Sm}$ ,  $^{177}\text{Lu}$ ,  $^{159}\text{Gd}$ ,  $^{149}\text{Pm}$ ,  $^{140}\text{La}$ ,  $^{175}\text{Yb}$ ,  $^{166}\text{Ho}$ ,  $^{90}\text{Y}$ ,  $^{47}\text{Sc}$ ,  $^{186}\text{Re}$ ,  $^{188}\text{Re}$ ,  $^{142}\text{Pr}$ ,  $^{105}\text{Rh}$ ,  $^{97}\text{Ru}$ ; luminescent labels, such as luminol; and fluorescent labels, such as fluorescein and rhodamine, and biotin.

In addition to assaying levels of polypeptide of the present invention in a biological sample, proteins can also be detected in vivo by imaging. Antibody labels or markers for in vivo imaging of protein include those detectable by X-radiography, NMR or ESR. For X-radiography, suitable labels include radioisotopes such as barium or cesium, which emit



detectable radiation but are not overtly harmful to the subject. Suitable markers for NMR and ESR include those with a detectable characteristic spin, such as deuterium, which may be incorporated into the antibody by labeling of nutrients for the relevant hybridoma.

A protein-specific antibody or antibody fragment which has been labeled with an appropriate detectable imaging moiety, such as a radioisotope (for example,  $^{131}\text{I}$ ,  $^{112}\text{In}$ ,  $^{99\text{m}}\text{Tc}$ ,  $^{131}\text{I}$ ,  $^{125}\text{I}$ ,  $^{123}\text{I}$ ,  $^{121}\text{I}$ ), carbon ( $^{14}\text{C}$ ), sulfur ( $^{35}\text{S}$ ), tritium ( $^3\text{H}$ ), indium ( $^{115\text{m}}\text{In}$ ,  $^{113\text{m}}\text{In}$ ,  $^{112}\text{In}$ ,  $^{111}\text{In}$ ), and technetium ( $^{99}\text{Tc}$ ,  $^{99\text{m}}\text{Tc}$ ), thallium ( $^{201}\text{Tl}$ ), gallium ( $^{68}\text{Ga}$ ,  $^{67}\text{Ga}$ ), palladium ( $^{103}\text{Pd}$ ), molybdenum ( $^{99}\text{Mo}$ ), xenon ( $^{133}\text{Xe}$ ), fluorine ( $^{18}\text{F}$ ,  $^{153}\text{Sm}$ ,  $^{177}\text{Lu}$ ,  $^{159}\text{Gd}$ ,  $^{149}\text{Pm}$ ,  $^{140}\text{La}$ ,  $^{175}\text{Yb}$ ,  $^{166}\text{Ho}$ ,  $^{90}\text{Y}$ ,  $^{47}\text{Sc}$ ,  $^{186}\text{Re}$ ,  $^{188}\text{Re}$ ,  $^{142}\text{Pr}$ ,  $^{105}\text{Rh}$ ,  $^{97}\text{Ru}$ ), a radio-opaque substance, or a material detectable by nuclear magnetic resonance, is introduced (for example, parenterally, subcutaneously or intraperitoneally) into the mammal to be examined for immune system disorder. It will be understood in the art that the size of the subject and the imaging system used will determine the quantity of imaging moiety needed to produce diagnostic images. In the case of a radioisotope moiety, for a human subject, the quantity of radioactivity injected will normally range from about 5 to 20 millicuries of  $^{99\text{m}}\text{Tc}$ . The labeled antibody or antibody fragment will then preferentially accumulate at the location of cells which express the polypeptide encoded by a polynucleotide of the invention. *In vivo* tumor imaging is described in S.W. Burchiel et al., "Immunopharmacokinetics of Radiolabeled Antibodies and Their Fragments" (Chapter 13 in *Tumor Imaging: The Radiochemical Detection of Cancer*, S.W. Burchiel and B. A. Rhodes, eds., Masson Publishing Inc. (1982)).

In one embodiment, the invention provides a method for the specific delivery of compositions of the invention to cells by administering polypeptides of the invention (e.g., polypeptides encoded by polynucleotides of the invention and/or antibodies) that are associated with heterologous polypeptides or nucleic acids. In one example, the invention provides a method for delivering a therapeutic protein into the targeted cell. In another example, the invention provides a method for delivering a single stranded nucleic acid (e.g., antisense or ribozymes) or double stranded nucleic acid (e.g., DNA that can integrate into the cell's genome or replicate episomally and that can be transcribed) into the targeted cell.

In another embodiment, the invention provides a method for the specific destruction of cells (e.g., the destruction of tumor cells) by administering polypeptides of the invention in association with toxins or cytotoxic prodrugs.

By "toxin" is meant one or more compounds that bind and activate endogenous cytotoxic effector systems, radioisotopes, holotoxins, modified toxins, catalytic subunits of toxins, or any molecules or enzymes not normally present in or on the surface of a cell that under defined conditions cause the cell's death. Toxins that may be used according to the methods of the invention include, but are not limited to, radioisotopes known in the art, compounds such as, for example, antibodies (or complement fixing containing portions thereof) that bind an inherent or induced endogenous cytotoxic effector system, thymidine kinase, endonuclease, RNase, alpha toxin, ricin, abrin, *Pseudomonas* exotoxin A, diphtheria toxin, saporin, momordin, gelonin, pokeweed antiviral protein, alpha-sarcin and cholera toxin. "Toxin" also includes a cytostatic or cytotoxic agent, a therapeutic agent or a radioactive metal ion, e.g., alpha-emitters such as, for example,  $^{213}\text{Bi}$ , or other radioisotopes such as, for example,  $^{103}\text{Pd}$ ,  $^{133}\text{Xe}$ ,  $^{131}\text{I}$ ,  $^{68}\text{Ge}$ ,  $^{57}\text{Co}$ ,  $^{65}\text{Zn}$ ,  $^{85}\text{Sr}$ ,  $^{32}\text{P}$ ,  $^{35}\text{S}$ ,  $^{90}\text{Y}$ ,  $^{153}\text{Sm}$ ,  $^{153}\text{Gd}$ ,  $^{169}\text{Yb}$ ,  $^{51}\text{Cr}$ ,  $^{54}\text{Mn}$ ,  $^{75}\text{Se}$ ,  $^{113}\text{Sn}$ ,  $^{90}\text{Yttrium}$ ,  $^{117}\text{Tin}$ ,  $^{186}\text{Rhenium}$ ,  $^{166}\text{Holmium}$ , and  $^{188}\text{Rhenium}$ ; luminescent labels, such as luminol; and fluorescent labels, such as fluorescein and rhodamine, and biotin.

Techniques known in the art may be applied to label polypeptides of the invention (including antibodies). Such techniques include, but are not limited to, the use of bifunctional conjugating agents (see e.g., U.S. Patent Nos. 5,756,065; 5,714,631; 5,696,239; 5,652,361; 5,505,931; 5,489,425; 5,435,990; 5,428,139; 5,342,604; 5,274,119; 4,994,560; and 5,808,003; the contents of each of which are hereby incorporated by reference in its entirety).

Thus, the invention provides a diagnostic method of a disorder, which involves (a) assaying the expression level of a colon cancer polypeptide of the present invention in cells or body fluid of an individual, or more preferably, assaying the expression level of a colon cancer polypeptide of the present invention in colon cells or sera of an individual; and (b) comparing the assayed polypeptide expression level with a standard polypeptide expression level, whereby an increase or decrease in the assayed polypeptide expression level compared to the standard expression level is indicative of a disorder. With respect to cancer, the presence of a relatively high amount of transcript in biopsied tissue from an individual may indicate a predisposition for the development of the disease, or may provide a means for detecting the disease prior to the appearance of actual clinical symptoms. A more definitive diagnosis of this type may allow health professionals to employ preventative measures or

aggressive treatment earlier thereby preventing the development or further progression of the cancer.

Moreover, colon cancer antigen polypeptides of the present invention can be used to treat or prevent diseases or conditions such as, for example, neural disorders, immune system disorders, muscular disorders, reproductive disorders, gastrointestinal disorders, pulmonary disorders, cardiovascular disorders, renal disorders, proliferative disorders, and/or cancerous diseases and conditions, preferably proliferative disorders of the colon, and/or cancerous disease and conditions. For example, patients can be administered a polypeptide of the present invention in an effort to replace absent or decreased levels of the polypeptide (e.g., insulin), to supplement absent or decreased levels of a different polypeptide (e.g., hemoglobin S for hemoglobin B, SOD, catalase, DNA repair proteins), to inhibit the activity of a polypeptide (e.g., an oncogene or tumor suppressor), to activate the activity of a polypeptide (e.g., by binding to a receptor), to reduce the activity of a membrane bound receptor by competing with it for free ligand (e.g., soluble TNF receptors used in reducing inflammation), or to bring about a desired response (e.g., blood vessel growth inhibition, enhancement of the immune response to proliferative cells or tissues).

Similarly, antibodies directed to a polypeptide of the present invention can also be used to treat disease (as described supra, and elsewhere herein). For example, administration of an antibody directed to a polypeptide of the present invention can bind, and/or neutralize the polypeptide, and/or reduce overproduction of the polypeptide. Similarly, administration of an antibody can activate the polypeptide, such as by binding to a polypeptide bound to a membrane (receptor).

At the very least, the polypeptides of the present invention can be used as molecular weight markers on SDS-PAGE gels or on molecular sieve gel filtration columns using methods well known to those of skill in the art. Polypeptides can also be used to raise antibodies, which in turn are used to measure protein expression from a recombinant cell, as a way of assessing transformation of the host cell. Moreover, the polypeptides of the present invention can be used to test the following biological activities.

### Gene Therapy Methods

Another aspect of the present invention is to gene therapy methods for treating or preventing disorders, diseases and conditions. The gene therapy methods relate to the introduction of nucleic acid (DNA, RNA and antisense DNA or RNA) sequences into an animal to achieve expression of the polypeptide of the present invention. This method requires a polynucleotide which codes for a polypeptide of the present invention operatively linked to a promoter and any other genetic elements necessary for the expression of the polypeptide by the target tissue. Such gene therapy and delivery techniques are known in the art, see, for example, WO90/11092, which is herein incorporated by reference.

Thus, for example, cells from a patient may be engineered with a polynucleotide (DNA or RNA) comprising a promoter operably linked to a polynucleotide of the present invention ex vivo, with the engineered cells then being provided to a patient to be treated with the polypeptide of the present invention. Such methods are well-known in the art. For example, see Belldégrun, A., et al., J. Natl. Cancer Inst. 85: 207-216 (1993); Ferrantini, M. et al., Cancer Research 53: 1107-1112 (1993); Ferrantini, M. et al., J. Immunology 153: 4604-4615 (1994); Kaido, T., et al., Int. J. Cancer 60: 221-229 (1995); Ogura, H., et al., Cancer Research 50: 5102-5106 (1990); Santodonato, L., et al., Human Gene Therapy 7:1-10 (1996); Santodonato, L., et al., Gene Therapy 4:1246-1255 (1997); and Zhang, J.-F. et al., Cancer Gene Therapy 3: 31-38 (1996)), which are herein incorporated by reference. In one embodiment, the cells which are engineered are arterial cells. The arterial cells may be reintroduced into the patient through direct injection to the artery, the tissues surrounding the artery, or through catheter injection.

As discussed in more detail below, the polynucleotide constructs can be delivered by any method that delivers injectable materials to the cells of an animal, such as, injection into the interstitial space of tissues (heart, muscle, skin, lung, liver, and the like). The polynucleotide constructs may be delivered in a pharmaceutically acceptable liquid or aqueous carrier.

In one embodiment, the polynucleotide of the present invention is delivered as a naked polynucleotide. The term "naked" polynucleotide, DNA or RNA refers to sequences that are free from any delivery vehicle that acts to assist, promote or facilitate entry into the cell, including viral sequences, viral particles, liposome formulations, lipofectin or precipitating agents and the like. However, the polynucleotide of the present invention can

also be delivered in liposome formulations and lipofectin formulations and the like can be prepared by methods well known to those skilled in the art. Such methods are described, for example, in U.S. Patent Nos. 5,593,972, 5,589,466, and 5,580,859, which are herein incorporated by reference.

5       The polynucleotide vector constructs used in the gene therapy method are preferably constructs that will not integrate into the host genome nor will they contain sequences that allow for replication. Appropriate vectors include pWLNEO, pSV2CAT, pOG44, pXT1 and pSG available from Stratagene; pSVK3, pBPV, pMSG and pSVL available from Pharmacia; and pEF1/V5, pcDNA3.1, and pRc/CMV2 available from Invitrogen. Other suitable vectors  
10 will be readily apparent to the skilled artisan.

Any strong promoter known to those skilled in the art can be used for driving the expression of the polynucleotide sequence. Suitable promoters include adenoviral promoters, such as the adenoviral major late promoter; or heterologous promoters, such as the cytomegalovirus (CMV) promoter; the respiratory syncytial virus (RSV) promoter; inducible  
15 promoters, such as the MMT promoter, the metallothionein promoter; heat shock promoters; the albumin promoter; the ApoA1 promoter; human globin promoters; viral thymidine kinase promoters, such as the Herpes Simplex thymidine kinase promoter; retroviral LTRs; the b-actin promoter; and human growth hormone promoters. The promoter also may be the native promoter for the polynucleotide of the present invention.

20       Unlike other gene therapy techniques, one major advantage of introducing naked nucleic acid sequences into target cells is the transitory nature of the polynucleotide synthesis in the cells. Studies have shown that non-replicating DNA sequences can be introduced into cells to provide production of the desired polypeptide for periods of up to six months.

The polynucleotide construct can be delivered to the interstitial space of tissues within  
25 the an animal, including of muscle, skin, brain, lung, liver, spleen, bone marrow, thymus, heart, lymph, blood, bone, cartilage, pancreas, kidney, gall bladder, stomach, intestine, testis, ovary, uterus, rectum, nervous system, eye, gland, and connective tissue. Interstitial space of the tissues comprises the intercellular, fluid, mucopolysaccharide matrix among the reticular fibers of organ tissues, elastic fibers in the walls of vessels or chambers, collagen fibers of  
30 fibrous tissues, or that same matrix within connective tissue ensheathing muscle cells or in the lacunae of bone. It is similarly the space occupied by the plasma of the circulation and the lymph fluid of the lymphatic channels. Delivery to the interstitial space of muscle tissue is

preferred for the reasons discussed below. They may be conveniently delivered by injection into the tissues comprising these cells. They are preferably delivered to and expressed in persistent, non-dividing cells which are differentiated, although delivery and expression may be achieved in non-differentiated or less completely differentiated cells, such as, for example, stem cells of blood or skin fibroblasts. In vivo muscle cells are particularly competent in their ability to take up and express polynucleotides.

For the naked nucleic acid sequence injection, an effective dosage amount of DNA or RNA will be in the range of from about 0.05 mg/kg body weight to about 50 mg/kg body weight. Preferably the dosage will be from about 0.005 mg/kg to about 20 mg/kg and more preferably from about 0.05 mg/kg to about 5 mg/kg. Of course, as the artisan of ordinary skill will appreciate, this dosage will vary according to the tissue site of injection. The appropriate and effective dosage of nucleic acid sequence can readily be determined by those of ordinary skill in the art and may depend on the condition being treated and the route of administration.

The preferred route of administration is by the parenteral route of injection into the interstitial space of tissues. However, other parenteral routes may also be used, such as, inhalation of an aerosol formulation particularly for delivery to lungs or bronchial tissues, throat or mucous membranes of the nose. In addition, naked DNA constructs can be delivered to arteries during angioplasty by the catheter used in the procedure.

The naked polynucleotides are delivered by any method known in the art, including, but not limited to, direct needle injection at the delivery site, intravenous injection, topical administration, catheter infusion, and so-called "gene guns". These delivery methods are known in the art.

The constructs may also be delivered with delivery vehicles such as viral sequences, viral particles, liposome formulations, lipofectin, precipitating agents, etc. Such methods of delivery are known in the art.

In certain embodiments, the polynucleotide constructs are complexed in a liposome preparation. Liposomal preparations for use in the instant invention include cationic (positively charged), anionic (negatively charged) and neutral preparations. However, cationic liposomes are particularly preferred because a tight charge complex can be formed between the cationic liposome and the polyanionic nucleic acid. Cationic liposomes have been shown to mediate intracellular delivery of plasmid DNA (Felgner et al., Proc. Natl. Acad. Sci. USA (1987) 84:7413-7416, which is herein incorporated by reference); mRNA

(Malone et al., Proc. Natl. Acad. Sci. USA (1989) 86:6077-6081, which is herein incorporated by reference); and purified transcription factors (Debs et al., J. Biol. Chem. (1990) 265:10189-10192, which is herein incorporated by reference), in functional form.

Cationic liposomes are readily available. For example,  
5 N[1-2,3-dioleoyloxy]propyl]-N,N,N-triethylammonium (DOTMA) liposomes are particularly useful and are available under the trademark Lipofectin, from GIBCO BRL, Grand Island, N.Y. (See, also, Felgner et al., Proc. Natl Acad. Sci. USA (1987) 84:7413-7416, which is herein incorporated by reference). Other commercially available liposomes include transfectace (DDAB/DOPE) and DOTAP/DOPE (Boehringer).

10 Other cationic liposomes can be prepared from readily available materials using techniques well known in the art. See, e.g. PCT Publication No. WO 90/11092 (which is herein incorporated by reference) for a description of the synthesis of DOTAP (1,2-bis(oleoyloxy)-3-(trimethylammonio)propane) liposomes. Preparation of DOTMA liposomes is explained in the literature, see, e.g., P. Felgner et al., Proc. Natl. Acad. Sci. USA  
15 84:7413-7417, which is herein incorporated by reference. Similar methods can be used to prepare liposomes from other cationic lipid materials.

Similarly, anionic and neutral liposomes are readily available, such as from Avanti Polar Lipids (Birmingham, Ala.), or can be easily prepared using readily available materials. Such materials include phosphatidyl, choline, cholesterol, phosphatidyl ethanolamine,  
20 dioleoylphosphatidyl choline (DOPC), dioleoylphosphatidyl glycerol (DOPG), dioleoylphosphatidyl ethanolamine (DOPE), among others. These materials can also be mixed with the DOTMA and DOTAP starting materials in appropriate ratios. Methods for making liposomes using these materials are well known in the art.

For example, commercially dioleoylphosphatidyl choline (DOPC),  
25 dioleoylphosphatidyl glycerol (DOPG), and dioleoylphosphatidyl ethanolamine (DOPE) can be used in various combinations to make conventional liposomes, with or without the addition of cholesterol. Thus, for example, DOPG/DOPC vesicles can be prepared by drying 50 mg each of DOPG and DOPC under a stream of nitrogen gas into a sonication vial. The sample is placed under a vacuum pump overnight and is hydrated the following day with  
30 deionized water. The sample is then sonicated for 2 hours in a capped vial, using a Heat Systems model 350 sonicator equipped with an inverted cup (bath type) probe at the maximum setting while the bath is circulated at 15EC. Alternatively, negatively charged

vesicles can be prepared without sonication to produce multilamellar vesicles or by extrusion through nucleopore membranes to produce unilamellar vesicles of discrete size. Other methods are known and available to those of skill in the art.

The liposomes can comprise multilamellar vesicles (MLVs), small unilamellar vesicles (SUVs), or large unilamellar vesicles (LUVs), with SUVs being preferred. The various liposome-nucleic acid complexes are prepared using methods well known in the art. See, e.g., Straubinger et al., *Methods of Immunology* (1983), 101:512-527, which is herein incorporated by reference. For example, MLVs containing nucleic acid can be prepared by depositing a thin film of phospholipid on the walls of a glass tube and subsequently hydrating with a solution of the material to be encapsulated. SUVs are prepared by extended sonication of MLVs to produce a homogeneous population of unilamellar liposomes. The material to be entrapped is added to a suspension of preformed MLVs and then sonicated. When using liposomes containing cationic lipids, the dried lipid film is resuspended in an appropriate solution such as sterile water or an isotonic buffer solution such as 10 mM Tris/NaCl, sonicated, and then the preformed liposomes are mixed directly with the DNA. The liposome and DNA form a very stable complex due to binding of the positively charged liposomes to the cationic DNA. SUVs find use with small nucleic acid fragments. LUVs are prepared by a number of methods, well known in the art. Commonly used methods include  $\text{Ca}^{2+}$ -EDTA chelation (Papahadjopoulos et al., *Biochim. Biophys. Acta* (1975) 394:483; Wilson et al., *Cell* (1979) 17:77); ether injection (Deamer, D. and Bangham, A., *Biochim. Biophys. Acta* (1976) 443:629; Ostro et al., *Biochem. Biophys. Res. Commun.* (1977) 76:836; Fraley et al., *Proc. Natl. Acad. Sci. USA* (1979) 76:3348); detergent dialysis (Enoch, H. and Strittmatter, P., *Proc. Natl. Acad. Sci. USA* (1979) 76:145); and reverse-phase evaporation (REV) (Fraley et al., *J. Biol. Chem.* (1980) 255:10431; Szoka, F. and Papahadjopoulos, D., *Proc. Natl. Acad. Sci. USA* (1978) 75:145; Schaefer-Ridder et al., *Science* (1982) 215:166), which are herein incorporated by reference.

Generally, the ratio of DNA to liposomes will be from about 10:1 to about 1:10. Preferably, the ration will be from about 5:1 to about 1:5. More preferably, the ration will be about 3:1 to about 1:3. Still more preferably, the ratio will be about 1:1.

U.S. Patent No. 5,676,954 (which is herein incorporated by reference) reports on the injection of genetic material, complexed with cationic liposomes carriers, into mice. U.S. Patent Nos. 4,897,355, 4,946,787, 5,049,386, 5,459,127, 5,589,466, 5,693,622, 5,580,859,



5,703,055, and international publication no. WO 94/9469 (which are herein incorporated by reference) provide cationic lipids for use in transfecting DNA into cells and mammals. U.S. Patent Nos. 5,589,466, 5,693,622, 5,580,859, 5,703,055, and international publication no. WO 94/9469 (which are herein incorporated by reference) provide methods for delivering  
5 DNA-cationic lipid complexes to mammals.

In certain embodiments, cells are engineered, *ex vivo* or *in vivo*, using a retroviral particle containing RNA which comprises a sequence encoding a polypeptide of the present invention. Retroviruses from which the retroviral plasmid vectors may be derived include, but are not limited to, Moloney Murine Leukemia Virus, spleen necrosis virus, Rous sarcoma  
10 Virus, Harvey Sarcoma Virus, avian leukosis virus, gibbon ape leukemia virus, human immunodeficiency virus, Myeloproliferative Sarcoma Virus, and mammary tumor virus.

The retroviral plasmid vector is employed to transduce packaging cell lines to form producer cell lines. Examples of packaging cells which may be transfected include, but are not limited to, the PE501, PA317, R-2, R-AM, PA12, T19-14X, VT-19-17-H2, RCRE,  
15 RCRIP, GP+E-86, GP+envAm12, and DAN cell lines as described in Miller, Human Gene Therapy 1:5-14 (1990), which is incorporated herein by reference in its entirety. The vector may transduce the packaging cells through any means known in the art. Such means include, but are not limited to, electroporation, the use of liposomes, and  $\text{CaPO}_4$  precipitation. In one alternative, the retroviral plasmid vector may be encapsulated into a liposome, or coupled to a  
20 lipid, and then administered to a host.

The producer cell line generates infectious retroviral vector particles which include polynucleotide encoding a polypeptide of the present invention. Such retroviral vector particles then may be employed, to transduce eukaryotic cells, either *in vitro* or *in vivo*. The transduced eukaryotic cells will express a polypeptide of the present invention.

25 In certain other embodiments, cells are engineered, *ex vivo* or *in vivo*, with polynucleotide contained in an adenovirus vector. Adenovirus can be manipulated such that it encodes and expresses a polypeptide of the present invention, and at the same time is inactivated in terms of its ability to replicate in a normal lytic viral life cycle. Adenovirus expression is achieved without integration of the viral DNA into the host cell chromosome,  
30 thereby alleviating concerns about insertional mutagenesis. Furthermore, adenoviruses have been used as live enteric vaccines for many years with an excellent safety profile (Schwartz, A. R. et al. (1974) Am. Rev. Respir. Dis.109:233-238). Finally, adenovirus mediated gene

transfer has been demonstrated in a number of instances including transfer of alpha-1-antitrypsin and CFTR to the lungs of cotton rats (Rosenfeld, M. A. et al. (1991) Science 252:431-434; Rosenfeld et al., (1992) Cell 68:143-155). Furthermore, extensive studies to attempt to establish adenovirus as a causative agent in human cancer were uniformly negative (Green, M. et al. (1979) Proc. Natl. Acad. Sci. USA 76:6606).

Suitable adenoviral vectors useful in the present invention are described, for example, in Kozarsky and Wilson, Curr. Opin. Genet. Devel. 3:499-503 (1993); Rosenfeld et al., Cell 68:143-155 (1992); Engelhardt et al., Human Genet. Ther. 4:759-769 (1993); Yang et al., Nature Genet. 7:362-369 (1994); Wilson et al., Nature 365:691-692 (1993); and U.S. Patent No. 5,652,224, which are herein incorporated by reference. For example, the adenovirus vector Ad2 is useful and can be grown in human 293 cells. These cells contain the E1 region of adenovirus and constitutively express E1a and E1b, which complement the defective adenoviruses by providing the products of the genes deleted from the vector. In addition to Ad2, other varieties of adenovirus (e.g., Ad3, Ad5, and Ad7) are also useful in the present invention.

Preferably, the adenoviruses used in the present invention are replication deficient. Replication deficient adenoviruses require the aid of a helper virus and/or packaging cell line to form infectious particles. The resulting virus is capable of infecting cells and can express a polynucleotide of interest which is operably linked to a promoter, but cannot replicate in most cells. Replication deficient adenoviruses may be deleted in one or more of all or a portion of the following genes: E1a, E1b, E3, E4, E2a, or L1 through L5.

In certain other embodiments, the cells are engineered, ex vivo or in vivo, using an adeno-associated virus (AAV). AAVs are naturally occurring defective viruses that require helper viruses to produce infectious particles (Muzyczka, N., Curr. Topics in Microbiol. Immunol. 158:97 (1992)). It is also one of the few viruses that may integrate its DNA into non-dividing cells. Vectors containing as little as 300 base pairs of AAV can be packaged and can integrate, but space for exogenous DNA is limited to about 4.5 kb. Methods for producing and using such AAVs are known in the art. See, for example, U.S. Patent Nos. 5,139,941, 5,173,414, 5,354,678, 5,436,146, 5,474,935, 5,478,745, and 5,589,377.

For example, an appropriate AAV vector for use in the present invention will include all the sequences necessary for DNA replication, encapsidation, and host-cell integration. The polynucleotide construct is inserted into the AAV vector using standard cloning

methods, such as those found in Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Press (1989). The recombinant AAV vector is then transfected into packaging cells which are infected with a helper virus, using any standard technique, including lipofection, electroporation, calcium phosphate precipitation, etc. Appropriate  
5 helper viruses include adenoviruses, cytomegaloviruses, vaccinia viruses, or herpes viruses. Once the packaging cells are transfected and infected, they will produce infectious AAV viral particles which contain the polynucleotide construct. These viral particles are then used to transduce eukaryotic cells, either ex vivo or in vivo. The transduced cells will contain the polynucleotide construct integrated into its genome, and will express a polypeptide of the  
10 invention.

Another method of gene therapy involves operably associating heterologous control regions and endogenous polynucleotide sequences (e.g. encoding a polypeptide of the present invention) via homologous recombination (see, e.g., U.S. Patent No. 5,641,670, issued June 24, 1997; International Publication No. WO 96/29411, published September 26, 1996;  
15 International Publication No. WO 94/12650, published August 4, 1994; Koller et al., *Proc. Natl. Acad. Sci. USA* 86:8932-8935 (1989); and Zijlstra et al., *Nature* 342:435-438 (1989). This method involves the activation of a gene which is present in the target cells, but which is not normally expressed in the cells, or is expressed at a lower level than desired.

Polynucleotide constructs are made, using standard techniques known in the art,  
20 which contain the promoter with targeting sequences flanking the promoter. Suitable promoters are described herein. The targeting sequence is sufficiently complementary to an endogenous sequence to permit homologous recombination of the promoter-targeting sequence with the endogenous sequence. The targeting sequence will be sufficiently near the 5' end of the desired endogenous polynucleotide sequence so the promoter will be operably  
25 linked to the endogenous sequence upon homologous recombination.

The promoter and the targeting sequences can be amplified using PCR. Preferably, the amplified promoter contains distinct restriction enzyme sites on the 5' and 3' ends. Preferably, the 3' end of the first targeting sequence contains the same restriction enzyme site as the 5' end of the amplified promoter and the 5' end of the second targeting sequence  
30 contains the same restriction site as the 3' end of the amplified promoter. The amplified promoter and targeting sequences are digested and ligated together.

The promoter-targeting sequence construct is delivered to the cells, either as naked polynucleotide, or in conjunction with transfection-facilitating agents, such as liposomes, viral sequences, viral particles, whole viruses, lipofection, precipitating agents, etc., described in more detail above. The P promoter-targeting sequence can be delivered by any method, 5 included direct needle injection, intravenous injection, topical administration, catheter infusion, particle accelerators, etc. The methods are described in more detail below.

The promoter-targeting sequence construct is taken up by cells. Homologous recombination between the construct and the endogenous sequence takes place, such that an endogenous sequence is placed under the control of the promoter. The promoter then drives 10 the expression of the endogenous sequence.

Preferably, the polynucleotide encoding a polypeptide of the present invention contains a secretory signal sequence that facilitates secretion of the protein. Typically, the signal sequence is positioned in the coding region of the polynucleotide to be expressed 15 towards or at the 5' end of the coding region. The signal sequence may be homologous or heterologous to the polynucleotide of interest and may be homologous or heterologous to the cells to be transfected. Additionally, the signal sequence may be chemically synthesized using methods known in the art.

Any mode of administration of any of the above-described polynucleotides constructs can be used so long as the mode results in the expression of one or more molecules in an 20 amount sufficient to provide a therapeutic effect. This includes direct needle injection, systemic injection, catheter infusion, biolistic injectors, particle accelerators (i.e., "gene guns"), gel foam sponge depots, other commercially available depot materials, osmotic pumps (e.g., Alza minipumps), oral or suppository solid (tablet or pill) pharmaceutical formulations, and decanting or topical applications during surgery. For example, direct 25 injection of naked calcium phosphate-precipitated plasmid into rat liver and rat spleen or a protein-coated plasmid into the portal vein has resulted in gene expression of the foreign gene in the rat livers (Kaneda et al., Science 243:375 (1989)).

A preferred method of local administration is by direct injection. Preferably, a recombinant molecule of the present invention complexed with a delivery vehicle is 30 administered by direct injection into or locally within the area of arteries. Administration of a composition locally within the area of arteries refers to injecting the composition centimeters and preferably, millimeters within arteries.

Another method of local administration is to contact a polynucleotide construct of the present invention in or around a surgical wound. For example, a patient can undergo surgery and the polynucleotide construct can be coated on the surface of tissue inside the wound or the construct can be injected into areas of tissue inside the wound.

5       Therapeutic compositions useful in systemic administration, include recombinant molecules of the present invention complexed to a targeted delivery vehicle of the present invention. Suitable delivery vehicles for use with systemic administration comprise liposomes comprising ligands for targeting the vehicle to a particular site.

Preferred methods of systemic administration, include intravenous injection, aerosol,  
10   oral and percutaneous (topical) delivery. Intravenous injections can be performed using methods standard in the art. Aerosol delivery can also be performed using methods standard in the art (see, for example, Stribling et al., Proc. Natl. Acad. Sci. USA 189:11277-11281, 1992, which is incorporated herein by reference). Oral delivery can be performed by complexing a polynucleotide construct of the present invention to a carrier capable of  
15   withstanding degradation by digestive enzymes in the gut of an animal. Examples of such carriers, include plastic capsules or tablets, such as those known in the art. Topical delivery can be performed by mixing a polynucleotide construct of the present invention with a lipophilic reagent (e.g., DMSO) that is capable of passing into the skin.

Determining an effective amount of substance to be delivered can depend upon a  
20   number of factors including, for example, the chemical structure and biological activity of the substance, the age and weight of the animal, the precise condition requiring treatment and its severity, and the route of administration. The frequency of treatments depends upon a number of factors, such as the amount of polynucleotide constructs administered per dose, as well as the health and history of the subject. The precise amount, number of doses, and  
25   timing of doses will be determined by the attending physician or veterinarian.

Therapeutic compositions of the present invention can be administered to any animal, preferably to mammals and birds. Preferred mammals include humans, dogs, cats, mice, rats, rabbits sheep, cattle, horses and pigs, with humans being particularly preferred.

### 30   Biological Activities

Polynucleotides or polypeptides, or agonists or antagonists of the present invention, can be used in assays to test for one or more biological activities. If these polynucleotides or

polypeptides, or agonists or antagonists of the present invention, do exhibit activity in a particular assay, it is likely that these molecules may be involved in the diseases associated with the biological activity. Thus, the polynucleotides and polypeptides, and agonists or antagonists could be used to treat the associated disease.

5

#### **Immune Activity**

A polypeptide or polynucleotide, or agonists or antagonists of the present invention may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the proliferation, differentiation, or mobilization (chemotaxis) of immune cells.

10 Immune cells develop through a process called hematopoiesis, producing myeloid (platelets, red blood cells, neutrophils, and macrophages) and lymphoid (B and T lymphocytes) cells from pluripotent stem cells. The etiology of these immune deficiencies or disorders may be genetic, somatic, such as cancer or some autoimmune disorders, acquired (e.g., by chemotherapy or toxins), or infectious. Moreover, polynucleotides or polypeptides, or  
15 agonists or antagonists of the present invention can be used as a marker or detector of a particular immune system disease or disorder.

Polynucleotides or polypeptides, or agonists or antagonists of the present invention may be useful in treating or detecting deficiencies or disorders of hematopoietic cells. Polynucleotides or polypeptides, or agonists or antagonists of the present invention could be  
20 used to increase differentiation and proliferation of hematopoietic cells, including the pluripotent stem cells, in an effort to treat those disorders associated with a decrease in certain (or many) types hematopoietic cells. Examples of immunologic deficiency syndromes include, but are not limited to: blood protein disorders (e.g. agammaglobulinemia, dysgammaglobulinemia), ataxia telangiectasia, common variable  
25 immunodeficiency, Digeorge Syndrome, HIV infection, HTLV-BLV infection, leukocyte adhesion deficiency syndrome, lymphopenia, phagocyte bactericidal dysfunction, severe combined immunodeficiency (SCIDs), Wiskott-Aldrich Disorder, anemia, thrombocytopenia, or hemoglobinuria.

Moreover, polynucleotides or polypeptides, or agonists or antagonists of the present  
30 invention could also be used to modulate hemostatic (the stopping of bleeding) or thrombolytic activity (clot formation). For example, by increasing hemostatic or thrombolytic activity, polynucleotides or polypeptides, or agonists or antagonists of the

present invention could be used to treat blood coagulation disorders (e.g., afibrinogenemia, factor deficiencies), blood platelet disorders (e.g. thrombocytopenia), or wounds resulting from trauma, surgery, or other causes. Alternatively, polynucleotides or polypeptides, or agonists or antagonists of the present invention that can decrease hemostatic or thrombolytic activity could be used to inhibit or dissolve clotting. These molecules could be important in the treatment of heart attacks (infarction), strokes, or scarring.

Polynucleotides or polypeptides, or agonists or antagonists of the present invention may also be useful in treating or detecting autoimmune disorders. Many autoimmune disorders result from inappropriate recognition of self as foreign material by immune cells. This inappropriate recognition results in an immune response leading to the destruction of the host tissue. Therefore, the administration of polynucleotides or polypeptides, or agonists or antagonists of the present invention that can inhibit an immune response, particularly the proliferation, differentiation, or chemotaxis of T-cells, may be an effective therapy in preventing autoimmune disorders.

Examples of autoimmune disorders that can be treated or detected include, but are not limited to: Addison's Disease, hemolytic anemia, antiphospholipid syndrome, rheumatoid arthritis, dermatitis, allergic encephalomyelitis, glomerulonephritis, Goodpasture's Syndrome, Graves' Disease, Multiple Sclerosis, Myasthenia Gravis, Neuritis, Ophthalmia, Bullous Pemphigoid, Pemphigus, Polyendocrinopathies, Purpura, Reiter's Disease, Stiff-Man Syndrome, Autoimmune Thyroiditis, Systemic Lupus Erythematosus, Autoimmune Pulmonary Inflammation, Guillain-Barre Syndrome, insulin dependent diabetes mellitus, and autoimmune inflammatory eye disease.

Similarly, allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems, may also be treated by polynucleotides or polypeptides, or agonists or antagonists of the present invention. Moreover, these molecules can be used to treat anaphylaxis, hypersensitivity to an antigenic molecule, or blood group incompatibility.

Polynucleotides or polypeptides, or agonists or antagonists of the present invention may also be used to treat and/or prevent organ rejection or graft-versus-host disease (GVHD). Organ rejection occurs by host immune cell destruction of the transplanted tissue through an immune response. Similarly, an immune response is also involved in GVHD, but, in this case, the foreign transplanted immune cells destroy the host tissues. The administration of

polynucleotides or polypeptides, or agonists or antagonists of the present invention that inhibits an immune response, particularly the proliferation, differentiation, or chemotaxis of T-cells, may be an effective therapy in preventing organ rejection or GVHD.

Similarly, polynucleotides or polypeptides, or agonists or antagonists of the present invention may also be used to modulate inflammation. For example, polynucleotides or polypeptides, or agonists or antagonists of the present invention may inhibit the proliferation and differentiation of cells involved in an inflammatory response. These molecules can be used to treat inflammatory conditions, both chronic and acute conditions, including chronic prostatitis, granulomatous prostatitis and malacoplakia, inflammation associated with infection (e.g., septic shock, sepsis, or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine induced lung injury, inflammatory bowel disease, Crohn's disease, or resulting from over production of cytokines (e.g., TNF or IL-1.)

#### 15 **Hyperproliferative Disorders**

Polynucleotides or polypeptides, or agonists or antagonists of the present invention can be used to treat or detect hyperproliferative disorders, including neoplasms. Polynucleotides or polypeptides, or agonists or antagonists of the present invention may inhibit the proliferation of the disorder through direct or indirect interactions. Alternatively, Polynucleotides or polypeptides, or agonists or antagonists of the present invention may proliferate other cells which can inhibit the hyperproliferative disorder.

For example, by increasing an immune response, particularly increasing antigenic qualities of the hyperproliferative disorder or by proliferating, differentiating, or mobilizing T-cells, hyperproliferative disorders can be treated. This immune response may be increased by either enhancing an existing immune response, or by initiating a new immune response. Alternatively, decreasing an immune response may also be a method of treating hyperproliferative disorders, such as a chemotherapeutic agent.

Examples of hyperproliferative disorders that can be treated or detected by Polynucleotides or polypeptides, or agonists or antagonists of the present invention include, but are not limited to neoplasms located in the: colon, abdomen, bone, breast, digestive system, liver, pancreas, peritoneum, endocrine glands (adrenal, parathyroid, pituitary,



testicles, ovary, thymus, thyroid), eye, head and neck, nervous (central and peripheral), lymphatic system, pelvic, skin, soft tissue, spleen, thoracic, and urogenital.

Similarly, other hyperproliferative disorders can also be treated or detected by polynucleotides or polypeptides, or agonists or antagonists of the present invention.

5 Examples of such hyperproliferative disorders include, but are not limited to: hypergammaglobulinemia, lymphoproliferative disorders, paraproteinemias, purpura, sarcoidosis, Sezary Syndrome, Waldenström's Macroglobulinemia, Gaucher's Disease, histiocytosis, and any other hyperproliferative disease, besides neoplasia, located in an organ system listed above.

10 One preferred embodiment utilizes polynucleotides of the present invention to inhibit aberrant cellular division, by gene therapy using the present invention, and/or protein fusions or fragments thereof.

Thus, the present invention provides a method for treating cell proliferative disorders by inserting into an abnormally proliferating cell a polynucleotide of the present invention,  
15 wherein said polynucleotide represses said expression.

Another embodiment of the present invention provides a method of treating cell-proliferative disorders in individuals comprising administration of one or more active gene copies of the present invention to an abnormally proliferating cell or cells. In a preferred embodiment, polynucleotides of the present invention is a DNA construct comprising a  
20 recombinant expression vector effective in expressing a DNA sequence encoding said polynucleotides. In another preferred embodiment of the present invention, the DNA construct encoding the polynucleotides of the present invention is inserted into cells to be treated utilizing a retrovirus, or more preferably an adenoviral vector (See G J. Nabel, et. al., PNAS 1999 96: 324-326, which is hereby incorporated by reference). In a most preferred  
25 embodiment, the viral vector is defective and will not transform non-proliferating cells, only proliferating cells. Moreover, in a preferred embodiment, the polynucleotides of the present invention inserted into proliferating cells either alone, or in combination with or fused to other polynucleotides, can then be modulated via an external stimulus (i.e. magnetic, specific small molecule, chemical, or drug administration, etc.), which acts upon the promoter  
30 upstream of said polynucleotides to induce expression of the encoded protein product. As such the beneficial therapeutic affect of the present invention may be expressly modulated

(i.e. to increase, decrease, or inhibit expression of the present invention) based upon said external stimulus.

Polynucleotides of the present invention may be useful in repressing expression of oncogenic genes or antigens. By "repressing expression of the oncogenic genes " is intended  
5 the suppression of the transcription of the gene, the degradation of the gene transcript (pre-message RNA), the inhibition of splicing, the destruction of the messenger RNA, the prevention of the post-translational modifications of the protein, the destruction of the protein, or the inhibition of the normal function of the protein.

For local administration to abnormally proliferating cells, polynucleotides of the  
10 present invention may be administered by any method known to those of skill in the art including, but not limited to transfection, electroporation, microinjection of cells, or in vehicles such as liposomes, lipofectin, or as naked polynucleotides, or any other method described throughout the specification. The polynucleotide of the present invention may be delivered by known gene delivery systems such as, but not limited to, retroviral vectors  
15 (Gilboa, J. Virology 44:845 (1982); Hocke, Nature 320:275 (1986); Wilson, et al., Proc. Natl. Acad. Sci. U.S.A. 85:3014), vaccinia virus system (Chakrabarty et al., Mol. Cell Biol. 5:3403 (1985) or other efficient DNA delivery systems (Yates et al., Nature 313:812 (1985)) known to those skilled in the art. These references are exemplary only and are hereby incorporated by reference. In order to specifically deliver or transfect cells which are abnormally  
20 proliferating and spare non-dividing cells, it is preferable to utilize a retrovirus, or adenoviral (as described in the art and elsewhere herein) delivery system known to those of skill in the art. Since host DNA replication is required for retroviral DNA to integrate and the retrovirus will be unable to self replicate due to the lack of the retrovirus genes needed for its life cycle. Utilizing such a retroviral delivery system for polynucleotides of the present invention will  
25 target said gene and constructs to abnormally proliferating cells and will spare the non-dividing normal cells.

The polynucleotides of the present invention may be delivered directly to cell proliferative disorder/disease sites in internal organs, body cavities and the like by use of imaging devices used to guide an injecting needle directly to the disease site. The  
30 polynucleotides of the present invention may also be administered to disease sites at the time of surgical intervention.

By "cell proliferative disease" is meant any human or animal disease or disorder, affecting any one or any combination of organs, cavities, or body parts, which is characterized by single or multiple local abnormal proliferations of cells, groups of cells, or tissues, whether benign or malignant.

- 5 Any amount of the polynucleotides of the present invention may be administered as long as it has a biologically inhibiting effect on the proliferation of the treated cells. Moreover, it is possible to administer more than one of the polynucleotide of the present invention simultaneously to the same site. By "biologically inhibiting" is meant partial or total growth inhibition as well as decreases in the rate of proliferation or growth of the cells.
- 10 The biologically inhibitory dose may be determined by assessing the effects of the polynucleotides of the present invention on target malignant or abnormally proliferating cell growth in tissue culture, tumor growth in animals and cell cultures, or any other method known to one of ordinary skill in the art.

- The present invention is further directed to antibody-based therapies which involve
- 15 administering of anti-polypeptides and anti-polynucleotide antibodies to a mammalian, preferably human, patient for treating one or more of the described disorders. Methods for producing anti-polypeptides and anti-polynucleotide antibodies polyclonal and monoclonal antibodies are described in detail elsewhere herein. Such antibodies may be provided in pharmaceutically acceptable compositions as known in the art or as described herein.

- 20 A summary of the ways in which the antibodies of the present invention may be used therapeutically includes binding polynucleotides or polypeptides of the present invention locally or systemically in the body or by direct cytotoxicity of the antibody, e.g. as mediated by complement (CDC) or by effector cells (ADCC). Some of these approaches are described in more detail below. Armed with the teachings provided herein, one of ordinary skill in the
- 25 art will know how to use the antibodies of the present invention for diagnostic, monitoring or therapeutic purposes without undue experimentation.

- In particular, the antibodies, fragments and derivatives of the present invention are useful for treating a subject having or developing cell proliferative and/or differentiation disorders as described herein. Such treatment comprises administering a single or multiple
- 30 doses of the antibody, or a fragment, derivative, or a conjugate thereof.

The antibodies of this invention may be advantageously utilized in combination with other monoclonal or chimeric antibodies, or with lymphokines or hematopoietic growth

factors, for example, which serve to increase the number or activity of effector cells which interact with the antibodies.

It is preferred to use high affinity and/or potent in vivo inhibiting and/or neutralizing antibodies against polypeptides or polynucleotides of the present invention. fragments or regions thereof, for both immunoassays directed to and therapy of disorders related to polynucleotides or polypeptides, including fragments thereof, of the present invention. Such antibodies, fragments, or regions, will preferably have an affinity for polynucleotides or polypeptides, including fragments thereof. Preferred binding affinities include those with a dissociation constant or  $K_d$  less than  $5 \times 10^{-6}M$ ,  $10^{-6}M$ ,  $5 \times 10^{-7}M$ ,  $10^{-7}M$ ,  $5 \times 10^{-8}M$ ,  $10^{-8}M$ ,  $5 \times 10^{-9}M$ ,  $10^{-9}M$ ,  $5 \times 10^{-10}M$ ,  $10^{-10}M$ ,  $5 \times 10^{-11}M$ ,  $10^{-11}M$ ,  $5 \times 10^{-12}M$ ,  $10^{-12}M$ ,  $5 \times 10^{-13}M$ ,  $10^{-13}M$ ,  $5 \times 10^{-14}M$ ,  $10^{-14}M$ ,  $5 \times 10^{-15}M$ , and  $10^{-15}M$ .

Moreover, polypeptides of the present invention are useful in inhibiting the angiogenesis of proliferative cells or tissues, either alone, as a protein fusion, or in combination with other polypeptides directly or indirectly, as described elsewhere herein. In a most preferred embodiment, said anti-angiogenesis effect may be achieved indirectly, for example, through the inhibition of hematopoietic, tumor-specific cells, such as tumor-associated macrophages (See Joseph IB, et al. J Natl Cancer Inst, 90(21):1648-53 (1998), which is hereby incorporated by reference). Antibodies directed to polypeptides or polynucleotides of the present invention may also result in inhibition of angiogenesis directly, or indirectly (See Witte L, et al., Cancer Metastasis Rev. 17(2):155-61 (1998), which is hereby incorporated by reference)).

Polypeptides, including protein fusions, of the present invention, or fragments thereof may be useful in inhibiting proliferative cells or tissues through the induction of apoptosis. Said polypeptides may act either directly, or indirectly to induce apoptosis of proliferative cells and tissues, for example in the activation of a death-domain receptor, such as tumor necrosis factor (TNF) receptor-1, CD95 (Fas/APO-1), TNF-receptor-related apoptosis-mediated protein (TRAMP) and TNF-related apoptosis-inducing ligand (TRAIL) receptor-1 and -2 (See Schulze-Osthoff K, et al., Eur J Biochem 254(3):439-59 (1998), which is hereby incorporated by reference). Moreover, in another preferred embodiment of the present invention, said polypeptides may induce apoptosis through other mechanisms, such as in the activation of other proteins which will activate apoptosis, or through stimulating the expression of said proteins, either alone or in combination with small molecule drugs or

adjuvants, such as apoptonin, galectins, thioredoxins, antiinflammatory proteins (See for example, Mutat Res 400(1-2):447-55 (1998), Med Hypotheses.50(5):423-33 (1998), Chem Biol Interact. Apr 24;111-112:23-34 (1998), J Mol Med.76(6):402-12 (1998), Int J Tissue React;20(1):3-15 (1998), which are all hereby incorporated by reference).

5 Polypeptides, including protein fusions to, or fragments thereof, of the present invention are useful in inhibiting the metastasis of proliferative cells or tissues. Inhibition may occur as a direct result of administering polypeptides, or antibodies directed to said polypeptides as described elsewhere herein, or indirectly, such as activating the expression of proteins known to inhibit metastasis, for example alpha 4 integrins, (See, e.g., Curr Top  
10 Microbiol Immunol 1998;231:125-41, which is hereby incorporated by reference). Such therapeutic affects of the present invention may be achieved either alone, or in combination with small molecule drugs or adjuvants.

In another embodiment, the invention provides a method of delivering compositions containing the polypeptides of the invention (e.g., compositions containing polypeptides or  
15 polypeptide antibodies associated with heterologous polypeptides, heterologous nucleic acids, toxins, or prodrugs) to targeted cells expressing the polypeptide of the present invention. Polypeptides or polypeptide antibodies of the invention may be associated with with heterologous polypeptides, heterologous nucleic acids, toxins, or prodrugs via hydrophobic, hydrophilic, ionic and/or covalent interactions. Polypeptides, protein fusions to, or  
20 fragments thereof, of the present invention are useful in enhancing the immunogenicity and/or antigenicity of proliferating cells or tissues, either directly, such as would occur if the polypeptides of the present invention 'vaccinated' the immune response to respond to proliferative antigens and immunogens, or indirectly, such as in activating the expression of proteins known to enhance the immune response (e.g. chemokines), to said antigens and  
25 immunogens.

#### **Cardiovascular Disorders**

Polynucleotides or polypeptides, or agonists or antagonists of the present invention, may be used to treat cardiovascular disorders, including peripheral artery disease, such as  
30 limb ischemia.

Cardiovascular disorders include cardiovascular abnormalities, such as arterio-arterial fistula, arteriovenous fistula, cerebral arteriovenous malformations, congenital heart defects,

pulmonary atresia, and Scimitar Syndrome. Congenital heart defects include aortic coarctation, cor triatriatum, coronary vessel anomalies, crisscross heart, dextrocardia, patent ductus arteriosus, Ebstein's anomaly, Eisenmenger complex, hypoplastic left heart syndrome, levocardia, tetralogy of fallot, transposition of great vessels, double outlet right ventricle, 5 tricuspid atresia, persistent truncus arteriosus, and heart septal defects, such as aortopulmonary septal defect, endocardial cushion defects, Lutembacher's Syndrome, trilog of Fallot, ventricular heart septal defects.

Cardiovascular disorders also include heart disease, such as arrhythmias, carcinoid heart disease, high cardiac output, low cardiac output, cardiac tamponade, endocarditis 10 (including bacterial), heart aneurysm, cardiac arrest, congestive heart failure, congestive cardiomyopathy, paroxysmal dyspnea, cardiac edema, heart hypertrophy, congestive cardiomyopathy, left ventricular hypertrophy, right ventricular hypertrophy, post-infarction heart rupture, ventricular septal rupture, heart valve diseases, myocardial diseases, myocardial ischemia, pericardial effusion, pericarditis (including constrictive and 15 tuberculous), pneumopericardium, postpericardiotomy syndrome, pulmonary heart disease, rheumatic heart disease, ventricular dysfunction, hyperemia, cardiovascular pregnancy complications, Scimitar Syndrome, cardiovascular syphilis, and cardiovascular tuberculosis.

Arrhythmias include sinus arrhythmia, atrial fibrillation, atrial flutter, bradycardia, extrasystole, Adams-Stokes Syndrome, bundle-branch block, sinoatrial block, long QT 20 syndrome, parasystole, Lown-Ganong-Levine Syndrome, Mahaim-type pre-excitation syndrome, Wolff-Parkinson-White syndrome, sick sinus syndrome, tachycardias, and ventricular fibrillation. Tachycardias include paroxysmal tachycardia, supraventricular tachycardia, accelerated idioventricular rhythm, atrioventricular nodal reentry tachycardia, ectopic atrial tachycardia, ectopic junctional tachycardia, sinoatrial nodal reentry tachycardia, 25 sinus tachycardia, Torsades de Pointes, and ventricular tachycardia.

Heart valve disease include aortic valve insufficiency, aortic valve stenosis, hear murmurs, aortic valve prolapse, mitral valve prolapse, tricuspid valve prolapse, mitral valve insufficiency, mitral valve stenosis, pulmonary atresia, pulmonary valve insufficiency, pulmonary valve stenosis, tricuspid atresia, tricuspid valve insufficiency, and tricuspid valve 30 stenosis.

Myocardial diseases include alcoholic cardiomyopathy, congestive cardiomyopathy, hypertrophic cardiomyopathy, aortic subvalvular stenosis, pulmonary subvalvular stenosis,

restrictive cardiomyopathy, Chagas cardiomyopathy, endocardial fibroelastosis, endomyocardial fibrosis, Kearns Syndrome, myocardial reperfusion injury, and myocarditis.

Myocardial ischemias include coronary disease, such as angina pectoris, coronary aneurysm, coronary arteriosclerosis, coronary thrombosis, coronary vasospasm, myocardial infarction and myocardial stunning.

Cardiovascular diseases also include vascular diseases such as aneurysms, angiodysplasia, angiomas, bacillary angiomas, Hippiel-Lindau Disease, Klippel-Trenaunay-Weber Syndrome, Sturge-Weber Syndrome, angioneurotic edema, aortic diseases, Takayasu's Arteritis, aortitis, Leriche's Syndrome, arterial occlusive diseases, arteritis, 10 enarteritis, polyarteritis nodosa, cerebrovascular disorders, diabetic angiopathies, diabetic retinopathy, embolisms, thrombosis, erythromelalgia, hemorrhoids, hepatic veno-occlusive disease, hypertension, hypotension, ischemia, peripheral vascular diseases, phlebitis, pulmonary veno-occlusive disease, Raynaud's disease, CREST syndrome, retinal vein occlusion, Scimitar syndrome, superior vena cava syndrome, telangiectasia, ataxia 15 telangiectasia, hereditary hemorrhagic telangiectasia, varicocele, varicose veins, varicose ulcer, vasculitis, and venous insufficiency.

Aneurysms include dissecting aneurysms, false aneurysms, infected aneurysms, ruptured aneurysms, aortic aneurysms, cerebral aneurysms, coronary aneurysms, heart aneurysms, and iliac aneurysms.

Arterial occlusive diseases include arteriosclerosis, intermittent claudication, carotid stenosis, fibromuscular dysplasias, mesenteric vascular occlusion, Moyamoya disease, renal artery obstruction, retinal artery occlusion, and thromboangiitis obliterans.

Cerebrovascular disorders include carotid artery diseases, cerebral amyloid angiopathy, cerebral aneurysm, cerebral anoxia, cerebral arteriosclerosis, cerebral arteriovenous malformation, cerebral artery diseases, cerebral embolism and thrombosis, 25 carotid artery thrombosis, sinus thrombosis, Wallenberg's syndrome, cerebral hemorrhage, epidural hematoma, subdural hematoma, subarachnoid hemorrhage, cerebral infarction, cerebral ischemia (including transient), subclavian steal syndrome, periventricular leukomalacia, vascular headache, cluster headache, migraine, and vertebrobasilar 30 insufficiency.

Embolisms include air embolisms, amniotic fluid embolisms, cholesterol embolisms, blue toe syndrome, fat embolisms, pulmonary embolisms, and thromboembolisms.

Thrombosis include coronary thrombosis, hepatic vein thrombosis, retinal vein occlusion, carotid artery thrombosis, sinus thrombosis, Wallenberg's syndrome, and thrombophlebitis.

Ischemia includes cerebral ischemia, ischemic colitis, compartment syndromes, anterior compartment syndrome, myocardial ischemia, reperfusion injuries, and peripheral limb ischemia. Vasculitis includes aortitis, arteritis, Behcet's Syndrome, Churg-Strauss Syndrome, mucocutaneous lymph node syndrome, thromboangiitis obliterans, hypersensitivity vasculitis, Schoenlein-Henoch purpura, allergic cutaneous vasculitis, and Wegener's granulomatosis.

Polynucleotides or polypeptides, or agonists or antagonists of the present invention, are especially effective for the treatment of critical limb ischemia and coronary disease.

Polypeptides may be administered using any method known in the art, including, but not limited to, direct needle injection at the delivery site, intravenous injection, topical administration, catheter infusion, biolistic injectors, particle accelerators, gelfoam sponge depots, other commercially available depot materials, osmotic pumps, oral or suppository solid pharmaceutical formulations, decanting or topical applications during surgery, aerosol delivery. Such methods are known in the art. Polypeptides may be administered as part of a Therapeutic, described in more detail below. Methods of delivering polynucleotides are described in more detail herein.

#### **Anti-Angiogenesis Activity**

The naturally occurring balance between endogenous stimulators and inhibitors of angiogenesis is one in which inhibitory influences predominate. Rastinejad *et al.*, *Cell* 56:345-355 (1989). In those rare instances in which neovascularization occurs under normal physiological conditions, such as wound healing, organ regeneration, embryonic development, and female reproductive processes, angiogenesis is stringently regulated and spatially and temporally delimited. Under conditions of pathological angiogenesis such as that characterizing solid tumor growth, these regulatory controls fail. Unregulated angiogenesis becomes pathologic and sustains progression of many neoplastic and non-neoplastic diseases. A number of serious diseases are dominated by abnormal neovascularization including solid tumor growth and metastases, arthritis, some types of eye disorders, and psoriasis. See, e.g., reviews by Moses *et al.*, *Biotech.* 9:630-634 (1991); Folkman *et al.*, *N. Engl. J. Med.*, 333:1757-1763 (1995); Auerbach *et al.*, *J. Microvasc. Res.*



29:401-411 (1985); Folkman, *Advances in Cancer Research*, eds. Klein and Weinhouse, Academic Press, New York, pp. 175-203 (1985); Patz, *Am. J. Ophthalmol.* 94:715-743 (1982); and Folkman *et al.*, *Science* 221:719-725 (1983). In a number of pathological conditions, the process of angiogenesis contributes to the disease state. For example, 5 significant data have accumulated which suggest that the growth of solid tumors is dependent on angiogenesis. Folkman and Klagsbrun, *Science* 235:442-447 (1987).

The polynucleotides encoding a polypeptide of the present invention may be administered along with other polynucleotides encoding an angiogenic protein. Examples of angiogenic proteins include, but are not limited to, acidic and basic fibroblast growth factors. 10 VEGF-1, VEGF-2, VEGF-3, epidermal growth factor alpha and beta, platelet-derived endothelial cell growth factor, platelet-derived growth factor, tumor necrosis factor alpha, hepatocyte growth factor, insulin like growth factor, colony stimulating factor, macrophage colony stimulating factor, granulocyte/macrophage colony stimulating factor, and nitric oxide synthase.

15 The present invention provides for treatment of diseases or disorders associated with neovascularization by administration of the polynucleotides and/or polypeptides of the invention, as well as agonists or antagonists of the present invention. Malignant and metastatic conditions which can be treated with the polynucleotides and polypeptides, or agonists or antagonists of the invention include, but are not limited to, malignancies, solid 20 tumors, and cancers described herein and otherwise known in the art (for a review of such disorders, see Fishman *et al.*, *Medicine*, 2d Ed., J. B. Lippincott Co., Philadelphia (1985)). Thus, the present invention provides a method of treating an angiogenesis-related disease and/or disorder, comprising administering to an individual in need thereof a therapeutically effective amount of a polynucleotide, polypeptide, antagonist and/or agonist 25 of the invention. For example, polynucleotides, polypeptides, antagonists and/or agonists may be utilized in a variety of additional methods in order to therapeutically treat a cancer or tumor. Cancers which may be treated with polynucleotides, polypeptides, antagonists and/or agonists include, but are not limited to solid tumors, including colon, rectum, prostate, lung, breast, ovarian, stomach, pancreas, larynx, esophagus, testes, liver, parotid, biliary tract, 30 cervix, uterus, endometrium, kidney, bladder, thyroid cancer; primary tumors and metastases; melanomas; glioblastoma; Kaposi's sarcoma; leiomyosarcoma; non-small cell lung cancer; colorectal cancer; advanced malignancies; and blood born tumors such as leukemias. For

example, polynucleotides, polypeptides, antagonists and/or agonists may be delivered topically, in order to treat cancers such as skin cancer, head and neck tumors, breast tumors, and Kaposi's sarcoma.

Within yet other aspects, polynucleotides, polypeptides, antagonists and/or agonists  
5 may be utilized to treat superficial forms of bladder cancer by, for example, intravesical administration. Polynucleotides, polypeptides, antagonists and/or agonists may be delivered directly into the tumor, or near the tumor site, via injection or a catheter. Of course, as the artisan of ordinary skill will appreciate, the appropriate mode of administration will vary according to the cancer to be treated. Other modes of delivery are discussed herein.

10 Polynucleotides, polypeptides, antagonists and/or agonists may be useful in treating other disorders, besides cancers, which involve angiogenesis. These disorders include, but are not limited to: benign tumors, for example hemangiomas, acoustic neuromas, neurofibromas, trachomas, and pyogenic granulomas; arteriosclerotic plaques; ocular angiogenic diseases, for example, diabetic retinopathy, retinopathy of prematurity, macular  
15 degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, retinoblastoma, uveitis and Pterygia (abnormal blood vessel growth) of the eye; rheumatoid arthritis; psoriasis; delayed wound healing; endometriosis; vasculogenesis; granulations; hypertrophic scars (keloids); nonunion fractures; scleroderma; trachoma; vascular adhesions; myocardial angiogenesis; coronary collaterals; cerebral collaterals; arteriovenous  
20 malformations; ischemic limb angiogenesis; Osler-Webber Syndrome; plaque neovascularization; telangiectasia; hemophilic joints; angiofibroma; fibromuscular dysplasia; wound granulation; Crohn's disease; and atherosclerosis.

For example, within one aspect of the present invention methods are provided for treating hypertrophic scars and keloids, comprising the step of administering a  
25 polynucleotide, polypeptide, antagonist and/or agonist of the invention to a hypertrophic scar or keloid.

Within one embodiment of the present invention polynucleotides, polypeptides, antagonists and/or agonists are directly injected into a hypertrophic scar or keloid, in order to prevent the progression of these lesions. This therapy is of particular value in the  
30 prophylactic treatment of conditions which are known to result in the development of hypertrophic scars and keloids (e.g., burns), and is preferably initiated after the proliferative phase has had time to progress (approximately 14 days after the initial injury), but before

hypertrophic scar or keloid development. As noted above, the present invention also provides methods for treating neovascular diseases of the eye, including for example, corneal neovascularization, neovascular glaucoma, proliferative diabetic retinopathy, retrolental fibroplasia and macular degeneration.

5        Moreover, Ocular disorders associated with neovascularization which can be treated with the polynucleotides and polypeptides of the present invention (including agonists and/or antagonists) include, but are not limited to: neovascular glaucoma, diabetic retinopathy, retinoblastoma, retrolental fibroplasia, uveitis, retinopathy of prematurity macular degeneration, corneal graft neovascularization, as well as other eye inflammatory diseases,  
10    ocular tumors and diseases associated with choroidal or iris neovascularization. See, e.g., reviews by Waltman *et al.*, *Am. J. Ophthalmol.* 85:704-710 (1978) and Gartner *et al.*, *Surv. Ophthalmol.* 22:291-312 (1978).

      Thus, within one aspect of the present invention methods are provided for treating neovascular diseases of the eye such as corneal neovascularization (including corneal graft  
15    neovascularization), comprising the step of administering to a patient a therapeutically effective amount of a compound (as described above) to the cornea, such that the formation of blood vessels is inhibited. Briefly, the cornea is a tissue which normally lacks blood vessels. In certain pathological conditions however, capillaries may extend into the cornea from the pericorneal vascular plexus of the limbus. When the cornea becomes vascularized,  
20    it also becomes clouded, resulting in a decline in the patient's visual acuity. Visual loss may become complete if the cornea completely opacitates. A wide variety of disorders can result in corneal neovascularization, including for example, corneal infections (e.g., trachoma, herpes simplex keratitis, leishmaniasis and onchocerciasis), immunological processes (e.g., graft rejection and Stevens-Johnson's syndrome), alkali burns, trauma, inflammation (of any  
25    cause), toxic and nutritional deficiency states, and as a complication of wearing contact lenses.

      Within particularly preferred embodiments of the invention, may be prepared for topical administration in saline (combined with any of the preservatives and antimicrobial agents commonly used in ocular preparations), and administered in eyedrop form. The  
30    solution or suspension may be prepared in its pure form and administered several times daily. Alternatively, anti-angiogenic compositions, prepared as described above, may also be administered directly to the cornea. Within preferred embodiments, the anti-angiogenic

composition is prepared with a muco-adhesive polymer which binds to cornea. Within further embodiments, the anti-angiogenic factors or anti-angiogenic compositions may be utilized as an adjunct to conventional steroid therapy. Topical therapy may also be useful prophylactically in corneal lesions which are known to have a high probability of inducing an angiogenic response (such as chemical burns). In these instances the treatment, likely in combination with steroids, may be instituted immediately to help prevent subsequent complications.

Within other embodiments, the compounds described above may be injected directly into the corneal stroma by an ophthalmologist under microscopic guidance. The preferred site of injection may vary with the morphology of the individual lesion, but the goal of the administration would be to place the composition at the advancing front of the vasculature (i.e., interspersed between the blood vessels and the normal cornea). In most cases this would involve perilimbic corneal injection to "protect" the cornea from the advancing blood vessels. This method may also be utilized shortly after a corneal insult in order to prophylactically prevent corneal neovascularization. In this situation the material could be injected in the perilimbic cornea interspersed between the corneal lesion and its undesired potential limbic blood supply. Such methods may also be utilized in a similar fashion to prevent capillary invasion of transplanted corneas. In a sustained-release form injections might only be required 2-3 times per year. A steroid could also be added to the injection solution to reduce inflammation resulting from the injection itself.

Within another aspect of the present invention, methods are provided for treating neovascular glaucoma, comprising the step of administering to a patient a therapeutically effective amount of a polynucleotide, polypeptide, antagonist and/or agonist to the eye, such that the formation of blood vessels is inhibited. In one embodiment, the compound may be administered topically to the eye in order to treat early forms of neovascular glaucoma. Within other embodiments, the compound may be implanted by injection into the region of the anterior chamber angle. Within other embodiments, the compound may also be placed in any location such that the compound is continuously released into the aqueous humor. Within another aspect of the present invention, methods are provided for treating proliferative diabetic retinopathy, comprising the step of administering to a patient a therapeutically effective amount of a polynucleotide, polypeptide, antagonist and/or agonist to the eyes, such that the formation of blood vessels is inhibited.

Within particularly preferred embodiments of the invention, proliferative diabetic retinopathy may be treated by injection into the aqueous humor or the vitreous, in order to increase the local concentration of the polynucleotide, polypeptide, antagonist and/or agonist in the retina. Preferably, this treatment should be initiated prior to the acquisition of severe disease requiring photocoagulation.

Within another aspect of the present invention, methods are provided for treating retrolental fibroplasia, comprising the step of administering to a patient a therapeutically effective amount of a polynucleotide, polypeptide, antagonist and/or agonist to the eye, such that the formation of blood vessels is inhibited. The compound may be administered topically, via intravitreal injection and/or via intraocular implants.

Additionally, disorders which can be treated with the polynucleotides, polypeptides, agonists and/or antagonists include, but are not limited to, hemangioma, arthritis, psoriasis, angiofibroma, atherosclerotic plaques, delayed wound healing, granulations, hemophilic joints, hypertrophic scars, nonunion fractures, Osler-Weber syndrome, pyogenic granuloma, scleroderma, trachoma, and vascular adhesions.

Moreover, disorders and/or states, which can be treated with the polynucleotides, polypeptides, agonists and/or antagonists include, but are not limited to, solid tumors, blood born tumors such as leukemias, tumor metastasis, Kaposi's sarcoma, benign tumors, for example hemangiomas, acoustic neuromas, neurofibromas, trachomas, and pyogenic granulomas, rheumatoid arthritis, psoriasis, ocular angiogenic diseases, for example, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, retinoblastoma, and uveitis, delayed wound healing, endometriosis, vasculogenesis, granulations, hypertrophic scars (keloids), nonunion fractures, scleroderma, trachoma, vascular adhesions, myocardial angiogenesis, coronary collaterals, cerebral collaterals, arteriovenous malformations, ischemic limb angiogenesis, Osler-Webber Syndrome, plaque neovascularization, telangiectasia, hemophilic joints, angiofibroma fibromuscular dysplasia, wound granulation, Crohn's disease, atherosclerosis, birth control agent by preventing vascularization required for embryo implantation controlling menstruation, diseases that have angiogenesis as a pathologic consequence such as cat scratch disease (Rochelie minalia quintosa), ulcers (*Helicobacter pylori*), Bartonellosis and bacillary angiomatosis.

In one aspect of the birth control method, an amount of the compound sufficient to block embryo implantation is administered before or after intercourse and fertilization have occurred, thus providing an effective method of birth control, possibly a "morning after" method. Polynucleotides, polypeptides, agonists and/or agonists may also be used in  
5 controlling menstruation or administered as either a peritoneal lavage fluid or for peritoneal implantation in the treatment of endometriosis.

Polynucleotides, polypeptides, agonists and/or agonists of the present invention may be incorporated into surgical sutures in order to prevent stitch granulomas.

Polynucleotides, polypeptides, agonists and/or agonists may be utilized in a wide  
10 variety of surgical procedures. For example, within one aspect of the present invention a compositions (in the form of, for example, a spray or film) may be utilized to coat or spray an area prior to removal of a tumor, in order to isolate normal surrounding tissues from malignant tissue, and/or to prevent the spread of disease to surrounding tissues. Within other aspects of the present invention, compositions (e.g., in the form of a spray) may be delivered  
15 via endoscopic procedures in order to coat tumors, or inhibit angiogenesis in a desired locale. Within yet other aspects of the present invention, surgical meshes which have been coated with anti- angiogenic compositions of the present invention may be utilized in any procedure wherein a surgical mesh might be utilized. For example, within one embodiment of the invention a surgical mesh laden with an anti-angiogenic composition may be utilized during  
20 abdominal cancer resection surgery (e.g., subsequent to colon resection) in order to provide support to the structure, and to release an amount of the anti-angiogenic factor.

Within further aspects of the present invention, methods are provided for treating tumor excision sites, comprising administering a polynucleotide, polypeptide, agonist and/or agonist to the resection margins of a tumor subsequent to excision, such that the local  
25 recurrence of cancer and the formation of new blood vessels at the site is inhibited. Within one embodiment of the invention, the anti-angiogenic compound is administered directly to the tumor excision site (e.g., applied by swabbing, brushing or otherwise coating the resection margins of the tumor with the anti-angiogenic compound). Alternatively, the anti-angiogenic compounds may be incorporated into known surgical pastes prior to  
30 administration. Within particularly preferred embodiments of the invention, the anti-angiogenic compounds are applied after hepatic resections for malignancy, and after neurosurgical operations.

Within one aspect of the present invention, polynucleotides, polypeptides, agonists and/or agonists may be administered to the resection margin of a wide variety of tumors, including for example, breast, colon, brain and hepatic tumors. For example, within one embodiment of the invention, anti-angiogenic compounds may be administered to the site of a neurological tumor subsequent to excision, such that the formation of new blood vessels at the site are inhibited.

The polynucleotides, polypeptides, agonists and/or agonists of the present invention may also be administered along with other anti-angiogenic factors. Representative examples of other anti-angiogenic factors include: Anti-Invasive Factor, retinoic acid and derivatives thereof, paclitaxel, Suramin, Tissue Inhibitor of Metalloproteinase-1, Tissue Inhibitor of Metalloproteinase-2, Plasminogen Activator Inhibitor-1, Plasminogen Activator Inhibitor-2, and various forms of the lighter "d group" transition metals.

Lighter "d group" transition metals include, for example, vanadium, molybdenum, tungsten, titanium, niobium, and tantalum species. Such transition metal species may form transition metal complexes. Suitable complexes of the above-mentioned transition metal species include oxo transition metal complexes.

Representative examples of vanadium complexes include oxo vanadium complexes such as vanadate and vanadyl complexes. Suitable vanadate complexes include metavanadate and orthovanadate complexes such as, for example, ammonium metavanadate, sodium metavanadate, and sodium orthovanadate. Suitable vanadyl complexes include, for example, vanadyl acetylacetonate and vanadyl sulfate including vanadyl sulfate hydrates such as vanadyl sulfate mono- and trihydrates.

Representative examples of tungsten and molybdenum complexes also include oxo complexes. Suitable oxo tungsten complexes include tungstate and tungsten oxide complexes. Suitable tungstate complexes include ammonium tungstate, calcium tungstate, sodium tungstate dihydrate, and tungstic acid. Suitable tungsten oxides include tungsten (IV) oxide and tungsten (VI) oxide. Suitable oxo molybdenum complexes include molybdate, molybdenum oxide, and molybdenyl complexes. Suitable molybdate complexes include ammonium molybdate and its hydrates, sodium molybdate and its hydrates, and potassium molybdate and its hydrates. Suitable molybdenum oxides include molybdenum (VI) oxide, molybdenum (VI) oxide, and molybdic acid. Suitable molybdenyl complexes include, for

example. molybdenyl acetylacetonate. Other suitable tungsten and molybdenum complexes include hydroxo derivatives derived from, for example, glycerol, tartaric acid, and sugars.

A wide variety of other anti-angiogenic factors may also be utilized within the context of the present invention. Representative examples include platelet factor 4; protamine sulphate; sulphated chitin derivatives (prepared from queen crab shells), (Murata et al., Cancer Res. 51:22-26, 1991); Sulphated Polysaccharide Peptidoglycan Complex (SP- PG) (the function of this compound may be enhanced by the presence of steroids such as estrogen, and tamoxifen citrate); Staurosporine; modulators of matrix metabolism, including for example, proline analogs, cishydroxyproline, d,L-3,4-dehydroproline, Thiaproline, alpha,alpha-dipyridyl, aminopropionitrile fumarate; 4-propyl-5-(4-pyridinyl)-2(3H)-oxazolone; Methotrexate; Mitoxantrone; Heparin; Interferons; 2 Macroglobulin-serum; ChIMP-3 (Pavloff et al., J. Bio. Chem. 267:17321-17326, 1992); Chymostatin (Tomkinson et al., Biochem J. 286:475-480, 1992); Cyclodextrin Tetradecasulfate; Eponemycin; Camptothecin; Fumagillin (Ingber et al., Nature 348:555-557, 1990); Gold Sodium Thiomaleate ("GST"; Matsubara and Ziff, J. Clin. Invest. 79:1440-1446, 1987); anticollagenase-serum; alpha2-antiplasmin (Holmes et al., J. Biol. Chem. 262(4):1659-1664, 1987); Bisantrene (National Cancer Institute); Lobenzarit disodium (N-(2)-carboxyphenyl-4-chloroanthronilic acid disodium or "CCA"; Takeuchi et al., Agents Actions 36:312-316, 1992); Thalidomide; Angostatic steroid; AGM-1470; carboxynaminolimidazole; and metalloproteinase inhibitors such as BB94.

#### Diseases at the Cellular Level

Diseases associated with increased cell survival or the inhibition of apoptosis that could be treated or detected by polynucleotides or polypeptides, as well as antagonists or agonists of the present invention, include cancers (such as follicular lymphomas, carcinomas with p53 mutations, and hormone-dependent tumors, including, but not limited to colon cancer, cardiac tumors, pancreatic cancer, melanoma, retinoblastoma, glioblastoma, lung cancer, intestinal cancer, testicular cancer, stomach cancer, neuroblastoma, myxoma, myoma, lymphoma, endothelioma, osteoblastoma, osteoclastoma, osteosarcoma, chondrosarcoma, adenoma, breast cancer, prostate cancer, Kaposi's sarcoma and ovarian cancer); autoimmune disorders (such as, multiple sclerosis, Sjogren's syndrome, Hashimoto's thyroiditis, biliary cirrhosis, Behcet's disease, Crohn's disease, polymyositis, systemic lupus erythematosus and



immune-related glomerulonephritis and rheumatoid arthritis) and viral infections (such as herpes viruses, pox viruses and adenoviruses), inflammation, graft v. host disease, acute graft rejection, and chronic graft rejection. In preferred embodiments, polynucleotides, polypeptides, and/or antagonists of the invention are used to inhibit growth, progression, and/or metasis of cancers, in particular those listed above.

Additional diseases or conditions associated with increased cell survival that could be treated or detected by polynucleotides or polypeptides, or agonists or antagonists of the present invention include, but are not limited to, progression, and/or metastases of malignancies and related disorders such as leukemia (including acute leukemias (e.g., acute lymphocytic leukemia, acute myelocytic leukemia (including myeloblastic, promyelocytic, myelomonocytic, monocytic, and erythroleukemia)) and chronic leukemias (e.g., chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia)), polycythemia vera, lymphomas (e.g., Hodgkin's disease and non-Hodgkin's disease), multiple myeloma, Waldenstrom's macroglobulinemia, heavy chain disease, and solid tumors including, but not limited to, sarcomas and carcinomas such as fibrosarcoma, myxosarcoma, liposarcoma, chondrosarcoma, osteogenic sarcoma, chordoma, angiosarcoma, endotheliosarcoma, lymphangiosarcoma, lymphangioendotheliosarcoma, synovioma, mesothelioma, Ewing's tumor, leiomyosarcoma, rhabdomyosarcoma, colon carcinoma, pancreatic cancer, breast cancer, ovarian cancer, prostate cancer, squamous cell carcinoma, basal cell carcinoma, adenocarcinoma, sweat gland carcinoma, sebaceous gland carcinoma, papillary carcinoma, papillary adenocarcinomas, cystadenocarcinoma, medullary carcinoma, bronchogenic carcinoma, renal cell carcinoma, hepatoma, bile duct carcinoma, choriocarcinoma, seminoma, embryonal carcinoma, Wilm's tumor, cervical cancer, testicular tumor, lung carcinoma, small cell lung carcinoma, bladder carcinoma, epithelial carcinoma, glioma, astrocytoma, medulloblastoma, craniopharyngioma, ependymoma, pinealoma, hemangioblastoma, acoustic neuroma, oligodendroglioma, menangioma, melanoma, neuroblastoma, and retinoblastoma.

Diseases associated with increased apoptosis that could be treated or detected by polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, include AIDS; neurodegenerative disorders (such as Alzheimer's disease, Parkinson's disease, Amyotrophic lateral sclerosis, Retinitis pigmentosa, Cerebellar degeneration and brain tumor or prior associated disease); autoimmune disorders (such as, multiple sclerosis, Sjogren's

syndrome. Hashimoto's thyroiditis, biliary cirrhosis, Behcet's disease, Crohn's disease, polymyositis, systemic lupus erythematosus and immune-related glomerulonephritis and rheumatoid arthritis) myelodysplastic syndromes (such as aplastic anemia), graft v. host disease, ischemic injury (such as that caused by myocardial infarction, stroke and reperfusion injury), liver injury (e.g., hepatitis related liver injury, ischemia/reperfusion injury, cholestosis (bile duct injury) and liver cancer); toxin-induced liver disease (such as that caused by alcohol), septic shock, cachexia and anorexia.

#### **Wound Healing and Epithelial Cell Proliferation**

10 In accordance with yet a further aspect of the present invention, there is provided a process for utilizing polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, for therapeutic purposes, for example, to stimulate epithelial cell proliferation and basal keratinocytes for the purpose of wound healing, and to stimulate hair follicle production and healing of dermal wounds. Polynucleotides or polypeptides, as well as  
15 agonists or antagonists of the present invention, may be clinically useful in stimulating wound healing including surgical wounds, excisional wounds, deep wounds involving damage of the dermis and epidermis, eye tissue wounds, dental tissue wounds, oral cavity wounds, diabetic ulcers, dermal ulcers, cubitus ulcers, arterial ulcers, venous stasis ulcers, burns resulting from heat exposure or chemicals, and other abnormal wound healing  
20 conditions such as uremia, malnutrition, vitamin deficiencies and complications associated with systemic treatment with steroids, radiation therapy and antineoplastic drugs and antimetabolites. Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could be used to promote dermal reestablishment subsequent to dermal loss

25 Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could be used to increase the adherence of skin grafts to a wound bed and to stimulate re-epithelialization from the wound bed. The following are types of grafts that polynucleotides or polypeptides, agonists or antagonists of the present invention, could be used to increase adherence to a wound bed: autografts, artificial skin, allografts, autodermic  
30 graft, autoepidermic grafts, avascular grafts, Blair-Brown grafts, bone graft, brephoplastic grafts, cutis graft, delayed graft, dermic graft, epidermic graft, fascia graft, full thickness graft, heterologous graft, xenograft, homologous graft, hyperplastic graft, lamellar graft,

mesh graft, mucosal graft, Ollier-Thiersch graft, omentum graft, patch graft, pedicle graft, penetrating graft, split skin graft, thick split graft. Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, can be used to promote skin strength and to improve the appearance of aged skin.

5 It is believed that polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, will also produce changes in hepatocyte proliferation, and epithelial cell proliferation in the lung, breast, pancreas, stomach, small intestine, and large intestine. Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could promote proliferation of epithelial cells such as sebocytes, hair follicles, hepatocytes,  
10 type II pneumocytes, mucin-producing goblet cells, and other epithelial cells and their progenitors contained within the skin, lung, liver, and gastrointestinal tract. Polynucleotides or polypeptides, agonists or antagonists of the present invention, may promote proliferation of endothelial cells, keratinocytes, and basal keratinocytes.

Polynucleotides or polypeptides, as well as agonists or antagonists of the present  
15 invention, could also be used to reduce the side effects of gut toxicity that result from radiation, chemotherapy treatments or viral infections. Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, may have a cytoprotective effect on the small intestine mucosa. Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, may also stimulate healing of mucositis (mouth ulcers)  
20 that result from chemotherapy and viral infections.

Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could further be used in full regeneration of skin in full and partial thickness skin defects, including burns, (i.e., repopulation of hair follicles, sweat glands, and sebaceous glands), treatment of other skin defects such as psoriasis. Polynucleotides or polypeptides, as  
25 well as agonists or antagonists of the present invention, could be used to treat epidermolysis bullosa, a defect in adherence of the epidermis to the underlying dermis which results in frequent, open and painful blisters by accelerating reepithelialization of these lesions. Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could also be used to treat gastric and duodenal ulcers and help heal by scar formation of the  
30 mucosal lining and regeneration of glandular mucosa and duodenal mucosal lining more rapidly. Inflammatory bowel diseases, such as Crohn's disease and ulcerative colitis, are diseases which result in destruction of the mucosal surface of the small or large intestine,

respectively. Thus, polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could be used to promote the resurfacing of the mucosal surface to aid more rapid healing and to prevent progression of inflammatory bowel disease. Treatment with polynucleotides or polypeptides, agonists or antagonists of the present invention, is expected to have a significant effect on the production of mucus throughout the gastrointestinal tract and could be used to protect the intestinal mucosa from injurious substances that are ingested or following surgery. Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could be used to treat diseases associated with the under expression.

Moreover, polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could be used to prevent and heal damage to the lungs due to various pathological states. Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, which could stimulate proliferation and differentiation and promote the repair of alveoli and bronchiolar epithelium to prevent or treat acute or chronic lung damage. For example, emphysema, which results in the progressive loss of alveoli, and inhalation injuries, i.e., resulting from smoke inhalation and burns, that cause necrosis of the bronchiolar epithelium and alveoli could be effectively treated using polynucleotides or polypeptides, agonists or antagonists of the present invention. Also, polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could be used to stimulate the proliferation of and differentiation of type II pneumocytes, which may help treat or prevent disease such as hyaline membrane diseases, such as infant respiratory distress syndrome and bronchopulmonary dysplasia, in premature infants.

Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could stimulate the proliferation and differentiation of hepatocytes and, thus, could be used to alleviate or treat liver diseases and pathologies such as fulminant liver failure caused by cirrhosis, liver damage caused by viral hepatitis and toxic substances (i.e., acetaminophen, carbon tetrachloride and other hepatotoxins known in the art).

In addition, polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could be used to treat or prevent the onset of diabetes mellitus. In patients with newly diagnosed Types I and II diabetes, where some islet cell function remains, polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could be used to maintain the islet function so as to alleviate, delay or prevent permanent

manifestation of the disease. Also, polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could be used as an auxiliary in islet cell transplantation to improve or promote islet cell function.

## 5 Neurological Diseases

In accordance with yet a further aspect of the present invention, there is provided a process for utilizing polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, for therapeutic purposes, for example, to stimulate neurological cell  
10 proliferation and/or differentiation. Therefore, polynucleotides, polypeptides, agonists and/or antagonists of the invention may be used to treat and/or detect neurologic diseases. Moreover, polynucleotides or polypeptides, or agonists or antagonists of the invention, can be used as a marker or detector of a particular nervous system disease or disorder.

Examples of neurologic diseases which can be treated or detected with  
15 polynucleotides, polypeptides, agonists, and/or antagonists of the present invention include brain diseases, such as metabolic brain diseases which includes phenylketonuria such as maternal phenylketonuria, pyruvate carboxylase deficiency, pyruvate dehydrogenase complex deficiency, Wernicke's Encephalopathy, brain edema, brain neoplasms such as cerebellar neoplasms which include infratentorial neoplasms, cerebral ventricle neoplasms  
20 such as choroid plexus neoplasms, hypothalamic neoplasms, supratentorial neoplasms, canavan disease, cerebellar diseases such as cerebellar ataxia which include spinocerebellar degeneration such as ataxia telangiectasia, cerebellar dyssynergia, Friederich's Ataxia, Machado-Joseph Disease, olivopontocerebellar atrophy, cerebellar neoplasms such as infratentorial neoplasms, diffuse cerebral sclerosis such as encephalitis periaxialis, globoid  
25 cell leukodystrophy, metachromatic leukodystrophy and subacute sclerosing panencephalitis, cerebrovascular disorders (such as carotid artery diseases which include carotid artery thrombosis, carotid stenosis and Moyamoya Disease, cerebral amyloid angiopathy, cerebral aneurysm, cerebral anoxia, cerebral arteriosclerosis, cerebral arteriovenous malformations, cerebral artery diseases, cerebral embolism and thrombosis such as carotid artery thrombosis,  
30 sinus thrombosis and Wallenberg's Syndrome, cerebral hemorrhage such as epidural hematoma, subdural hematoma and subarachnoid hemorrhage, cerebral infarction, cerebral ischemia such as transient cerebral ischemia, Subclavian Steal Syndrome and vertebrobasilar insufficiency, vascular dementia such as multi-infarct dementia, periventricular leukomalacia,

vascular headache such as cluster headache, migraine, dementia such as AIDS Dementia Complex, presenile dementia such as Alzheimer's Disease and Creutzfeldt-Jakob Syndrome, senile dementia such as Alzheimer's Disease and progressive supranuclear palsy, vascular dementia such as multi-infarct dementia, encephalitis which include encephalitis periaxialis, 5 viral encephalitis such as epidemic encephalitis, Japanese Encephalitis, St. Louis Encephalitis, tick-borne encephalitis and West Nile Fever, acute disseminated encephalomyelitis, meningoencephalitis such as uveomeningoencephalitic syndrome, Postencephalitic Parkinson Disease and subacute sclerosing panencephalitis, encephalomalacia such as periventricular leukomalacia, epilepsy such as generalized epilepsy 10 which includes infantile spasms, absence epilepsy, myoclonic epilepsy which includes MERRF Syndrome, tonic-clonic epilepsy, partial epilepsy such as complex partial epilepsy, frontal lobe epilepsy and temporal lobe epilepsy, post-traumatic epilepsy, status epilepticus such as Epilepsia Partialis Continua, Hallervorden-Spatz Syndrome, hydrocephalus such as Dandy-Walker Syndrome and normal pressure hydrocephalus, hypothalamic diseases such as 15 hypothalamic neoplasms, cerebral malaria, narcolepsy which includes cataplexy, bulbar poliomyelitis, cerebri pseudotumor, Rett Syndrome, Reye's Syndrome, thalamic diseases, cerebral toxoplasmosis, intracranial tuberculoma and Zellweger Syndrome, central nervous system infections such as AIDS Dementia Complex, Brain Abscess, subdural empyema, encephalomyelitis such as Equine Encephalomyelitis, Venezuelan Equine Encephalomyelitis, 20 Necrotizing Hemorrhagic Encephalomyelitis, Visna, cerebral malaria, meningitis such as arachnoiditis, aseptic meningitis such as viral meningitis which includes lymphocytic choriomeningitis. Bacterial meningitis which includes Haemophilus Meningitis, Listeria Meningitis. Meningococcal Meningitis such as Waterhouse-Friderichsen Syndrome, Pneumococcal Meningitis and meningeal tuberculosis, fungal meningitis such as 25 Cryptococcal Meningitis, subdural effusion, meningoencephalitis such as uveomeningoencephalitic syndrome, myelitis such as transverse myelitis, neurosyphilis such as tabes dorsalis, poliomyelitis which includes bulbar poliomyelitis and postpoliomyelitis syndrome, prion diseases (such as Creutzfeldt-Jakob Syndrome, Bovine Spongiform Encephalopathy, Gerstmann-Straussler Syndrome, Kuru, Scrapie) cerebral toxoplasmosis, 30 central nervous system neoplasms such as brain neoplasms that include cerebellar neoplasms such as infratentorial neoplasms, cerebral ventricle neoplasms such as choroid plexus neoplasms, hypothalamic neoplasms and supratentorial neoplasms, meningeal

neoplasms, spinal cord neoplasms which include epidural neoplasms, demyelinating diseases such as Canavan Diseases, diffuse cerebral scleritis which includes adrenoleukodystrophy, encephalitis periaxialis, globoid cell leukodystrophy, diffuse cerebral sclerosis such as metachromatic leukodystrophy, allergic encephalomyelitis, necrotizing hemorrhagic  
5 encephalomyelitis, progressive multifocal leukoencephalopathy, multiple sclerosis, central pontine myelinolysis, transverse myelitis, neuromyelitis optica, Scrapie, Swayback, Chronic Fatigue Syndrome, Visna, High Pressure Nervous Syndrome, Meningism, spinal cord diseases such as amyotonia congenita, amyotrophic lateral sclerosis, spinal muscular atrophy such as Werdnig-Hoffmann Disease, spinal cord compression, spinal cord neoplasms such as  
10 epidural neoplasms, syringomyelia, Tabes Dorsalis, Stiff-Man Syndrome, mental retardation such as Angelman Syndrome, Cri-du-Chat Syndrome, De Lange's Syndrome, Down Syndrome, Gangliosidoses such as gangliosidoses G(M1), Sandhoff Disease, Tay-Sachs Disease, Hartnup Disease, homocystinuria, Laurence-Moon- Biedl Syndrome, Lesch-Nyhan Syndrome, Maple Syrup Urine Disease, mucopolipidosis such as fucosidosis, neuronal ceroid-  
15 lipofuscinosis, oculocerebrorenal syndrome, phenylketonuria such as maternal phenylketonuria, Prader-Willi Syndrome, Rett Syndrome, Rubinstein-Taybi Syndrome, Tuberous Sclerosis, WAGR Syndrome, nervous system abnormalities such as holoprosencephaly, neural tube defects such as anencephaly which includes hydrangencephaly, Arnold-Chairi Deformity, encephalocele, meningocele,  
20 meningomyelocele, spinal dysraphism such as spina bifida cystica and spina bifida occulta, hereditary motor and sensory neuropathies which include Charcot-Marie Disease, Hereditary optic atrophy, Refsum's Disease, hereditary spastic paraplegia, Werdnig-Hoffmann Disease, Hereditary Sensory and Autonomic Neuropathies such as Congenital Analgesia and Familial Dysautonomia, Neurologic manifestations (such as agnosia that include Gerstmann's  
25 Syndrome, Amnesia such as retrograde amnesia, apraxia, neurogenic bladder, cataplexy, communicative disorders such as hearing disorders that includes deafness, partial hearing loss, loudness recruitment and tinnitus, language disorders such as aphasia which include agraphia, anomia, broca aphasia, and Wernicke Aphasia, Dyslexia such as Acquired Dyslexia, language development disorders, speech disorders such as aphasia which includes  
30 anomia, broca aphasia and Wernicke Aphasia. articulation disorders, communicative disorders such as speech disorders which include dysarthria, echolalia, mutism and stuttering, voice disorders such as aphonia and hoarseness, decerebrate state, delirium, fasciculation,

hallucinations. meningism. movement disorders such as angelman syndrome, ataxia, athetosis. chorea. dystonia. hypokinesia, muscle hypotonia. myoclonus. tic, torticollis and tremor, muscle hypertonia such as muscle rigidity such as stiff-man syndrome, muscle spasticity, paralysis such as facial paralysis which includes Herpes Zoster Oticus, 5 Gastroparesis. Hemiplegia, ophthalmoplegia such as diplopia, Duane's Syndrome, Horner's Syndrome, Chronic progressive external ophthalmoplegia such as Kearns Syndrome, Bulbar Paralysis, Tropical Spastic Paraparesis. Paraplegia such as Brown-Sequard Syndrome, quadriplegia, respiratory paralysis and vocal cord paralysis, paresis, phantom limb, taste disorders such as ageusia and dysgeusia, vision disorders such as amblyopia, blindness, color 10 vision defects, diplopia, hemianopsia. scotoma and subnormal vision, sleep disorders such as hypersomnia which includes Kleine-Levin Syndrome, insomnia, and somnambulism, spasm such as trismus. unconsciousness such as coma, persistent vegetative state and syncope and vertigo, neuromuscular diseases such as amyotonia congenita, amyotrophic lateral sclerosis, Lambert-Eaton Myasthenic Syndrome, motor neuron disease, muscular atrophy such as 15 spinal muscular atrophy, Charcot-Marie Disease and Werdnig-Hoffmann Disease, Postpoliomyelitis Syndrome, Muscular Dystrophy, Myasthenia Gravis, Myotonia Atrophica, Myotonia Confenita, Nemaline Myopathy, Familial Periodic Paralysis, Multiplex Paramyoclonus, Tropical Spastic Paraparesis and Stiff-Man Syndrome, peripheral nervous system diseases such as acrodynia, amyloid neuropathies, autonomic nervous system diseases 20 such as Adie's Syndrome, Barre-Lieou Syndrome, Familial Dysautonomia, Horner's Syndrome, Reflex Sympathetic Dystrophy and Shy-Drager Syndrome, Cranial Nerve Diseases such as Acoustic Nerve Diseases such as Acoustic Neuroma which includes Neurofibromatosis 2, Facial Nerve Diseases such as Facial Neuralgia, Melkersson-Rosenthal Syndrome, ocular motility disorders which includes amblyopia, nystagmus, oculomotor nerve 25 paralysis, ophthalmoplegia such as Duane's Syndrome, Horner's Syndrome, Chronic Progressive External Ophthalmoplegia which includes Kearns Syndrome, Strabismus such as Esotropia and Exotropia, Oculomotor Nerve Paralysis, Optic Nerve Diseases such as Optic Atrophy which includes Hereditary Optic Atrophy, Optic Disk Drusen. Optic Neuritis such as Neuromyelitis Optica, Papilledema, Trigeminal Neuralgia, Vocal Cord Paralysis, 30 Demyelinating Diseases such as Neuromyelitis Optica and Swayback. Diabetic neuropathies such as diabetic foot, nerve compression syndromes such as carpal tunnel syndrome, tarsal tunnel syndrome, thoracic outlet syndrome such as cervical rib syndrome, ulnar nerve



- compression syndrome, neuralgia such as causalgia, cervico-brachial neuralgia, facial neuralgia and trigeminal neuralgia, neuritis such as experimental allergic neuritis, optic neuritis, polyneuritis, polyradiculoneuritis and radiculities such as polyradiculitis, hereditary motor and sensory neuropathies such as Charcot-Marie Disease. Hereditary Optic Atrophy, Refsum's Disease, Hereditary Spastic Paraplegia and Werdnig-Hoffmann Disease. Hereditary Sensory and Autonomic Neuropathies which include Congenital Analgesia and Familial Dysautonomia, POEMS Syndrome, Sciatica, Gustatory Sweating and Tetany).

#### **Infectious Disease**

- 10 Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention can be used to treat or detect infectious agents. For example, by increasing the immune response, particularly increasing the proliferation and differentiation of B and/or T cells, infectious diseases may be treated. The immune response may be increased by either enhancing an existing immune response, or by initiating a new immune response.
- 15 Alternatively, polynucleotides or polypeptides, as well as agonists or antagonists of the present invention may also directly inhibit the infectious agent, without necessarily eliciting an immune response.

- Viruses are one example of an infectious agent that can cause disease or symptoms that can be treated or detected by a polynucleotide or polypeptide and/or agonist or antagonist of the present invention. Examples of viruses, include, but are not limited to Examples of viruses, include, but are not limited to the following DNA and RNA viruses and viral families: Arbovirus, Adenoviridae, Arenaviridae, Arterivirus, Birnaviridae, Bunyaviridae, Caliciviridae, Circoviridae, Coronaviridae, Dengue, EBV, HIV, Flaviviridae, Hepadnaviridae (Hepatitis), Herpesviridae (such as, Cytomegalovirus, Herpes Simplex, Herpes Zoster),
- 25 Mononegavirus (e.g., Paramyxoviridae, Morbillivirus, Rhabdoviridae), Orthomyxoviridae (e.g., Influenza A, Influenza B, and parainfluenza), Papiloma virus, Papovaviridae, Parvoviridae, Picornaviridae, Poxviridae (such as Smallpox or Vaccinia), Reoviridae (e.g., Rotavirus), Retroviridae (HTLV-I, HTLV-II, Lentivirus), and Togaviridae (e.g., Rubivirus). Viruses falling within these families can cause a variety of diseases or symptoms, including,
- 30 but not limited to: arthritis, bronchiolitis, respiratory syncytial virus, encephalitis, eye infections (e.g., conjunctivitis, keratitis), chronic fatigue syndrome, hepatitis (A, B, C, E, Chronic Active, Delta), Japanese B encephalitis, Junin, Chikungunya, Rift Valley fever,

yellow fever, meningitis, opportunistic infections (e.g., AIDS), pneumonia, Burkitt's Lymphoma, chickenpox, hemorrhagic fever, Measles, Mumps, Parainfluenza, Rabies, the common cold, Polio, leukemia, Rubella, sexually transmitted diseases, skin diseases (e.g., Kaposi's, warts), and viremia. polynucleotides or polypeptides, or agonists or antagonists of the invention, can be used to treat or detect any of these symptoms or diseases. In specific embodiments, polynucleotides, polypeptides, or agonists or antagonists of the invention are used to treat: meningitis, Dengue, EBV, and/or hepatitis (e.g., hepatitis B). In an additional specific embodiment polynucleotides, polypeptides, or agonists or antagonists of the invention are used to treat patients nonresponsive to one or more other commercially available hepatitis vaccines. In a further specific embodiment polynucleotides, polypeptides, or agonists or antagonists of the invention are used to treat AIDS.

Similarly, bacterial or fungal agents that can cause disease or symptoms and that can be treated or detected by a polynucleotide or polypeptide and/or agonist or antagonist of the present invention include, but not limited to, include, but not limited to, the following Gram-Negative and Gram-positive bacteria and bacterial families and fungi: Actinomycetales (e.g., Corynebacterium, Mycobacterium, Norcardia), Cryptococcus neoformans, Aspergillosis, Bacillaceae (e.g., Anthrax, Clostridium), Bacteroidaceae, Blastomycosis, Bordetella, Borrelia (e.g., Borrelia burgdorferi, Brucellosis, Candidiasis, Campylobacter, Coccidioidomycosis, Cryptococcosis, Dermatocycoses, E. coli (e.g., Enterotoxigenic E. coli and Enterohemorrhagic E. coli), Enterobacteriaceae (Klebsiella, Salmonella (e.g., Salmonella typhi, and Salmonella paratyphi), Serratia, Yersinia), Erysipelothrix, Helicobacter, Legionellosis, Leptospirosis, Listeria, Mycoplasmatales, Mycobacterium leprae, Vibrio cholerae, Neisseriaceae (e.g., Acinetobacter, Gonorrhea, Meningococcal), Meisseria meningitidis, Pasteurellaceae Infections (e.g., Actinobacillus, Heamophilus (e.g., Heamophilus influenza type B), Pasteurella), Pseudomonas, Rickettsiaceae, Chlamydiaceae, Syphilis, Shigella spp., Staphylococcal, Meningiococcal, Pneumococcal and Streptococcal (e.g., Streptococcus pneumoniae and Group B Streptococcus). These bacterial or fungal families can cause the following diseases or symptoms, including, but not limited to: bacteremia, endocarditis, eye infections (conjunctivitis, tuberculosis, uveitis), gingivitis, opportunistic infections (e.g., AIDS related infections), paronychia, prosthesis-related infections, Reiter's Disease, respiratory tract infections, such as Whooping Cough or Empyema, sepsis, Lyme Disease, Cat-Scratch Disease, Dysentery, Paratyphoid Fever, food poisoning, Typhoid,

pneumonia, Gonorrhea, meningitis (e.g., meningitis types A and B), Chlamydia, Syphilis, Diphtheria, Leprosy, Paratuberculosis, Tuberculosis, Lupus, Botulism, gangrene, tetanus, impetigo, Rheumatic Fever, Scarlet Fever, sexually transmitted diseases, skin diseases (e.g., cellulitis, dermatocycoses), toxemia, urinary tract infections, wound infections.

5 Polynucleotides or polypeptides, agonists or antagonists of the invention, can be used to treat or detect any of these symptoms or diseases. In specific embodiments, Polynucleotides, polypeptides, agonists or antagonists of the invention are used to treat: tetanus, Diphtheria, botulism, and/or meningitis type B.

Moreover, parasitic agents causing disease or symptoms that can be treated or

10 detected by a polynucleotide or polypeptide and/or agonist or antagonist of the present invention include, but not limited to, the following families or class: Amebiasis, Babesiosis, Coccidiosis, Cryptosporidiosis, Dientamoebiasis, Dourine, Ectoparasitic, Giardiasis, Helminthiasis, Leishmaniasis, Theileriasis, Toxoplasmosis, Trypanosomiasis, and Trichomonas and Sporozoans (e.g., Plasmodium virax, Plasmodium falciparum, Plasmodium

15 malariae and Plasmodium ovale). These parasites can cause a variety of diseases or symptoms, including, but not limited to: Scabies, Trombiculiasis, eye infections, intestinal disease (e.g., dysentery, giardiasis), liver disease, lung disease, opportunistic infections (e.g., AIDS related), malaria, pregnancy complications, and toxoplasmosis. polynucleotides or polypeptides, or agonists or antagonists of the invention, can be used to treat or detect any of

20 these symptoms or diseases.

Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention of the present invention could either be by administering an effective amount of a polypeptide to the patient, or by removing cells from the patient, supplying the cells with a polynucleotide of the present invention, and returning the engineered cells to the patient (ex

25 vivo therapy). Moreover, the polypeptide or polynucleotide of the present invention can be used as an antigen in a vaccine to raise an immune response against infectious disease.

### **Regeneration**

Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention can be used to differentiate, proliferate, and attract cells, leading to the regeneration

30 of tissues. (See, Science 276:59-87 (1997).) The regeneration of tissues could be used to repair, replace, or protect tissue damaged by congenital defects, trauma (wounds, burns,

incisions, or ulcers). age, disease (e.g. osteoporosis, osteoarthritis, periodontal disease, liver failure), surgery, including cosmetic plastic surgery, fibrosis, reperfusion injury, or systemic cytokine damage.

Tissues that could be regenerated using the present invention include organs (e.g., pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac),  
5 vasculature (including vascular and lymphatics), nervous, hematopoietic, and skeletal (bone, cartilage, tendon, and ligament) tissue. Preferably, regeneration occurs without or decreased scarring. Regeneration also may include angiogenesis.

Moreover, polynucleotides or polypeptides, as well as agonists or antagonists of the  
10 present invention, may increase regeneration of tissues difficult to heal. For example, increased tendon/ligament regeneration would quicken recovery time after damage. Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention could also be used prophylactically in an effort to avoid damage. Specific diseases that could be treated include of tendinitis, carpal tunnel syndrome, and other tendon or ligament defects.  
15 A further example of tissue regeneration of non-healing wounds includes pressure ulcers, ulcers associated with vascular insufficiency, surgical, and traumatic wounds.

Similarly, nerve and brain tissue could also be regenerated by using polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, to proliferate and differentiate nerve cells. Diseases that could be treated using this method include central and  
20 peripheral nervous system diseases, neuropathies, or mechanical and traumatic disorders (e.g., spinal cord disorders, head trauma, cerebrovascular disease, and stroke). Specifically, diseases associated with peripheral nerve injuries, peripheral neuropathy (e.g., resulting from chemotherapy or other medical therapies), localized neuropathies, and central nervous system diseases (e.g., Alzheimer's disease, Parkinson's disease, Huntington's disease, amyotrophic  
25 lateral sclerosis, and Shy-Drager syndrome), could all be treated using the polynucleotides or polypeptides, as well as agonists or antagonists of the present invention.

### Chemotaxis

Polynucleotides or polypeptides, as well as agonists or antagonists of the present  
30 invention may have chemotaxis activity. A chemotactic molecule attracts or mobilizes cells (e.g., monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells) to a particular site in the body, such as inflammation, infection, or site of

hyperproliferation. The mobilized cells can then fight off and/or heal the particular trauma or abnormality.

Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention may increase chemotactic activity of particular cells. These chemotactic molecules can then be used to treat inflammation, infection, hyperproliferative disorders, or any immune system disorder by increasing the number of cells targeted to a particular location in the body. For example, chemotactic molecules can be used to treat wounds and other trauma to tissues by attracting immune cells to the injured location. Chemotactic molecules of the present invention can also attract fibroblasts, which can be used to treat wounds.

It is also contemplated that polynucleotides or polypeptides, as well as agonists or antagonists of the present invention may inhibit chemotactic activity. These molecules could also be used to treat disorders. Thus, polynucleotides or polypeptides, as well as agonists or antagonists of the present invention could be used as an inhibitor of chemotaxis.

#### 15 **Binding Activity**

A polypeptide of the present invention may be used to screen for molecules that bind to the polypeptide or for molecules to which the polypeptide binds. The binding of the polypeptide and the molecule may activate (agonist), increase, inhibit (antagonist), or decrease activity of the polypeptide or the molecule bound. Examples of such molecules include antibodies, oligonucleotides, proteins (e.g., receptors), or small molecules.

Preferably, the molecule is closely related to the natural ligand of the polypeptide, e.g., a fragment of the ligand, or a natural substrate, a ligand, a structural or functional mimetic. (See, Coligan et al., Current Protocols in Immunology 1(2):Chapter 5 (1991).) Similarly, the molecule can be closely related to the natural receptor to which the polypeptide binds, or at least, a fragment of the receptor capable of being bound by the polypeptide (e.g., active site). In either case, the molecule can be rationally designed using known techniques.

Preferably, the screening for these molecules involves producing appropriate cells which express the polypeptide. Preferred cells include cells from mammals, yeast, *Drosophila*, or *E. coli*. Cells expressing the polypeptide (or cell membrane containing the expressed polypeptide) are then preferably contacted with a test compound potentially containing the molecule to observe binding, stimulation, or inhibition of activity of either the polypeptide or the molecule.

The assay may simply test binding of a candidate compound to the polypeptide, wherein binding is detected by a label, or in an assay involving competition with a labeled competitor. Further, the assay may test whether the candidate compound results in a signal generated by binding to the polypeptide.

5 Alternatively, the assay can be carried out using cell-free preparations, polypeptide/molecule affixed to a solid support, chemical libraries, or natural product mixtures. The assay may also simply comprise the steps of mixing a candidate compound with a solution containing a polypeptide, measuring polypeptide/molecule activity or binding, and comparing the polypeptide/molecule activity or binding to a standard.

10 Preferably, an ELISA assay can measure polypeptide level or activity in a sample (e.g., biological sample) using a monoclonal or polyclonal antibody. The antibody can measure polypeptide level or activity by either binding, directly or indirectly, to the polypeptide or by competing with the polypeptide for a substrate.

15 Additionally, the receptor to which the polypeptide of the present invention binds can be identified by numerous methods known to those of skill in the art, for example, ligand panning and FACS sorting (Coligan, et al., Current Protocols in Immun., 1(2), Chapter 5, (1991)). For example, expression cloning is employed wherein polyadenylated RNA is prepared from a cell responsive to the polypeptides, for example, NIH3T3 cells which are known to contain multiple receptors for the FGF family proteins, and SC-3 cells, and a cDNA  
20 library created from this RNA is divided into pools and used to transfect COS cells or other cells that are not responsive to the polypeptides. Transfected cells which are grown on glass slides are exposed to the polypeptide of the present invention, after they have been labelled. The polypeptides can be labeled by a variety of means including iodination or inclusion of a recognition site for a site-specific protein kinase.

25 Following fixation and incubation, the slides are subjected to auto-radiographic analysis. Positive pools are identified and sub-pools are prepared and re-transfected using an iterative sub-pooling and re-screening process, eventually yielding a single clones that encodes the putative receptor.

30 As an alternative approach for receptor identification, the labeled polypeptides can be photoaffinity linked with cell membrane or extract preparations that express the receptor molecule. Cross-linked material is resolved by PAGE analysis and exposed to X-ray film. The labeled complex containing the receptors of the polypeptides can be excised, resolved

into peptide fragments, and subjected to protein microsequencing. The amino acid sequence obtained from microsequencing would be used to design a set of degenerate oligonucleotide probes to screen a cDNA library to identify the genes encoding the putative receptors.

Moreover, the techniques of gene-shuffling, motif-shuffling, exon-shuffling, and/or  
5 codon-shuffling (collectively referred to as "DNA shuffling") may be employed to modulate the activities of the polypeptide of the present invention thereby effectively generating agonists and antagonists of the polypeptide of the present invention. *See generally*, U.S. Patent Nos. 5,605,793, 5,811,238, 5,830,721, 5,834,252, and 5,837,458, and Patten, P. A., *et al.*, *Curr. Opinion Biotechnol.* 8:724-33 (1997); Harayama, S. *Trends Biotechnol.* 16(2):76-  
10 82 (1998); Hansson, L. O., *et al.*, *J. Mol. Biol.* 287:265-76 (1999); and Lorenzo, M. M. and Blasco, R. *Biotechniques* 24(2):308-13 (1998) (each of these patents and publications are hereby incorporated by reference). In one embodiment, alteration of polynucleotides and corresponding polypeptides may be achieved by DNA shuffling. DNA shuffling involves the assembly of two or more DNA segments into a desired molecule by homologous, or site-  
15 specific, recombination. In another embodiment, polynucleotides and corresponding polypeptides may be altered by being subjected to random mutagenesis by error-prone PCR, random nucleotide insertion or other methods prior to recombination. In another embodiment, one or more components, motifs, sections, parts, domains, fragments, etc., of the polypeptide of the present invention may be recombined with one or more components,  
20 motifs, sections, parts, domains, fragments, etc. of one or more heterologous molecules. In preferred embodiments, the heterologous molecules are family members. In further preferred embodiments, the heterologous molecule is a growth factor such as, for example, platelet-derived growth factor (PDGF), insulin-like growth factor (IGF-I), transforming growth factor (TGF)-alpha, epidermal growth factor (EGF), fibroblast growth factor (FGF),  
25 TGF-beta, bone morphogenetic protein (BMP)-2, BMP-4, BMP-5, BMP-6, BMP-7, activins A and B, decapentaplegic(dpp), 60A, OP-2, dorsalin, growth differentiation factors (GDFs), nodal, MIS, inhibin-alpha, TGF-beta1, TGF-beta2, TGF-beta3, TGF-beta5, and glial-derived neurotrophic factor (GDNF).

Other preferred fragments are biologically active fragments of the polypeptide of the  
30 present invention. Biologically active fragments are those exhibiting activity similar, but not necessarily identical, to an activity of the polypeptide of the present invention. The

biological activity of the fragments may include an improved desired activity, or a decreased undesirable activity.

Additionally, this invention provides a method of screening compounds to identify those which modulate the action of the polypeptide of the present invention. An example of  
5 such an assay comprises combining a mammalian fibroblast cell, a the polypeptide of the present invention, the compound to be screened and  $^3\text{[H]}$  thymidine under cell culture conditions where the fibroblast cell would normally proliferate. A control assay may be performed in the absence of the compound to be screened and compared to the amount of fibroblast proliferation in the presence of the compound to determine if the compound  
10 stimulates proliferation by determining the uptake of  $^3\text{[H]}$  thymidine in each case. The amount of fibroblast cell proliferation is measured by liquid scintillation chromatography which measures the incorporation of  $^3\text{[H]}$  thymidine. Both agonist and antagonist compounds may be identified by this procedure.

In another method, a mammalian cell or membrane preparation expressing a receptor  
15 for a polypeptide of the present invention is incubated with a labeled polypeptide of the present invention in the presence of the compound. The ability of the compound to enhance or block this interaction could then be measured. Alternatively, the response of a known second messenger system following interaction of a compound to be screened and the receptor is measured and the ability of the compound to bind to the receptor and elicit a  
20 second messenger response is measured to determine if the compound is a potential agonist or antagonist. Such second messenger systems include but are not limited to, cAMP guanylate cyclase, ion channels or phosphoinositide hydrolysis.

All of these above assays can be used as diagnostic or prognostic markers. The molecules discovered using these assays can be used to treat disease or to bring about a  
25 particular result in a patient (e.g., blood vessel growth) by activating or inhibiting the polypeptide/molecule. Moreover, the assays can discover agents which may inhibit or enhance the production of the polypeptides of the invention from suitably manipulated cells or tissues.

Therefore, the invention includes a method of identifying compounds which bind to a  
30 polypeptide of the invention comprising the steps of: (a) incubating a candidate binding compound with a polypeptide of the present invention; and (b) determining if binding has



occurred. Moreover, the invention includes a method of identifying agonists/antagonists comprising the steps of: (a) incubating a candidate compound with a polypeptide of the present invention, (b) assaying a biological activity, and (b) determining if a biological activity of the polypeptide has been altered.

5

#### **Targeted Delivery**

In another embodiment, the invention provides a method of delivering compositions to targeted cells expressing a receptor for a polypeptide of the invention, or cells expressing a cell bound form of a polypeptide of the invention.

10 As discussed herein, polypeptides or antibodies of the invention may be associated with heterologous polypeptides, heterologous nucleic acids, toxins, or prodrugs via hydrophobic, hydrophilic, ionic and/or covalent interactions. In one embodiment, the invention provides a method for the specific delivery of compositions of the invention to cells by administering polypeptides of the invention (including antibodies) that are associated with  
15 heterologous polypeptides or nucleic acids. In one example, the invention provides a method for delivering a therapeutic protein into the targeted cell. In another example, the invention provides a method for delivering a single stranded nucleic acid (e.g., antisense or ribozymes) or double stranded nucleic acid (e.g., DNA that can integrate into the cell's genome or replicate episomally and that can be transcribed) into the targeted cell.

20 In another embodiment, the invention provides a method for the specific destruction of cells (e.g., the destruction of tumor cells) by administering polypeptides of the invention (e.g., polypeptides of the invention or antibodies of the invention) in association with toxins or cytotoxic prodrugs.

By "toxin" is meant compounds that bind and activate endogenous cytotoxic effector  
25 systems, radioisotopes, holotoxins, modified toxins, catalytic subunits of toxins, or any molecules or enzymes not normally present in or on the surface of a cell that under defined conditions cause the cell's death. Toxins that may be used according to the methods of the invention include, but are not limited to, radioisotopes known in the art, compounds such as, for example, antibodies (or complement fixing containing portions thereof) that bind an  
30 inherent or induced endogenous cytotoxic effector system, thymidine kinase, endonuclease, RNase, alpha toxin, ricin, abrin, *Pseudomonas* exotoxin A, diphtheria toxin, saporin,

momordin, gelonin, pokeweed antiviral protein, alpha-sarcin and cholera toxin. By "cytotoxic prodrug" is meant a non-toxic compound that is converted by an enzyme, normally present in the cell, into a cytotoxic compound. Cytotoxic prodrugs that may be used according to the methods of the invention include, but are not limited to, glutamyl  
5 derivatives of benzoic acid mustard alkylating agent, phosphate derivatives of etoposide or mitomycin C, cytosine arabinoside, daunorubisin, and phenoxycetamide derivatives of doxorubicin.

### Drug Screening

10 Further contemplated is the use of the polypeptides of the present invention, or the polynucleotides encoding these polypeptides, to screen for molecules which modify the activities of the polypeptides of the present invention. Such a method would include contacting the polypeptide of the present invention with a selected compound(s) suspected of having antagonist or agonist activity, and assaying the activity of these polypeptides  
15 following binding.

This invention is particularly useful for screening therapeutic compounds by using the polypeptides of the present invention, or binding fragments thereof, in any of a variety of drug screening techniques. The polypeptide or fragment employed in such a test may be affixed to a solid support, expressed on a cell surface, free in solution, or located  
20 intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or fragment. Drugs are screened against such transformed cells in competitive binding assays. One may measure, for example, the formulation of complexes between the agent being tested and a polypeptide of the present invention.

25 Thus, the present invention provides methods of screening for drugs or any other agents which affect activities mediated by the polypeptides of the present invention. These methods comprise contacting such an agent with a polypeptide of the present invention or a fragment thereof and assaying for the presence of a complex between the agent and the polypeptide or a fragment thereof, by methods well known in the art. In such a competitive  
30 binding assay, the agents to screen are typically labeled. Following incubation, free agent is separated from that present in bound form, and the amount of free or uncomplexed label is a

measure of the ability of a particular agent to bind to the polypeptides of the present invention.

Another technique for drug screening provides high throughput screening for compounds having suitable binding affinity to the polypeptides of the present invention, and is described in great detail in European Patent Application 84/03564, published on September 13, 1984, which is incorporated herein by reference herein. Briefly stated, large numbers of different small peptide test compounds are synthesized on a solid substrate, such as plastic pins or some other surface. The peptide test compounds are reacted with polypeptides of the present invention and washed. Bound polypeptides are then detected by methods well known in the art. Purified polypeptides are coated directly onto plates for use in the aforementioned drug screening techniques. In addition, non-neutralizing antibodies may be used to capture the peptide and immobilize it on the solid support.

This invention also contemplates the use of competitive drug screening assays in which neutralizing antibodies capable of binding polypeptides of the present invention specifically compete with a test compound for binding to the polypeptides or fragments thereof. In this manner, the antibodies are used to detect the presence of any peptide which shares one or more antigenic epitopes with a polypeptide of the invention.

#### Antisense And Ribozyme (Antagonists)

In specific embodiments, antagonists according to the present invention are nucleic acids corresponding to the sequences contained in SEQ ID NO:X, or the complementary strand thereof, and/or to nucleotide sequences contained in the cDNA contained in the related cDNA clone identified in Table 1. In one embodiment, antisense sequence is generated internally, by the organism, in another embodiment, the antisense sequence is separately administered (see, for example, O'Connor, J., Neurochem. 56:560 (1991). Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988). Antisense technology can be used to control gene expression through antisense DNA or RNA, or through triple-helix formation. Antisense techniques are discussed for example, in Okano, J., Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988). Triple helix formation is discussed in, for instance, Lee et al., Nucleic Acids Research 6:3073 (1979); Cooney et al.,

Science 241:456 (1988); and Dervan et al., Science 251:1300 (1991). The methods are based on binding of a polynucleotide to a complementary DNA or RNA.

For example, the use of c-myc and c-myb antisense RNA constructs to inhibit the growth of the non-lymphocytic leukemia cell line HL-60 and other cell lines was previously described. (Wickstrom et al. (1988); Anfossi et al. (1989)). These experiments were performed in vitro by incubating cells with the oligoribonucleotide. A similar procedure for in vivo use is described in WO 91/15580. Briefly, a pair of oligonucleotides for a given antisense RNA is produced as follows: A sequence complimentary to the first 15 bases of the open reading frame is flanked by an EcoRI site on the 5' end and a HindIII site on the 3' end. Next, the pair of oligonucleotides is heated at 90°C for one minute and then annealed in 2X ligation buffer (20mM TRIS HCl pH 7.5, 10mM MgCl<sub>2</sub>, 10mM dithiothreitol (DTT) and 0.2 mM ATP) and then ligated to the EcoRI/Hind III site of the retroviral vector PMV7 (WO 91/15580).

For example, the 5' coding portion of a polynucleotide that encodes the polypeptide of the present invention may be used to design an antisense RNA oligonucleotide of from about 10 to 40 base pairs in length. A DNA oligonucleotide is designed to be complementary to a region of the gene involved in transcription thereby preventing transcription and the production of the receptor. The antisense RNA oligonucleotide hybridizes to the mRNA in vivo and blocks translation of the mRNA molecule into receptor polypeptide.

In one embodiment, the antisense nucleic acid of the invention is produced intracellularly by transcription from an exogenous sequence. For example, a vector or a portion thereof, is transcribed, producing an antisense nucleic acid (RNA) of the invention. Such a vector would contain a sequence encoding the antisense nucleic acid. Such a vector can remain episomal or become chromosomally integrated, as long as it can be transcribed to produce the desired antisense RNA. Such vectors can be constructed by recombinant DNA technology methods standard in the art. Vectors can be plasmid, viral, or others known in the art, used for replication and expression in vertebrate cells. Expression of the sequence encoding the polypeptide of the present invention or fragments thereof, can be by any promoter known in the art to act in vertebrate, preferably human cells. Such promoters can be inducible or constitutive. Such promoters include, but are not limited to, the SV40 early promoter region (Bernoist and Chambon, Nature 29:304-310 (1981), the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto et al., Cell 22:787-797

(1980), the herpes thymidine promoter (Wagner et al., Proc. Natl. Acad. Sci. U.S.A. 78:1441-1445 (1981), the regulatory sequences of the metallothionein gene (Brinster, et al., Nature 296:39-42 (1982)), etc.

The antisense nucleic acids of the invention comprise a sequence complementary to at least a portion of an RNA transcript of a gene of the present invention. However, absolute complementarity, although preferred, is not required. A sequence "complementary to at least a portion of an RNA," referred to herein, means a sequence having sufficient complementarity to be able to hybridize with the RNA, forming a stable duplex; in the case of double stranded antisense nucleic acids, a single strand of the duplex DNA may thus be tested, or triplex formation may be assayed. The ability to hybridize will depend on both the degree of complementarity and the length of the antisense nucleic acid. Generally, the larger the hybridizing nucleic acid, the more base mismatches with a RNA it may contain and still form a stable duplex (or triplex as the case may be). One skilled in the art can ascertain a tolerable degree of mismatch by use of standard procedures to determine the melting point of the hybridized complex.

Oligonucleotides that are complementary to the 5' end of the message, e.g., the 5' untranslated sequence up to and including the AUG initiation codon, should work most efficiently at inhibiting translation. However, sequences complementary to the 3' untranslated sequences of mRNAs have been shown to be effective at inhibiting translation of mRNAs as well. See generally, Wagner, R., 1994, Nature 372:333-335. Thus, oligonucleotides complementary to either the 5'- or 3'- non- translated, non-coding regions of polynucleotide sequences described herein could be used in an antisense approach to inhibit translation of endogenous mRNA. Oligonucleotides complementary to the 5' untranslated region of the mRNA should include the complement of the AUG start codon. Antisense oligonucleotides complementary to mRNA coding regions are less efficient inhibitors of translation but could be used in accordance with the invention. Whether designed to hybridize to the 5', 3'- or coding region of mRNA of the present invention, antisense nucleic acids should be at least six nucleotides in length, and are preferably oligonucleotides ranging from 6 to about 50 nucleotides in length. In specific aspects the oligonucleotide is at least 10 nucleotides, at least 17 nucleotides, at least 25 nucleotides or at least 50 nucleotides.

The polynucleotides of the invention can be DNA or RNA or chimeric mixtures or derivatives or modified versions thereof, single-stranded or double-stranded. The

oligonucleotide can be modified at the base moiety, sugar moiety, or phosphate backbone, for example, to improve stability of the molecule, hybridization, etc. The oligonucleotide may include other appended groups such as peptides (e.g., for targeting host cell receptors in vivo), or agents facilitating transport across the cell membrane (see, e.g., Letsinger et al., 5 1989, Proc. Natl. Acad. Sci. U.S.A. 86:6553-6556; Lemaitre et al., 1987, Proc. Natl. Acad. Sci. 84:648-652; PCT Publication No. WO88/09810, published December 15, 1988) or the blood-brain barrier (see, e.g., PCT Publication No. WO89/10134, published April 25, 1988), hybridization-triggered cleavage agents. (See, e.g., Krol et al., 1988, BioTechniques 6:958-976) or intercalating agents. (See, e.g., Zon, 1988, Pharm. Res. 5:539-549). To this end, the 10 oligonucleotide may be conjugated to another molecule, e.g., a peptide, hybridization triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent, etc.

The antisense oligonucleotide may comprise at least one modified base moiety which is selected from the group including, but not limited to, 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xantine, 4-acetylcytosine, 15 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta- 20 D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine.

25 The antisense oligonucleotide may also comprise at least one modified sugar moiety selected from the group including, but not limited to, arabinose, 2-fluoroarabinose, xylulose, and hexose.

In yet another embodiment, the antisense oligonucleotide comprises at least one modified phosphate backbone selected from the group including, but not limited to, a 30 phosphorothioate, a phosphorodithioate, a phosphoramidothioate, a phosphoramidate, a phosphordiamidate, a methylphosphonate, an alkyl phosphotriester, and a formacetal or analog thereof.

In yet another embodiment, the antisense oligonucleotide is an a-anomeric oligonucleotide. An a-anomeric oligonucleotide forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual b-units, the strands run parallel to each other (Gautier et al., 1987, Nucl. Acids Res. 15:6625-6641). The oligonucleotide is a 2'-O-methylribonucleotide (Inoue et al., 1987, Nucl. Acids Res. 15:6131-6148), or a chimeric RNA-DNA analogue (Inoue et al., 1987, FEBS Lett. 215:327-330).

Polynucleotides of the invention may be synthesized by standard methods known in the art, e.g. by use of an automated DNA synthesizer (such as are commercially available from Biosearch, Applied Biosystems, etc.). As examples, phosphorothioate oligonucleotides may be synthesized by the method of Stein et al. (1988, Nucl. Acids Res. 16:3209), methylphosphonate oligonucleotides can be prepared by use of controlled pore glass polymer supports (Sarin et al., 1988, Proc. Natl. Acad. Sci. U.S.A. 85:7448-7451), etc.

While antisense nucleotides complementary to the coding region sequence could be used, those complementary to the transcribed untranslated region are most preferred.

Potential antagonists according to the invention also include catalytic RNA, or a ribozyme (See, e.g., PCT International Publication WO 90/11364, published October 4, 1990; Sarver et al, Science 247:1222-1225 (1990). While ribozymes that cleave mRNA at site specific recognition sequences can be used to destroy mRNAs, the use of hammerhead ribozymes is preferred. Hammerhead ribozymes cleave mRNAs at locations dictated by flanking regions that form complementary base pairs with the target mRNA. The sole requirement is that the target mRNA have the following sequence of two bases: 5'-UG-3'. The construction and production of hammerhead ribozymes is well known in the art and is described more fully in Haseloff and Gerlach, Nature 334:585-591 (1988). There are numerous potential hammerhead ribozyme cleavage sites within the nucleotide sequence of SEQ ID NO:X. Preferably, the ribozyme is engineered so that the cleavage recognition site is located near the 5' end of the mRNA; i.e., to increase efficiency and minimize the intracellular accumulation of non-functional mRNA transcripts.

As in the antisense approach, the ribozymes of the invention can be composed of modified oligonucleotides (e.g. for improved stability, targeting, etc.) and should be delivered to cells which express in vivo. DNA constructs encoding the ribozyme may be introduced into the cell in the same manner as described above for the introduction of antisense encoding DNA. A preferred method of delivery involves using a DNA construct "encoding" the

ribozyme under the control of a strong constitutive promoter, such as, for example, pol III or pol II promoter, so that transfected cells will produce sufficient quantities of the ribozyme to destroy endogenous messages and inhibit translation. Since ribozymes unlike antisense molecules, are catalytic, a lower intracellular concentration is required for efficiency.

- 5           Antagonist/agonist compounds may be employed to inhibit the cell growth and proliferation effects of the polypeptides of the present invention on neoplastic cells and tissues, i.e. stimulation of angiogenesis of tumors, and, therefore, retard or prevent abnormal cellular growth and proliferation, for example, in tumor formation or growth.

- 10           The antagonist/agonist may also be employed to prevent hyper-vascular diseases, and prevent the proliferation of epithelial lens cells after extracapsular cataract surgery. Prevention of the mitogenic activity of the polypeptides of the present invention may also be desirable in cases such as restenosis after balloon angioplasty.

          The antagonist/agonist may also be employed to prevent the growth of scar tissue during wound healing.

- 15           The antagonist/agonist may also be employed to treat the diseases described herein.

- Thus, the invention provides a method of treating disorders or diseases, including but not limited to the disorders or diseases listed throughout this application, associated with overexpression of a polynucleotide of the present invention by administering to a patient (a) an antisense molecule directed to the polynucleotide of the present invention, and/or (b) a  
20           ribozyme directed to the polynucleotide of the present invention.

#### **Other Activities**

- A polypeptide, polynucleotide, agonist, or antagonist of the present invention, as a result of the ability to stimulate vascular endothelial cell growth, may be employed in  
25           treatment for stimulating re-vascularization of ischemic tissues due to various disease conditions such as thrombosis, arteriosclerosis, and other cardiovascular conditions. The polypeptide, polynucleotide, agonist, or antagonist of the present invention may also be employed to stimulate angiogenesis and limb regeneration, as discussed above.

- 30           A polypeptide, polynucleotide, agonist, or antagonist of the present invention may also be employed for treating wounds due to injuries, burns, post-operative tissue repair, and ulcers since they are mitogenic to various cells of different origins, such as fibroblast cells



and skeletal muscle cells, and therefore, facilitate the repair or replacement of damaged or diseased tissue.

5 A polypeptide, polynucleotide, agonist, or antagonist of the present invention may also be employed stimulate neuronal growth and to treat and prevent neuronal damage which occurs in certain neuronal disorders or neuro-degenerative conditions such as Alzheimer's disease, Parkinson's disease, and AIDS-related complex. A polypeptide, polynucleotide, agonist, or antagonist of the present invention may have the ability to stimulate chondrocyte growth, therefore, they may be employed to enhance bone and periodontal regeneration and aid in tissue transplants or bone grafts.

10 A polypeptide, polynucleotide, agonist, or antagonist of the present invention may be also be employed to prevent skin aging due to sunburn by stimulating keratinocyte growth.

A polypeptide, polynucleotide, agonist, or antagonist of the present invention may also be employed for preventing hair loss, since FGF family members activate hair-forming cells and promotes melanocyte growth. Along the same lines, a polypeptide, polynucleotide, 15 agonist, or antagonist of the present invention may be employed to stimulate growth and differentiation of hematopoietic cells and bone marrow cells when used in combination with other cytokines.

A polypeptide, polynucleotide, agonist, or antagonist of the present invention may also be employed to maintain organs before transplantation or for supporting cell culture of primary tissues. A polypeptide, polynucleotide, agonist, or antagonist of the present 20 invention may also be employed for inducing tissue of mesodermal origin to differentiate in early embryos.

A polypeptide, polynucleotide, agonist, or antagonist of the present invention may also increase or decrease the differentiation or proliferation of embryonic stem cells, besides, 25 as discussed above, hematopoietic lineage.

A polypeptide, polynucleotide, agonist, or antagonist of the present invention may also be used to modulate mammalian characteristics. such as body height, weight, hair color, eye color, skin, percentage of adipose tissue, pigmentation, size, and shape (e.g., cosmetic surgery). Similarly, a polypeptide, polynucleotide, agonist, or antagonist of the present 30 invention may be used to modulate mammalian metabolism affecting catabolism, anabolism, processing, utilization, and storage of energy.

A polypeptide, polynucleotide, agonist, or antagonist of the present invention may be used to change a mammal's mental state or physical state by influencing biorhythms, cardiac rhythms, depression (including depressive disorders), tendency for violence, tolerance for pain, reproductive capabilities (preferably by Activin or Inhibin-like activity),  
5 hormonal or endocrine levels, appetite, libido, memory, stress, or other cognitive qualities.

A polypeptide, polynucleotide, agonist, or antagonist of the present invention may also be used as a food additive or preservative, such as to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional components.

10 The above-recited applications have uses in a wide variety of hosts. Such hosts include, but are not limited to, human, murine, rabbit, goat, guinea pig, camel, horse, mouse, rat, hamster, pig, micro-pig, chicken, goat, cow, sheep, dog, cat, non-human primate, and human. In specific embodiments, the host is a mouse, rabbit, goat, guinea pig, chicken, rat, hamster, pig, sheep, dog or cat. In preferred embodiments, the host is a mammal. In most  
15 preferred embodiments, the host is a human.

#### **Other Preferred Embodiments**

Other preferred embodiments of the claimed invention include an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence  
20 of at least about 50 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X or the complementary strand thereto, and/or the cDNA in the related cDNA clone contained in the deposit.

Also preferred is a nucleic acid molecule wherein said sequence of contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of positions  
25 identified as "Start" and "End" in columns 7 and 8 as defined for SEQ ID NO:X in Table 1.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 150 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X or the complementary strand thereto, and/or the cDNA in the related cDNA clone contained in the deposit.

30 Further preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 500 contiguous

nucleotides in the nucleotide sequence of SEQ ID NO:X or the complementary strand thereto, and/or the cDNA in the related cDNA clone contained in the deposit.

5 A further preferred embodiment is a nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the nucleotide sequence of SEQ ID NO:X in the range of positions identified as "Start" and "End" in columns 7 and 8 as defined for SEQ ID NO:X in Table 1.

10 A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the complete nucleotide sequence of SEQ ID NO:X or the complementary strand thereto, and/or the cDNA in the related cDNA clone contained in the deposit.

Also preferred is an isolated nucleic acid molecule which hybridizes under stringent hybridization conditions to a nucleic acid molecule comprising a nucleotide sequence of SEQ ID NO:X or the complementary strand thereto, and/or the cDNA in the related cDNA clone contained in the deposit, wherein said nucleic acid molecule which hybridizes does not  
15 hybridize under stringent hybridization conditions to a nucleic acid molecule having a nucleotide sequence consisting of only A residues or of only T residues.

Also preferred is a composition of matter comprising a DNA molecule which comprises a cDNA clone contained in the deposit.

20 Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least 50 contiguous nucleotides in the nucleotide sequence of the cDNA in the related cDNA clone contained in the deposit.

Also preferred is an isolated nucleic acid molecule, wherein said sequence of at least 50 contiguous nucleotides is included in the nucleotide sequence of an open reading frame sequence encoded by the cDNA in the related cDNA clone contained in the deposit.

25 Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to sequence of at least 150 contiguous nucleotides in the nucleotide sequence encoded by the cDNA in the related cDNA clone contained in the deposit.

30 A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to sequence of at least 500 contiguous nucleotides in the nucleotide sequence encoded by the cDNA in the related cDNA clone contained in the deposit.

A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the complete nucleotide sequence encoded by the cDNA in the related cDNA clone contained in the deposit.

5 A further preferred embodiment is a method for detecting in a biological sample a nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X or the complementary strand thereto; and a nucleotide sequence encoded by the cDNA in the related cDNA clone contained in the deposit; which method comprises a step of comparing a nucleotide sequence of at least one  
10 nucleic acid molecule in said sample with a sequence selected from said group and determining whether the sequence of said nucleic acid molecule in said sample is at least 95% identical to said selected sequence.

Also preferred is the above method wherein said step of comparing sequences comprises determining the extent of nucleic acid hybridization between nucleic acid  
15 molecules in said sample and a nucleic acid molecule comprising said sequence selected from said group. Similarly, also preferred is the above method wherein said step of comparing sequences is performed by comparing the nucleotide sequence determined from a nucleic acid molecule in said sample with said sequence selected from said group. The nucleic acid molecules can comprise DNA molecules or RNA molecules.

20 A further preferred embodiment is a method for identifying the species, tissue or cell type of a biological sample which method comprises a step of detecting nucleic acid molecules in said sample, if any, comprising a nucleotide sequence that is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X or the complementary strand  
25 thereto; and a nucleotide sequence encoded by the cDNA in the related cDNA clone contained in the deposit.

Also preferred is the above method for identifying the species, tissue or cell type of a biological sample which comprises a step of detecting nucleic acid molecules comprising a nucleotide sequence in a panel of at least two nucleotide sequences, wherein at least one  
30 sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from said group.

Also preferred is a method for diagnosing in a subject a pathological condition associated with abnormal structure or expression of a nucleotide sequence of SEQ ID NO:X; or the cDNA contained in the related cDNA clone referenced in Table I which encodes a protein, wherein the method comprises a step of detecting in a biological sample obtained  
5 from said subject nucleic acid molecules, if any, comprising a nucleotide sequence that is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X or the complementary strand thereto; and a nucleotide sequence of the cDNA in the related cDNA clone contained in the deposit.

10 Also preferred is the above method for diagnosing a pathological condition which comprises a step of detecting nucleic acid molecules comprising a nucleotide sequence in a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from said group.

15 Also preferred is a composition of matter comprising isolated nucleic acid molecules wherein the nucleotide sequences of said nucleic acid molecules comprise a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X or the complementary strand  
20 thereto; and a nucleotide sequence encoded by the cDNA in the related cDNA clone contained in the deposit. The nucleic acid molecules can comprise DNA molecules or RNA molecules.

Also preferred is a composition of matter comprising isolated nucleic acid molecules wherein the nucleotide sequences of said nucleic acid molecules comprise a DNA microarray or "chip" of at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 40, 50, 100, 150, 200, 250, 300,  
25 500, 1000, 2000, 3000 or 4000 nucleotide sequences, wherein at least one sequence in said DNA microarray or "chip" is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X or the complementary strand thereto; and a nucleotide sequence encoded by  
30 the cDNA in the cDNA clone referenced in Table I. The nucleic acid molecules can comprise DNA molecules or RNA molecules.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 90% identical to a sequence of at least about 10 contiguous amino acids in the polypeptide sequence of SEQ ID NO:Y; a polypeptide encoded by SEQ ID NO:X; and/or a polypeptide encoded by the cDNA in the related cDNA clone contained in the deposit.

5 Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 30 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y; a polypeptide encoded by SEQ ID NO:X; and/or a polypeptide encoded by the cDNA in the related cDNA clone contained in the deposit.

Further preferred is an isolated polypeptide comprising an amino acid sequence at  
10 least 95% identical to a sequence of at least about 100 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y; a polypeptide encoded by SEQ ID NO:X; and/or a polypeptide encoded by the cDNA in the related cDNA clone contained in the deposit.

Further preferred is an isolated polypeptide comprising an amino acid sequence at  
15 least 95% identical to the complete amino acid sequence of SEQ ID NO:Y; a polypeptide encoded by SEQ ID NO:X; and/or a polypeptide encoded by the cDNA in the related cDNA clone contained in the deposit.

Further preferred is an isolated polypeptide comprising an amino acid sequence at least 90% identical to a sequence of at least about 10 contiguous amino acids in the complete amino acid sequence of a polypeptide encoded by the cDNA clone referenced in Table 1.

20 Also preferred is a polypeptide wherein said sequence of contiguous amino acids is included in the amino acid sequence of a portion of said polypeptide encoded by the cDNA clone referenced in Table 1; a polypeptide encoded by SEQ ID NO:X; and/or the polypeptide sequence of SEQ ID NO:Y.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least  
25 95% identical to a sequence of at least about 30 contiguous amino acids in the amino acid sequence of a polypeptide encoded by the cDNA clone referenced in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 100 contiguous amino acids in the amino acid sequence of a polypeptide encoded by the cDNA clone referenced in Table 1.

30 Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to the amino acid sequence of a polypeptide encoded by the cDNA clone referenced in Table 1.

Further preferred is an isolated antibody which binds specifically to a polypeptide comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: a polypeptide sequence of SEQ ID NO:Y; a polypeptide encoded by SEQ ID NO:X; and a polypeptide  
5 encoded by the cDNA in the related cDNA clone contained in the deposit.

Further preferred is a method for detecting in a biological sample a polypeptide comprising an amino acid sequence which is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: a polypeptide sequence of SEQ ID NO:Y; a polypeptide encoded by SEQ ID NO:X; and a polypeptide  
10 encoded by the cDNA in the related cDNA clone referenced in Table 1; which method comprises a step of comparing an amino acid sequence of at least one polypeptide molecule in said sample with a sequence selected from said group and determining whether the sequence of said polypeptide molecule in said sample is at least 90% identical to said sequence of at least 10 contiguous amino acids.

Also preferred is the above method wherein said step of comparing an amino acid sequence of at least one polypeptide molecule in said sample with a sequence selected from said group comprises determining the extent of specific binding of polypeptides in said sample to an antibody which binds specifically to a polypeptide comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a  
15 sequence selected from the group consisting of: a polypeptide sequence of SEQ ID NO:Y; a polypeptide encoded by SEQ ID NO:X; and a polypeptide encoded by the cDNA in the related cDNA clone referenced in Table 1.

Also preferred is the above method wherein said step of comparing sequences is performed by comparing the amino acid sequence determined from a polypeptide molecule in  
20 said sample with said sequence selected from said group.

Also preferred is a method for identifying the species, tissue or cell type of a biological sample which method comprises a step of detecting polypeptide molecules in said sample, if any, comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of:  
25 polypeptide sequence of SEQ ID NO:Y; a polypeptide encoded by SEQ ID NO:X; and a polypeptide encoded by the cDNA in the related cDNA clone referenced in Table 1.

Also preferred is the above method for identifying the species, tissue or cell type of a biological sample, which method comprises a step of detecting polypeptide molecules comprising an amino acid sequence in a panel of at least two amino acid sequences, wherein at least one sequence in said panel is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the above group.

Also preferred is a method for diagnosing in a subject a pathological condition associated with abnormal structure or expression of a nucleic acid sequence identified in Table 1 encoding a polypeptide, which method comprises a step of detecting in a biological sample obtained from said subject polypeptide molecules comprising an amino acid sequence in a panel of at least two amino acid sequences, wherein at least one sequence in said panel is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: polypeptide sequence of SEQ ID NO:Y; a polypeptide encoded by SEQ ID NO:X; and a polypeptide encoded by the cDNA in the related cDNA clone referenced in Table 1.

In any of these methods, the step of detecting said polypeptide molecules includes using an antibody.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a nucleotide sequence encoding a polypeptide wherein said polypeptide comprises an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: polypeptide sequence of SEQ ID NO:Y; a polypeptide encoded by SEQ ID NO:X; and a polypeptide encoded by the cDNA in the related cDNA clone referenced in Table 1.

Also preferred is an isolated nucleic acid molecule, wherein said nucleotide sequence encoding a polypeptide has been optimized for expression of said polypeptide in a prokaryotic host.

Also preferred is an isolated nucleic acid molecule, wherein said polypeptide comprises an amino acid sequence selected from the group consisting of: polypeptide sequence of SEQ ID NO:Y; a polypeptide encoded by SEQ ID NO:X; and a polypeptide encoded by the cDNA in the related cDNA clone referenced in Table 1.

Further preferred is a method of making a recombinant vector comprising inserting any of the above isolated nucleic acid molecule into a vector. Also preferred is the recombinant vector produced by this method. Also preferred is a method of making a



recombinant host cell comprising introducing the vector into a host cell, as well as the recombinant host cell produced by this method.

Also preferred is a method of making an isolated polypeptide comprising culturing this recombinant host cell under conditions such that said polypeptide is expressed and recovering said polypeptide. Also preferred is this method of making an isolated polypeptide, wherein said recombinant host cell is a eukaryotic cell and said polypeptide is a human protein comprising an amino acid sequence selected from the group consisting of: polypeptide sequence of SEQ ID NO:Y; a polypeptide encoded by SEQ ID NO:X; and a polypeptide encoded by the cDNA in the related cDNA clone referenced in Table 1. The isolated polypeptide produced by this method is also preferred.

Also preferred is a method of treatment of an individual in need of an increased level of a protein activity, which method comprises administering to such an individual a Therapeutic comprising an amount of an isolated polypeptide, polynucleotide, immunogenic fragment or analogue thereof, binding agent, antibody, or antigen binding fragment of the claimed invention effective to increase the level of said protein activity in said individual.

Also preferred is a method of treatment of an individual in need of a decreased level of a protein activity, which method comprised administering to such an individual a Therapeutic comprising an amount of an isolated polypeptide, polynucleotide, immunogenic fragment or analogue thereof, binding agent, antibody, or antigen binding fragment of the claimed invention effective to decrease the level of said protein activity in said individual.

Having generally described the invention, the same will be more readily understood by reference to the following examples, which are provided by way of illustration and are not intended as limiting.

*Examples**Example 1: Isolation of a Selected cDNA Clone From the Deposited Sample*

5

Each deposited cDNA clone is contained in a plasmid vector. Table 5 identifies the vectors used to construct the cDNA library from which each clone was isolated. In many cases, the vector used to construct the library is a phage vector from which a plasmid has been excised. The following correlates the related plasmid for each phage vector used in constructing the cDNA library. For example, where a particular clone is identified in Table 5 as being isolated in the vector "Lambda Zap," the corresponding deposited clone is in "pBluescript."

	<u>Vector Used to Construct Library</u>	<u>Corresponding Deposited Plasmid</u>
	Lambda Zap	pBluescript (pBS)
15	Uni-Zap XR	pBluescript (pBS)
	Zap Express	pBK
	lafmid BA	plafmid BA
	pSport1	pSport1
	pCMVSport 2.0	pCMVSport 2.0
20	pCMVSport 3.0	pCMVSport 3.0
	pCR <sup>®</sup> 2.1	pCR <sup>®</sup> 2.1

Vectors Lambda Zap (U.S. Patent Nos. 5,128,256 and 5,286,636), Uni-Zap XR (U.S. Patent Nos. 5,128,256 and 5,286,636), Zap Express (U.S. Patent Nos. 5,128,256 and 5,286,636), pBluescript (pBS) (Short, J. M. et al., Nucleic Acids Res. 16:7583-7600 (1988); Alting-Mees, M. A. and Short, J. M., Nucleic Acids Res. 17:9494 (1989)) and pBK (Alting-Mees, M. A. et al., Strategies 5:58-61 (1992)) are commercially available from Stratagene Cloning Systems, Inc., 11011 N. Torrey Pines Road, La Jolla, CA, 92037. pBS contains an ampicillin resistance gene and pBK contains a neomycin resistance gene. Both can be transformed into E. coli strain XL-1 Blue, also available from Stratagene. pBS comes in 4 forms SK+, SK-, KS+ and KS-. The S and K refers to the orientation of the polylinker to the T7 and T3 primer sequences which flank the polylinker region ("S" is for SacI and "K" is for KpnI which are the first sites on each respective end of the linker). "+" or "-" refer to the

orientation of the fl origin of replication ("ori"), such that in one orientation, single stranded rescue initiated from the fl ori generates sense strand DNA and in the other, antisense.

Vectors pSport1, pCMVSPORT 2.0 and pCMVSPORT 3.0, were obtained from Life Technologies, Inc., P. O. Box 6009, Gaithersburg, MD 20897. All Sport vectors contain an  
5    ampicillin resistance gene and may be transformed into E. coli strain DH10B, also available from Life Technologies. (See, for instance, Gruber, C. E., et al., Focus 15:59 (1993).) Vector lafmid BA (Bento Soares, Columbia University, NY) contains an ampicillin resistance gene and can be transformed into E. coli strain XL-1 Blue. Vector pCR<sup>®</sup>2.1, which is available from Invitrogen, 1600 Faraday Avenue, Carlsbad, CA 92008, contains an  
10    ampicillin resistance gene and may be transformed into E. coli strain DH10B, available from Life Technologies. (See, for instance, Clark, J. M., Nuc. Acids Res. 16:9677-9686 (1988) and Mead, D. et al., Bio/Technology 9: (1991).) Preferably, a polynucleotide of the present invention does not comprise the phage vector sequences identified for the particular clone in Table 5, as well as the corresponding plasmid vector sequences designated above.

15       The deposited material in the sample assigned the ATCC Deposit Number cited by reference to Table 2 and 5 for any given cDNA clone also may contain one or more additional plasmids, each comprising a cDNA clone different from that given clone. Thus, deposits sharing the same ATCC Deposit Number contain at least a plasmid for each cDNA clone referenced in Table 1.

**TABLE 5**

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
HUKA HUKB HUKC HUKD HUKF HUKF HUKG	Human Uterine Cancer	Lambda ZAP II	LP01
HCNA HCNB	Human Colon	Lambda Zap II	LP01
HFFA	Human Fetal Brain, random primed	Lambda Zap II	LP01
HTWA	Resting T-Cell	Lambda ZAP II	LP01
HBQA	Early Stage Human Brain, random primed	Lambda ZAP II	LP01
HLMB HLMF HLMG HLMH HLMJ HLMJ HLMN HLMN	breast lymph node CDNA library	Lambda ZAP II	LP01
HCQA HCOB	human colon cancer	Lambda ZAP II	LP01
HMEA HMEC HMEC HMEC HMEF HMEG HMEI HMEJ HMEK HMEK	Human Microvascular Endothelial Cells, fract. A	Lambda ZAP II	LP01
HUSA HUSC	Human Umbilical Vein Endothelial Cells, fract. A	Lambda ZAP II	LP01
HLQA HLQB	Hepatocellular Tumor	Lambda ZAP II	LP01
HHGA HHGB HHGC HHGD	Hemangiopericytoma	Lambda ZAP II	LP01
HSDM	Human Striatum Depression, re-rescue	Lambda ZAP II	LP01
HUSH	H Umbilical Vein Endothelial Cells, fract. A, re-excision	Lambda ZAP II	LP01
HSGS	Salivary gland, subtracted	Lambda ZAP II	LP01
HFXA HFXB HFXC HFXD HFXE HFXF HFXG HFXH	Brain frontal cortex	Lambda ZAP II	LP01
HPQA HPQB HPQC	PERM TF274	Lambda ZAP II	LP01
HFXJ HFXK	Brain Frontal Cortex, re-excision	Lambda ZAP II	LP01
HCWA HCWB HCWC HCWD HCWE HCWF HCWG HCWH HCWI HCWJ HCWK	CD34 positive cells (Cord Blood)	ZAP Express	LP02
HCUA HCUB HCUC	CD34 depleted Buffy Coat (Cord Blood)	ZAP Express	LP02
HRSM	A-14 cell line	ZAP Express	LP02
HRSA	A1-CELL LINE	ZAP Express	LP02
HCUD HCUE HCUF HCUG HCUH HCUH HCUH	CD34 depleted Buffy Coat (Cord Blood), re-excision	ZAP Express	LP02
HBXE HBXF HBXG	H. Whole Brain #2, re-excision	ZAP Express	LP02
HRLM	L8 cell line	ZAP Express	LP02
HBXA HBXB HBXC HBXD	Human Whole Brain #2 - Oligo dT > 1.5Kb	ZAP Express	LP02
HUDA HUDB HUDC	Testes	ZAP Express	LP02
HHTM HHTN HHTO	H. hypothalamus, fract. A, re-excision	ZAP Express	LP02
HHTL	H. hypothalamus, fract. A	ZAP Express	LP02
HASA HASD	Human Adult Spleen	Uni-ZAP XR	LP03
HFKC HFKD HFKC HFKF HFKG	Human Fetal Kidney	Uni-ZAP XR	LP03
HE8A HE8B HE8C HE8D HE8E HE8F HE8M HE8N	Human 8 Week Whole Embryo	Uni-ZAP XR	LP03
HGBA HGBD HGBE HGBF HGBG HGBH HGBI	Human Gall Bladder	Uni-ZAP XR	LP03
HLHA HLHB HLHC HLHD HLHE	Human Fetal Lung III	Uni-ZAP XR	LP03

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
HLHF HLHG HLHH HLHQ			
HPMA HPMB HPMC HPMD HPME HPMF HPMG HPMH	Human Placenta	Uni-ZAP XR	LP03
HPRA HPRB HPRC HPRD	Human Prostate	Uni-ZAP XR	LP03
HSIA HSIC HSID HSIE	Human Adult Small Intestine	Uni-ZAP XR	LP03
HTEA HTEB HTEC HTED HTEE HTEF HTEG HTEH HTEI HTEJ HTEK	Human Testes	Uni-ZAP XR	LP03
HTPA HTPB HTPC HTPD HTPF	Human Pancreas Tumor	Uni-ZAP XR	LP03
HTTA HTTB HTTC HTTD HTTE HTTF	Human Testes Tumor	Uni-ZAP XR	LP03
HAPA HAPB HAPC HAPM	Human Adult Pulmonary	Uni-ZAP XR	LP03
HETA HETB HETC HETD HETE HETF HETG HETH HETI	Human Endometrial Tumor	Uni-ZAP XR	LP03
HHFB HHFC HHFD HHFE HHFF HHFG HHFH HHFI	Human Fetal Heart	Uni-ZAP XR	LP03
HHPB HHPC HHPD HHPE HHPF HHPG HHPH	Human Hippocampus	Uni-ZAP XR	LP03
HCE1 HCE2 HCE3 HCE4 HCE5 HCEB HCEC HCED HCEE HCEF HCEG	Human Cerebellum	Uni-ZAP XR	LP03
HUVB HUVC HUVD HUVE	Human Umbilical Vein. Endo. remake	Uni-ZAP XR	LP03
HSTA HSTB HSTC HSTD	Human Skin Tumor	Uni-ZAP XR	LP03
HTAA HTAB HTAC HTAD HTAE	Human Activated T-Cells	Uni-ZAP XR	LP03
HFEA HFEB HFEC	Human Fetal Epithelium (Skin)	Uni-ZAP XR	LP03
HJPA HJPB HJPC HJPD	HUMAN JURKAT MEMBRANE BOUND POLYSOMES	Uni-ZAP XR	LP03
HESA	Human epithelioid sarcoma	Uni-Zap XR	LP03
HLTA HLTB HLTC HLTD HLTE HLTF	Human T-Cell Lymphoma	Uni-ZAP XR	LP03
HFTA HFTB HFTC HFTD	Human Fetal Dura Mater	Uni-ZAP XR	LP03
HRDA HRDB HRDC HRDD HRDE HRDF	Human Rhabdomyosarcoma	Uni-ZAP XR	LP03
HCAA HCAB HCAC	Cem cells cyclohexamide treated	Uni-ZAP XR	LP03
HRGA HRGB HRGC HRGD	Raji Cells. cyclohexamide treated	Uni-ZAP XR	LP03
HSUA HSUB HSUC HSUM	Supt Cells. cyclohexamide treated	Uni-ZAP XR	LP03
HT4A HT4C HT4D	Activated T-Cells. 12 hrs.	Uni-ZAP XR	LP03
HE9A HE9B HE9C HE9D HE9E HE9F HE9G HE9H HE9M HE9N	Nine Week Old Early Stage Human	Uni-ZAP XR	LP03
HATA HATB HATC HATD HATE	Human Adrenal Gland Tumor	Uni-ZAP XR	LP03
HT5A	Activated T-Cells. 24 hrs.	Uni-ZAP XR	LP03
HFGA HFGM	Human Fetal Brain	Uni-ZAP XR	LP03
HNEA HNEB HNEC HNED HNEE	Human Neutrophil	Uni-ZAP XR	LP03
HBGB HBGD	Human Primary Breast Cancer	Uni-ZAP XR	LP03
HBNA HBNB	Human Normal Breast	Uni-ZAP XR	LP03
HCAS	Cem Cells. cyclohexamide treated. subtra	Uni-ZAP XR	LP03
HHPS	Human Hippocampus. subtracted	pBS	LP03
HKCS HKCU	Human Colon Cancer. subtracted	pBS	LP03

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
HRGS	Raji cells, cyclohexamide treated, subtracted	pBS	LP03
HSUT	Supt cells, cyclohexamide treated, differentially expressed	pBS	LP03
HT4S	Activated T-Cells, 12 hrs. subtracted	Uni-ZAP XR	LP03
HCDA HCDB HCDC HCDD HCDE	Human Chondrosarcoma	Uni-ZAP XR	LP03
HOAA HOAB HOAC	Human Osteosarcoma	Uni-ZAP XR	LP03
HTLA HTLB HTLC HTLD HTLE HTLF	Human adult testis, large inserts	Uni-ZAP XR	LP03
HLMA HLMD HLMD	Breast Lymph node cDNA library	Uni-ZAP XR	LP03
H6EA H6EB H6EC	HL-60, PMA 4H	Uni-ZAP XR	LP03
HTXA HTXB HTXC HTXD HTXE HTXF HTXG HTXH	Activated T-Cell (12hs)/Thiouridine labelledEco	Uni-ZAP XR	LP03
HNFA HNFB HNFC HNFD HNFE HNFF HNFG HNFI HNFI	Human Neutrophil, Activated	Uni-ZAP XR	LP03
HTOB HTOC	HUMAN TONSILS, FRACTION 2	Uni-ZAP XR	LP03
HMGB	Human OB MG63 control fraction I	Uni-ZAP XR	LP03
HOPB	Human OB HOS control fraction I	Uni-ZAP XR	LP03
HORB	Human OB HOS treated (10 nM E2) fraction I	Uni-ZAP XR	LP03
HSVA HSVB HSVC	Human Chronic Synovitis	Uni-ZAP XR	LP03
HROA	HUMAN STOMACH	Uni-ZAP XR	LP03
HBJA HBJB HBJC HBJD HBJE HBJF HBJG HBJH HBJI HBJJ HBJK	HUMAN B CELL LYMPHOMA	Uni-ZAP XR	LP03
HCRA HCRB HCRC	human corpus colosum	Uni-ZAP XR	LP03
HODA HODB HODC HODD	human ovarian cancer	Uni-ZAP XR	LP03
HDSA	Dermatofibrosarcoma Protuberance	Uni-ZAP XR	LP03
HMWA HMWB HMWC HMWD HMWE HMWF HMWG HMWH HMWI HMWJ	Bone Marrow Cell Line (RS4;11)	Uni-ZAP XR	LP03
HSOA	stomach cancer (human)	Uni-ZAP XR	LP03
HERA	SKIN	Uni-ZAP XR	LP03
HMDA	Brain-medulloblastoma	Uni-ZAP XR	LP03
HGLA HGLB HGLD	Glioblastoma	Uni-ZAP XR	LP03
HEAA	H. Atrophic Endometrium	Uni-ZAP XR	LP03
HBCA HBCB	H. Lymph node breast Cancer	Uni-ZAP XR	LP03
HPWT	Human Prostate BPH, re-excision	Uni-ZAP XR	LP03
HFVG HFVH HFVI	Fetal Liver, subtraction II	pBS	LP03
HNFI	Human Neutrophils, Activated, re-excision	pBS	LP03
HBMB HBMC HBMD	Human Bone Marrow, re-excision	pBS	LP03
HKML HKMM HKMN	H. Kidney Medulla, re-excision	pBS	LP03
HKIX HKIY	H. Kidney Cortex, subtracted	pBS	LP03
HADT	H. Amygdala Depression, subtracted	pBS	LP03
H6AS	HL-60, untreated, subtracted	Uni-ZAP XR	LP03
H6ES	HL-60, PMA 4H, subtracted	Uni-ZAP XR	LP03
H6BS	HL-60, RA 4h, Subtracted	Uni-ZAP XR	LP03

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
H6CS	HL-60, PMA 1d. subtracted	Uni-ZAP XR	LP03
HTXJ HTXK	Activated T-cell(12h)/Thiouridine-re-excision	Uni-ZAP XR	LP03
HMSA HMSB HMSC HMSD HMSE HMSF HMSG HMSH HMSI HMSJ HMSK	Monocyte activated	Uni-ZAP XR	LP03
HAGA HAGB HAGC HAGD HAGE HAGF	Human Amygdala	Uni-ZAP XR	LP03
HSRA HSRB HSRE	STROMAL -OSTEOCLASTOMA	Uni-ZAP XR	LP03
HSRD HSRF HSRG HSRH	Human Osteoclastoma Stromal Cells - unamplified	Uni-ZAP XR	LP03
HSQA HSQB HSQC HSQD HSQE HSQF HSQG	Stromal cell TF274	Uni-ZAP XR	LP03
HSKA HSKB HSKC HSKD HSKE HSKF HSKZ	Smooth muscle, serum treated	Uni-ZAP XR	LP03
HSLA HSLB HSLC HSLD HSLE HSLF HSLG	Smooth muscle control	Uni-ZAP XR	LP03
HSDA HSDD HSDE HSDF HSDG HSDH	Spinal cord	Uni-ZAP XR	LP03
HPWS	Prostate-BPH subtracted II	pBS	LP03
HSKV HSKX HSKY	Smooth Muscle- HASTE normalized	pBS	LP03
HFPB HFPC HFPD	H. Frontal cortex.epileptic:re-excision	Uni-ZAP XR	LP03
HSDI HSDJ HSDK	Spinal Cord, re-excision	Uni-ZAP XR	LP03
HSKN HSKO	Smooth Muscle Serum Treated, Norm	pBS	LP03
HSKG HSKH HSKI	Smooth muscle, serum induced.re-exc	pBS	LP03
HFCA HFCB HFCC HFCD HFCE HFCF	Human Fetal Brain	Uni-ZAP XR	LP04
HPTA HPTB HPTD	Human Pituitary	Uni-ZAP XR	LP04
HTHB HTHC HTHD	Human Thymus	Uni-ZAP XR	LP04
HE6B HE6C HE6D HE6E HE6F HE6G HE6S	Human Whole Six Week Old Embryo	Uni-ZAP XR	LP04
HSSA HSSB HSSC HSSD HSSE HSSF HSSG HSSH HSSI HSSJ HSSK HE7T	Human Synovial Sarcoma	Uni-ZAP XR	LP04
HEPA HEPB HEPC	7 Week Old Early Stage Human, subtracted	Uni-ZAP XR	LP04
HSNA HSNB HSNB HSNM HSNM	Human Epididymus	Uni-ZAP XR	LP04
HPFB HPFC HPFD HPFE	Human Synovium	Uni-ZAP XR	LP04
HE2A HE2D HE2E HE2H HE2I HE2M HE2N HE2O	Human Prostate Cancer, Stage C fraction	Uni-ZAP XR	LP04
HE2B HE2C HE2F HE2G HE2P HE2Q	12 Week Old Early Stage Human	Uni-ZAP XR	LP04
HPTS HPTT HPTU	12 Week Old Early Stage Human, II	Uni-ZAP XR	LP04
HAUA HAUB HAUC	Human Pituitary, subtracted	Uni-ZAP XR	LP04
HAQA HAQB HAQC HAQD	Amniotic Cells - TNF induced	Uni-ZAP XR	LP04
HWTA HWTB HWTC	Amniotic Cells - Primary Culture	Uni-ZAP XR	LP04
HBSD	wilm's tumor	Uni-ZAP XR	LP04
HSGB	Bone Cancer, re-excision	Uni-ZAP XR	LP04
HSJA HSJB HSJC	Salivary gland, re-excision	Uni-ZAP XR	LP04
HSXA HSXB HSXC HSXD	Smooth muscle-ILb induced	Uni-ZAP XR	LP04
	Human Substantia Nigra	Uni-ZAP XR	LP04

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
HSHA HSHB HSHC	Smooth muscle, IL1b induced	Uni-ZAP XR	LP04
HOUA HOU'B HOU'C HOU'D HOU'E	Adipocytes	Uni-ZAP XR	LP04
HPWA HPWB HPWC HPWD HPWE	Prostate BPH	Uni-ZAP XR	LP04
HELA HELB HELC HELD HELE HELF HELG HELH	Endothelial cells-control	Uni-ZAP XR	LP04
HEMA HEMB HEMC HEMD HEME HEMF HENG HEMH	Endothelial-induced	Uni-ZAP XR	LP04
HBIA HBIB HBIC	Human Brain, Striatum	Uni-ZAP XR	LP04
HSHA HSHB HHSC HHSD HHSE	Human Hypothalamus, Schizophrenia	Uni-ZAP XR	LP04
HNGA HNGB HNGC HNGD HNGE HNGF HNGG HNGH HNGI HNGJ	neutrophils control	Uni-ZAP XR	LP04
HNHA HNHB HNHC HNHD HNHE HNHF HNHG HNHH HNHI HNHI	Neutrophils IL-1 and LPS induced	Uni-ZAP XR	LP04
HSDB HSDC	STRIATUM DEPRESSION	Uni-ZAP XR	LP04
HHPT	Hypothalamus	Uni-ZAP XR	LP04
HSAT HSAU HSAV HSAW HSAX HSAY HSAZ	Anergic T-cell	Uni-ZAP XR	LP04
HBMS HBMT HBMU HBMV HBMW HBMX	Bone marrow	Uni-ZAP XR	LP04
HOEA HOEB HOEC HOED HOEE HOEF HOEJ	Osteoblasts	Uni-ZAP XR	LP04
HAIA HAIB HAIC HAID HAIE HAIF	Epithelial-TNF $\alpha$ and INF induced	Uni-ZAP XR	LP04
HTGA HTGB HTGC HTGD	Apoptotic T-cell	Uni-ZAP XR	LP04
HMCA HMCB HMCC HMCD HMCE	Macrophage-oxLDL	Uni-ZAP XR	LP04
HMAA HMA B HMA C HMA D HMAE HMAF HMAG	Macrophage (GM-CSF treated)	Uni-ZAP XR	LP04
HPHA	Normal Prostate	Uni-ZAP XR	LP04
HPIA HPIB HPIC	LNCAP prostate cell line	Uni-ZAP XR	LP04
HPJA HPJB HPJC	PC3 Prostate cell line	Uni-ZAP XR	LP04
HOSE HOSF HOSG	Human Osteoclastoma, re-excision	Uni-ZAP XR	LP04
HTGE HTGF	Apoptotic T-cell, re-excision	Uni-ZAP XR	LP04
HMAJ HMAK	H Macrophage (GM-CSF treated), re-excision	Uni-ZAP XR	LP04
HACB HACC HACD	Human Adipose Tissue, re-excision	Uni-ZAP XR	LP04
HFPA	H. Frontal Cortex, Epileptic	Uni-ZAP XR	LP04
HFAA HFAB HFAC HFAD HFAE	Alzheimers, spongy change	Uni-ZAP XR	LP04
HFAM	Frontal Lobe, Dementia	Uni-ZAP XR	LP04
HMIA HMIB HMIC	Human Manic Depression Tissue	Uni-ZAP XR	LP04
HTSA HTSE HTSF HTSG HTSH	Human Thymus	pBS	LP05
HPBA HPBB HPBC HPBD HPBE	Human Pineal Gland	pBS	LP05
HSAA HSAB HSAC	HSA 172 Cells	pBS	LP05
HSBA HSBB HSBC HSBM	HSC172 cells	pBS	LP05
HJAA HJAB HJAC HJAD	Jurkat T-cell G1 phase	pBS	LP05
HJBA HJBB HJBC HJBD	Jurkat T-Cell, S phase	pBS	LP05
HAFA HAFB	Aorta endothelial cells + TNF- $\alpha$	pBS	LP05
HAWA HAWB HAWC	Human White Adipose	pBS	LP05
HTNA HTNB	Human Thyroid	pBS	LP05



Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
HONA	Normal Ovary, Premenopausal	pBS	LP05
HARA HARB	Human Adult Retina	pBS	LP05
HLJA HLJB	Human Lung	pCMVSPORT 1	LP06
HOFM HOFN HOFO	H. Ovarian Tumor, II, OV5232	pCMVSPORT 2.0	LP07
HOGA HOGB HOGC	OV 10-3-95	pCMVSPORT 2.0	LP07
HCGL	CD34+cells, II	pCMVSPORT 2.0	LP07
HDLA	Hodgkin's Lymphoma I	pCMVSPORT 2.0	LP07
HDTA HDTB HDTC HDTD HDTE	Hodgkin's Lymphoma II	pCMVSPORT 2.0	LP07
HKAA HKAB HKAC HKAD HKAE HKAF HKAG HKAH	Keratinocyte	pCMVSPORT2.0	LP07
HCIM	CAPFINDER, Crohn's Disease, lib 2	pCMVSPORT 2.0	LP07
HKAL	Keratinocyte, lib 2	pCMVSPORT2.0	LP07
HKAT	Keratinocyte, lib 3	pCMVSPORT2.0	LP07
HNDA	Nasal polyps	pCMVSPORT2.0	LP07
HDRA	H. Primary Dendritic Cells.lib 3	pCMVSPORT2.0	LP07
HOHA HOHB HOHC	Human Osteoblasts II	pCMVSPORT2.0	LP07
HLDA HLDB HLDC	Liver, Hepatoma	pCMVSPORT3.0	LP08
HLDN HLDO HLDP	Human Liver, normal	pCMVSPORT3.0	LP08
HMTA	pBMC stimulated w/ poly I/C	pCMVSPORT3.0	LP08
HNTA	NTERA2, control	pCMVSPORT3.0	LP08
HDPA HDPB HDPC HDPD HDPF HDPG HDPI HDPI HDPI HDPK	Primary Dendritic Cells, lib 1	pCMVSPORT3.0	LP08
HDPM HDPN HDPO HDPP	Primary Dendritic cells,frac 2	pCMVSPORT3.0	LP08
HMUA HMUB HMUC	Myeloid Progenitor Cell Line	pCMVSPORT3.0	LP08
HHEA HHEB HHEC HHED	T Cell helper I	pCMVSPORT3.0	LP08
HHEM HHEN HHEO HHEP	T cell helper II	pCMVSPORT3.0	LP08
HEQA HEQB HEQC	Human endometrial stromal cells	pCMVSPORT3.0	LP08
HJMA HJMB	Human endometrial stromal cells-treated with progesterone	pCMVSPORT3.0	LP08
HSWA HSWB HSWC	Human endometrial stromal cells-treated with estradiol	pCMVSPORT3.0	LP08
HSYA HSYB HSYC	Human Thymus Stromal Cells	pCMVSPORT3.0	LP08
HLWA HLWB HLWC	Human Placenta	pCMVSPORT3.0	LP08
HRAA HRAB HRAC	Rejected Kidney, lib 4	pCMVSPORT3.0	LP08
HMTM	PCR, pBMC I/C treated	PCR11	LP09
HMJA	H. Meningioma, M6	pSport 1	LP10
HMKA HMKB HMKC HMKD HMKE	H. Meningioma, M1	pSport 1	LP10
HUSG HUSI	Human umbilical vein endothelial cells, IL-4 induced	pSport 1	LP10
HUSX HUSY	Human Umbilical Vein Endothelial Cells, uninduced	pSport 1	LP10
HOFA	Ovarian Tumor I, OV5232	pSport 1	LP10
HCFA HCFB HCFC HCFC	T-Cell PHA 16 hrs	pSport 1	LP10
HCFL HCFM HCFN HCFO	T-Cell PHA 24 hrs	pSport 1	LP10
HADA HADC HADD HADE HADF HADG	Human Adipose	pSport 1	LP10

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
HOVA HOVB HOVC	Human Ovary	pSport 1	LP10
HTWB HTWC HTWD HTWE HTWF	Resting T-Cell Library.II	pSport 1	LP10
HMMA	Spleen metastatic melanoma	pSport 1	LP10
HLYA HLYB HLYC HLYD HLYE	Spleen, Chronic lymphocytic leukemia	pSport 1	LP10
HCGA	CD34+ cell. I	pSport 1	LP10
HEOM HEON	Human Eosinophils	pSport 1	LP10
HTDA	Human Tonsil. Lib 3	pSport 1	LP10
HSPA	Salivary Gland. Lib 2	pSport 1	LP10
HCHA HCHB HCHC	Breast Cancer cell line. MDA 36	pSport 1	LP10
HCHM HCHN	Breast Cancer Cell line. angiogenic	pSport 1	LP10
HCIA	Crohn's Disease	pSport 1	LP10
HDAA HDAB HDAC	HEL cell line	pSport 1	LP10
HABA	Human Astrocyte	pSport 1	LP10
HUFA HUFB HUF C	Ulcerative Colitis	pSport 1	LP10
HNTM	NTERA2 + retinoic acid. 14 days	pSport 1	LP10
HDQA	Primary Dendritic cells.CapFinder2. frac 1	pSport 1	LP10
HDQM	Primary Dendritic Cells. CapFinder. frac 2	pSport 1	LP10
HLDX	Human Liver. normal.CapFinder	pSport 1	LP10
HULA HULB HULC	Human Dermal Endothelial Cells.untreated	pSport 1	LP10
HUMA	Human Dermal Endothelial cells,treated	pSport 1	LP10
HCJA	Human Stromal Endometrial fibroblasts. untreated	pSport 1	LP10
HCJM	Human Stromal endometrial fibroblasts. treated w/ estradiol	pSport 1	LP10
HEDA	Human Stromal endometrial fibroblasts. treated with progesterone	pSport 1	LP10
HFNA	Human ovary tumor cell OV350721	pSport 1	LP10
HKGA HKGB HKGC HKGD	Merkel Cells	pSport 1	LP10
HISA HISB HISC	Pancreas Islet Cell Tumor	pSport 1	LP10
HLSA	Skin. burned	pSport 1	LP10
HBZA	Prostate.BPH. Lib 2	pSport 1	LP10
HBZS	Prostate BPH.Lib 2. subtracted	pSport 1	LP10
HFIA HFIB HFIC	Synovial Fibroblasts (control)	pSport 1	LP10
HFIH HFII HFIJ	Synovial hypoxia	pSport 1	LP10
HFIT HFIU HFIV	Synovial IL-1/TNF stimulated	pSport 1	LP10
HGCA	Messangial cell. frac 1	pSport 1	LP10
HMVA HMVB HMVC	Bone Marrow Stromal Cell. untreated	pSport 1	LP10
HFIX HFY HFIZ	Synovial Fibroblasts (III/TNF). subt	pSport 1	LP10
HFOX HFOY HFOZ	Synovial hypoxia-RSF subtracted	pSport 1	LP10
HMQA HMQB HMQC HMQD	Human Activated Monocytes	Uni-ZAP XR	LP11
HLIA HLIB HLIC	Human Liver	pCMVSPORT 1	LP012
HHBA HHBB HHBC HHBD HHBE	Human Heart	pCMVSPORT 1	LP012
HBBA HBBB	Human Brain	pCMVSPORT 1	LP012

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
HLJA HLJB HLJC HLJD HLJE	Human Lung	pCMVSPORT 1	LP012
HOGA HOGB HOGC	Ovarian Tumor	pCMVSPORT 2.0	LP012
HTJM	Human Tonsils. Lib 2	pCMVSPORT 2.0	LP012
HAMF HAMG	KMH2	pCMVSPORT 3.0	LP012
HAJA HAJB HAJC	L428	pCMVSPORT 3.0	LP012
HWBA HWBB HWBC HWBD HWBE	Dendritic cells. pooled	pCMVSPORT 3.0	LP012
HWAA HWAB HWAC HWAD HWAE	Human Bone Marrow. treated	pCMVSPORT 3.0	LP012
HYAA HYAB HYAC	B Cell lymphoma	pCMVSPORT 3.0	LP012
HWHG HWHH HWHI	Healing groin wound, 6.5 hours post incision	pCMVSPORT 3.0	LP012
HWHP HWHQ HWHR	Healing groin wound: 7.5 hours post incision	pCMVSPORT 3.0	LP012
HARM	Healing groin wound - zero hr post-incision (control)	pCMVSPORT 3.0	LP012
HBIM	Olfactory epithelium: nasal cavity	pCMVSPORT 3.0	LP012
HWDA	Healing Abdomen wound: 70&90 min post incision	pCMVSPORT 3.0	LP012
HWEA	Healing Abdomen Wound:15 days post incision	pCMVSPORT 3.0	LP012
HWJA	Healing Abdomen Wound:21&29 days	pCMVSPORT 3.0	LP012
HNAL	Human Tongue. frac 2	pSport1	LP012
HMJA	H. Meningioma, M6	pSport1	LP012
HMKA HMKB HMKC HMKD HMKE	H. Meningioma, M1	pSport1	LP012
HOFA	Ovarian Tumor I. OV5232	pSport1	LP012
HCFA HCFB HCFC HCFD	T-Cell PHA 16 hrs	pSport1	LP012
HCFL HCFM HCFN HCFO	T-Cell PHA 24 hrs	pSport1	LP012
HMMA HMMB HMMC	Spleen metastatic melanoma	pSport1	LP012
HTDA	Human Tonsil. Lib 3	pSport1	LP012
HDBA	Human Fetal Thymus	pSport1	LP012
HDLA	Pericardium	pSport1	LP012
HBZA	Prostate.BPH. Lib 2	pSport1	LP012
HWCA	Larynx tumor	pSport1	LP012
HWKA	Normal lung	pSport1	LP012
HSMB	Bone marrow stroma.treated	pSport1	LP012
HBHM	Normal trachea	pSport1	LP012
HLFC	Human Larynx	pSport1	LP012
HLRB	Siebben Polyposis	pSport1	LP012
HNIA	Mammary Gland	pSport1	LP012
HNJB	Palate carcinoma	pSport1	LP012
HNKA	Palate normal	pSport1	LP012
HMZA	Pharynx carcinoma	pSport1	LP012
HABG	Cheek Carcinoma	pSport1	LP012
HMZM	Pharynx Carcinoma	pSport1	LP012
HDRM	Larynx Carcinoma	pSport1	LP012
HVAA	Pancreas normal PCA4 No	pSport1	LP012
HICA	Tongue carcinoma	pSport1	LP012

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
HUKA HUKB HUKC HUKD HUK E	Human Uterine Cancer	Lambda ZAP II	LP013
HFFA	Human Fetal Brain, random primed	Lambda ZAP II	LP013
HTUA	Activated T-cell labeled with 4-thiour	Lambda ZAP II	LP013
HBQA	Early Stage Human Brain, random primed	Lambda ZAP II	LP013
HMEB	Human microvascular Endothelial cells, fract. B	Lambda ZAP II	LP013
HUSH	Human Umbilical Vein Endothelial cells, fract. A, re-excision	Lambda ZAP II	LP013
HLQC HLOD	Hepatocellular tumor, re-excision	Lambda ZAP II	LP013
HTWJ HTWK HTWL	Resting T-cell, re-excision	Lambda ZAP II	LP013
HP6S	Human Whole 6 week Old Embryo (II), sub	pBluescript	LP013
HHPS	Human Hippocampus, subtracted	pBluescript	LP013
HL1S	LNAP, differential expression	pBluescript	LP013
HLHS HLHT	Early Stage Human Lung, Subtracted	pBluescript	LP013
HSUS	Supt cells, cyclohexamide treated, subtracted	pBluescript	LP013
HSUT	Supt cells, cyclohexamide treated, differentially expressed	pBluescript	LP013
HSDS	H. Striatum Depression, subtracted	pBluescript	LP013
HPTZ	Human Pituitary, Subtracted VII	pBluescript	LP013
HSDX	H. Striatum Depression, sub II	pBluescript	LP013
HSDZ	H. Striatum Depression, sub	pBluescript	LP013
HPBA HPBB HPBC HPBD HPBE	Human Pineal Gland	pBluescript SK-	LP013
HRTA	Colorectal Tumor	pBluescript SK-	LP013
HSBA HSBB HSBC HSBM	HSC172 cells	pBluescript SK-	LP013
HJAA HJAB HJAC HJAD	Jurkat T-cell G1 phase	pBluescript SK-	LP013
HJBA HJBB HJBC HJBD	Jurkat T-cell, S1 phase	pBluescript SK-	LP013
HTNA HTNB	Human Thyroid	pBluescript SK-	LP013
HAHA HAHB	Human Adult Heart	Uni-ZAP XR	LP013
HE6A	Whole 6 week Old Embryo	Uni-ZAP XR	LP013
HFCA HFCB HFCC HFCD HFCE	Human Fetal Brain	Uni-ZAP XR	LP013
HFKC HFKD HFKE HFKF HFKG	Human Fetal Kidney	Uni-ZAP XR	LP013
HGBA HGBD HGBE HGBF HGBG	Human Gall Bladder	Uni-ZAP XR	LP013
HPRA HPRB HPRC HPRD	Human Prostate	Uni-ZAP XR	LP013
HTEA HTEB HTEC HTED HTEE	Human Testes	Uni-ZAP XR	LP013
HTTA HTTB HTTC HTTD HTTE	Human Testes Tumor	Uni-ZAP XR	LP013
HYBA HYBB	Human Fetal Bone	Uni-ZAP XR	LP013
HFLA	Human Fetal Liver	Uni-ZAP XR	LP013
HHFB HHFC HHFD HHFE HHFF	Human Fetal Heart	Uni-ZAP XR	LP013
HUVB HUV C HUV D HUV E	Human Umbilical Vein, End. remake	Uni-ZAP XR	LP013
HTHB HTHC HTHD	Human Thymus	Uni-ZAP XR	LP013
HSTA HSTB HSTC HSTD	Human Skin Tumor	Uni-ZAP XR	LP013
HTAA HTAB HTAC HTAD HTAE	Human Activated T-cells	Uni-ZAP XR	LP013
HFEA HFEB HFEC	Human Fetal Epithelium (skin)	Uni-ZAP XR	LP013
HJPA HJPB HJPC HJPD	Human Jurkat Membrane Bound Polysomes	Uni-ZAP XR	LP013
HESA	Human Epithelioid Sarcoma	Uni-ZAP XR	LP013

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
HALS	Human Adult Liver. Subtracted	Uni-ZAP XR	LP013
HFTA HFTB HFTC HFTD	Human Fetal Dura Mater	Uni-ZAP XR	LP013
HCAA HCAB HCAC	Cem cells. cyclohexamide treated	Uni-ZAP XR	LP013
HRGA HRGB HRGC HRGD	Raji Cells. cyclohexamide treated	Uni-ZAP XR	LP013
HE9A HE9B HE9C HE9D HE9E	Nine Week Old Early Stage Human	Uni-ZAP XR	LP013
HSFA	Human Fibrosarcoma	Uni-ZAP XR	LP013
HATA HATB HATC HATD HATE	Human Adrenal Gland Tumor	Uni-ZAP XR	LP013
HTRA	Human Trachea Tumor	Uni-ZAP XR	LP013
HE2A HE2D HE2E HE2H HE2I	12 Week Old Early Stage Human	Uni-ZAP XR	LP013
HE2B HE2C HE2F HE2G HE2P	12 Week Old Early Stage Human. II	Uni-ZAP XR	LP013
HNEA HNEB HNEC HNED HNEE	Human Neutrophil	Uni-ZAP XR	LP013
HBGA	Human Primary Breast Cancer	Uni-ZAP XR	LP013
HPTS HPTT HPTU	Human Pituitary. subtracted	Uni-ZAP XR	LP013
HMQA HMQB HMQC HMQD	Human Activated Monocytes	Uni-ZAP XR	LP013
HOAA HOAB HOAC	Human Osteosarcoma	Uni-ZAP XR	LP013
HTOA HTOD HTOE HTOF HTOG	human tonsils	Uni-ZAP XR	LP013
HMGB	Human OB MG63 control fraction I	Uni-ZAP XR	LP013
HOPB	Human OB HOS control fraction I	Uni-ZAP XR	LP013
HOQB	Human OB HOS treated (1 nM E2) fraction I	Uni-ZAP XR	LP013
HAUA HAUB HAUC	Amniotic Cells - TNF induced	Uni-ZAP XR	LP013
HAQA HAQB HAQC HAQD	Amniotic Cells - Primary Culture	Uni-ZAP XR	LP013
HROA HROC	HUMAN STOMACH	Uni-ZAP XR	LP013
HBJA HBJB HBJC HBJD HBJE	HUMAN B CELL LYMPHOMA	Uni-ZAP XR	LP013
HODA HODB HODC HODD	human ovarian cancer	Uni-ZAP XR	LP013
HCPA	Corpus Callosum	Uni-ZAP XR	LP013
HSOA	stomach cancer (human)	Uni-ZAP XR	LP013
HERA	SKIN	Uni-ZAP XR	LP013
HMDA	Brain-medulloblastoma	Uni-ZAP XR	LP013
HGLA HGLB HGLD	Glioblastoma	Uni-ZAP XR	LP013
HWTA HWTB HWTC	wilm's tumor	Uni-ZAP XR	LP013
HEAA	H. Atrophic Endometrium	Uni-ZAP XR	LP013
HAPN HAPO HAPB HAQO HAPR	Human Adult Pulmonary:re-excision	Uni-ZAP XR	LP013
HLTG HLTH	Human T-cell lymphoma:re-excision	Uni-ZAP XR	LP013
HAHC HAHD HAHE	Human Adult Heart:re-excision	Uni-ZAP XR	LP013
HAGA HAGB HAGC HAGD HAGE	Human Amygdala	Uni-ZAP XR	LP013
HSJA HSJB HSJC	Smooth muscle-ILb induced	Uni-ZAP XR	LP013
HSJA HSHB HSHC	Smooth muscle, IL1b induced	Uni-ZAP XR	LP013
HPWA HPWB HPWC HPWD HPWE	Prostate BPH	Uni-ZAP XR	LP013
HPJA HPJB HPJC	LNCAP prostate cell line	Uni-ZAP XR	LP013
HPJA HPJB HPJC	PC3 Prostate cell line	Uni-ZAP XR	LP013
HBTA	Bone Marrow Stroma. TNF&LPS ind	Uni-ZAP XR	LP013
HMCB HMCG HMCH HMCJ HMCJ	Macrophage-oxLDL: re-excision	Uni-ZAP XR	LP013
HAGG HAGH HAGI	Human Amygdala:re-excision	Uni-ZAP XR	LP013
HACA	H. Adipose Tissue	Uni-ZAP XR	LP013
HKFB	K562 + PMA (36 hrs).re-excision	ZAP Express	LP013
HCWT HCWU HCWV	CD34 positive cells (cord blood).re-ex	ZAP Express	LP013

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
HBWA	Whole brain	ZAP Express	LP013
HBXA HBXB HBXC HBXD	Human Whole Brain #2 - Oligo dT > 1.5Kb	ZAP Express	LP013
HAVM	Temporal cortex-Alzheimer	pT-Adv	LP014
HAUT	Hippocampus, Alzheimer Subtracted	pT-Adv	LP014
HHAS	CHME Cell Line	Uni-ZAP XR	LP014
HAJR	Larynx normal	pSport 1	LP014
HWLE HWLF HWLG HWLH	Colon Normal	pSport 1	LP014
HCRM HCRN HCRO	Colon Carcinoma	pSport 1	LP014
HWLI HWLJ HWLK	Colon Normal	pSport 1	LP014
HWLQ HWLR HWLS HWLT	Colon Tumor	pSport 1	LP014
HBFM	Gastrocnemius Muscle	pSport 1	LP014
HBOD HBOE	Quadriceps Muscle	pSport 1	LP014
HBKD HBKE	Soleus Muscle	pSport 1	LP014
HCCM	Pancreatic Langerhans	pSport 1	LP014
HWGA	Larynx carcinoma	pSport 1	LP014
HWGM HWGN	Larynx carcinoma	pSport 1	LP014
HWLA HWLB HWLC	Normal colon	pSport 1	LP014
HWLM HWLN	Colon Tumor	pSport 1	LP014
HVAM HVAN HVAO	Pancreas Tumor	pSport 1	LP014
HWGO	Larynx carcinoma	pSport 1	LP014
HAQM HAQN	Salivary Gland	pSport 1	LP014
HASM	Stomach; normal	pSport 1	LP014
HBCM	Uterus; normal	pSport 1	LP014
HCDM	Testis; normal	pSport 1	LP014
HDJM	Brain; normal	pSport 1	LP014
HEFM	Adrenal Gland; normal	pSport 1	LP014
HBAA	Rectum normal	pSport 1	LP014
HFDM	Rectum tumour	pSport 1	LP014
HGAM	Colon, normal	pSport 1	LP014
HHMM	Colon, tumour	pSport 1	LP014
HCLB HCLC	Human Lung Cancer	Lambda Zap II	LP015
HRLA	L1 Cell line	ZAP Express	LP015
HHAM	Hypothalamus, Alzheimer's	pCMVSport 3.0	LP015
HKBA	Ku 812F Basophils Line	pSport 1	LP015
HS2S	Saos2, Dexamethosone Treated	pSport 1	LP016
HA5A	Lung Carcinoma A549 TNFalpha activated	pSport 1	LP016
HTFM	TF-1 Cell Line GM-CSF Treated	pSport 1	LP016
HYAS	Thyroid Tumour	pSport 1	LP016
HUTS	Larynx Normal	pSport 1	LP016
HXOA	Larynx Tumor	pSport 1	LP016
HEAH	Ea.hy.926 cell line	pSport 1	LP016
HINA	Adenocarcinoma Human	pSport 1	LP016
HRMA	Lung Mesothelium	pSport 1	LP016
HLCL	Human Pre-Differentiated Adipocytes	Uni-Zap XR	LP017
HS2A	Saos2 Cells	pSport 1	LP020

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
HS2I	Saos2 Cells: Vitamin D3 Treated	pSport 1	LP020
HUCM	CHME Cell Line, untreated	pSport 1	LP020
HEPN	Aryepiglottis Normal	pSport 1	LP020
HPSN	Sinus Piniformis Tumour	pSport 1	LP020
HNSA	Stomach Normal	pSport 1	LP020
HNSM	Stomach Tumour	pSport 1	LP020
HNLA	Liver Normal Met5No	pSport 1	LP020
HUTA	Liver Tumour Met 5 Tu	pSport 1	LP020
HOCN	Colon Normal	pSport 1	LP020
HOCT	Colon Tumor	pSport 1	LP020
HTNT	Tongue Tumour	pSport 1	LP020
HLXN	Larynx Normal	pSport 1	LP020
HLXT	Larynx Tumour	pSport 1	LP020
HTYN	Thymus	pSport 1	LP020
HPLN	Placenta	pSport 1	LP020
HTNG	Tongue Normal	pSport 1	LP020
HZAA	Thyroid Normal (SDCA2 No)	pSport 1	LP020
HWES	Thyroid Thyroiditis	pSport 1	LP020
HFHD	Ficoll Human Stromal Cells, 5Fu treated	pTriplEx2	LP021
HFHM, HFHN	Ficoll Human Stromal Cells, Untreated	pTriplEx2	LP021
HPCI	Hep G2 Cells, lambda library	lambda Zap-CMV XR	LP021
HBCA, HBCB, HBCC	H. Lymph node breast Cancer	Uni-ZAP XR	LP021
HCOK	Chondrocytes	pSPORT1	LP022
HDCA, HDCB, HDCC	Dendritic Cells From CD34 Cells	pSPORT1	LP022
HDMA, HDMB	CD40 activated monocyte dendritic cells	pSPORT1	LP022
HDDM, HDDN, HDDO	LPS activated derived dendritic cells	pSPORT1	LP022
HPCR	Hep G2 Cells, PCR library	lambda Zap-CMV XR	LP022
HAAA, HAAB, HAAC	Lung, Cancer (4005313 A3): Invasive Poorly Differentiated Lung Adenocarcinoma	pSPORT1	LP022
HIPB, HIPB, HIPC	Lung, Cancer (4005163 B7): Invasive, Poorly Diff. Adenocarcinoma, Metastatic	pSPORT1	LP022
HOOH, HOOI	Ovary, Cancer: (4004562 B6) Papillary Serous Cystic Neoplasm, Low Malignant Pot	pSPORT1	LP022
HIDA	Lung, Normal: (4005313 B1)	pSPORT1	LP022
HUJA, HUJB, HUJC, HUJD, HUJE	B-Cells	pCMVSPORT 3.0	LP022
HNOA, HNOB, HNOG, HNOD	Ovary, Normal: (9805C040R)	pSPORT1	LP022
HNLM	Lung, Normal: (4005313 B1)	pSPORT1	LP022
HSCL	Stromal Cells	pSPORT1	LP022
HAAX	Lung, Cancer: (4005313 A3) Invasive Poorly-differentiated Metastatic lung adenocarcinoma	pSPORT1	LP022
HUUA, HUUB, HUUC, HUUD	B-cells (unstimulated)	pTriplEx2	LP022
HWWA, HWWB, HWWC, HWWD, HWE, HWWF, HWWG	B-cells (stimulated)	pSPORT1	LP022
HCCC	Colon, Cancer: (9808C064R)	pCMVSPORT 3.0	LP023

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
HPDO HPDP HPDQ HPDR HPD	Ovary, Cancer (9809C332): Poorly differentiated adenocarcinoma	pSport 1	LP023
HPCO HPCP HPCQ HPCT	Ovary, Cancer (15395A1F): Grade II Papillary Carcinoma	pSport 1	LP023
HOCM HOCO HOCQ HOCQ	Ovary, Cancer: (15799A1F) Poorly differentiated carcinoma	pSport 1	LP023
HCBM HCBN HCBO	Breast, Cancer: (4004943 A5)	pSport 1	LP023
HNBT HNBU HNBV	Breast, Normal: (4005522B2)	pSport 1	LP023
HBCP HBCQ	Breast, Cancer: (4005522 A2)	pSport 1	LP023
HBCJ	Breast, Cancer: (9806C012R)	pSport 1	LP023
HSAM HSAN	Stromal cells 3.88	pSport 1	LP023
HVCA HV'CB HVCC HVCD	Ovary, Cancer: (4004332 A2)	pSport 1	LP023
HSCK HSEN HSEO	Stromal cells (HBM3.18)	pSport 1	LP023
HSCP HSCQ	stromal cell clone 2.5	pSport 1	LP023
HUXA	Breast Cancer: (4005385 A2)	pSport 1	LP023
HCOM HCON HCOO HCOP HCOQ	Ovary, Cancer (4004650 A3): Well-Differentiated Micropapillary Serous Carcinoma	pSport 1	LP023
HBNM	Breast, Cancer: (9802C020E)	pSport 1	LP023
HVVA HV'VB HVVC HVVD HVVE	Human Bone Marrow, treated	pSport 1	LP023



Two approaches can be used to isolate a particular clone from the deposited sample of plasmid DNAs cited for that clone in Table 5. First, a plasmid is directly isolated by screening the clones using a polynucleotide probe corresponding to the nucleotide sequence of SEQ ID NO:X.

5        Particularly, a specific polynucleotide with 30-40 nucleotides is synthesized using an Applied Biosystems DNA synthesizer according to the sequence reported. The oligonucleotide is labeled, for instance, with  $^{32}\text{P}$ - $\gamma$ -ATP using T4 polynucleotide kinase and purified according to routine methods. (E.g., Maniatis et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Press, Cold Spring, NY (1982).) The plasmid  
10        mixture is transformed into a suitable host, as indicated above (such as XL-1 Blue (Stratagene)) using techniques known to those of skill in the art, such as those provided by the vector supplier or in related publications or patents cited above. The transformants are plated on 1.5% agar plates (containing the appropriate selection agent, e.g., ampicillin) to a density of about 150 transformants (colonies) per plate. These plates are screened using  
15        Nylon membranes according to routine methods for bacterial colony screening (e.g., Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2nd Edit., (1989), Cold Spring Harbor Laboratory Press, pages 1.93 to 1.104), or other techniques known to those of skill in the art.

          Alternatively, two primers of 17-20 nucleotides derived from both ends of the  
20        nucleotide sequence of SEQ ID NO:X are synthesized and used to amplify the desired cDNA using the deposited cDNA plasmid as a template. The polymerase chain reaction is carried out under routine conditions, for instance, in 25  $\mu\text{l}$  of reaction mixture with 0.5  $\mu\text{g}$  of the above cDNA template. A convenient reaction mixture is 1.5-5 mM  $\text{MgCl}_2$ , 0.01% (w/v) gelatin, 20  $\mu\text{M}$  each of dATP, dCTP, dGTP, dTTP, 25 pmol of each primer and 0.25 Unit of  
25        Taq polymerase. Thirty five cycles of PCR (denaturation at 94°C for 1 min; annealing at 55°C for 1 min; elongation at 72°C for 1 min) are performed with a Perkin-Elmer Cetus automated thermal cycler. The amplified product is analyzed by agarose gel electrophoresis and the DNA band with expected molecular weight is excised and purified. The PCR product is verified to be the selected sequence by subcloning and sequencing the DNA  
30        product.

Several methods are available for the identification of the 5' or 3' non-coding portions of a gene which may not be present in the deposited clone. These methods include but are not

limited to. filter probing, clone enrichment using specific probes, and protocols similar or identical to 5' and 3' "RACE" protocols which are well known in the art. For instance, a method similar to 5' RACE is available for generating the missing 5' end of a desired full-length transcript. (Fromont-Racine et al., Nucleic Acids Res. 21(7):1683-1684 (1993).)

5 Briefly, a specific RNA oligonucleotide is ligated to the 5' ends of a population of RNA presumably containing full-length gene RNA transcripts. A primer set containing a primer specific to the ligated RNA oligonucleotide and a primer specific to a known sequence of the gene of interest is used to PCR amplify the 5' portion of the desired full-length gene. This amplified product may then be sequenced and used to generate the full  
10 length gene.

This above method starts with total RNA isolated from the desired source, although poly-A+ RNA can be used. The RNA preparation can then be treated with phosphatase if necessary to eliminate 5' phosphate groups on degraded or damaged RNA which may interfere with the later RNA ligase step. The phosphatase should then be inactivated and the  
15 RNA treated with tobacco acid pyrophosphatase in order to remove the cap structure present at the 5' ends of messenger RNAs. This reaction leaves a 5' phosphate group at the 5' end of the cap cleaved RNA which can then be ligated to an RNA oligonucleotide using T4 RNA ligase.

This modified RNA preparation is used as a template for first strand cDNA synthesis  
20 using a gene specific oligonucleotide. The first strand synthesis reaction is used as a template for PCR amplification of the desired 5' end using a primer specific to the ligated RNA oligonucleotide and a primer specific to the known sequence of the gene of interest. The resultant product is then sequenced and analyzed to confirm that the 5' end sequence belongs to the desired gene.

25

***Example 2: Isolation of Genomic Clones Corresponding to a Polynucleotide***

A human genomic P1 library (Genomic Systems, Inc.) is screened by PCR using primers selected for the sequence corresponding to SEQ ID NO:X, according to the method  
30 described in Example 1. (See also, Sambrook.)

***Example 3: Tissue specific expression analysis***

The Human Genome Sciences, Inc. (HGS) database is derived from sequencing tissue specific cDNA libraries. Libraries generated from a particular tissue are selected and the specific tissue expression pattern of EST groups or assembled contigs within these libraries is determined by comparison of the expression patterns of those groups or contigs within the entire database. ESTs which show tissue specific expression are selected.

The original clone from which the specific EST sequence was generated, is obtained from the catalogued library of clones and the insert amplified by PCR using methods known in the art. The PCR product is denatured then transferred in 96 well format to a nylon membrane (Schleicher and Scheull) generating an array filter of tissue specific clones. Housekeeping genes, maize genes, and known tissue specific genes are included on the filters. These targets can be used in signal normalization and to validate assay sensitivity. Additional targets are included to monitor probe length and specificity of hybridization.

Radioactively labeled hybridization probes are generated by first strand cDNA synthesis per the manufacturer's instructions (Life Technologies) from mRNA/RNA samples prepared from the specific tissue being analyzed. The hybridization probes are purified by gel exclusion chromatography, quantitated, and hybridized with the array filters in hybridization bottles at 65°C overnight. The filters are washed under stringent conditions and signals are captured using a Fuji phosphorimager.

Data is extracted using AIS software and following background subtraction, signal normalization is performed. This includes a normalization of filter-wide expression levels between different experimental runs. Genes that are differentially expressed in the tissue of interest are identified and the full length sequence of these clones is generated.

***Example 4: Chromosomal Mapping of the Polynucleotides***

An oligonucleotide primer set is designed according to the sequence at the 5' end of SEQ ID NO:X. This primer preferably spans about 100 nucleotides. This primer set is then used in a polymerase chain reaction under the following set of conditions : 30 seconds, 95°C; 1 minute, 56°C; 1 minute, 70°C. This cycle is repeated 32 times followed by one 5 minute

cycle at 70°C. Human, mouse, and hamster DNA is used as template in addition to a somatic cell hybrid panel containing individual chromosomes or chromosome fragments (Bios, Inc). The reactions is analyzed on either 8% polyacrylamide gels or 3.5 % agarose gels. Chromosome mapping is determined by the presence of an approximately 100 bp PCR  
5 fragment in the particular somatic cell hybrid.

***Example 5: Bacterial Expression of a Polypeptide***

A polynucleotide encoding a polypeptide of the present invention is amplified using  
10 PCR oligonucleotide primers corresponding to the 5' and 3' ends of the DNA sequence, as outlined in Example 1, to synthesize insertion fragments. The primers used to amplify the cDNA insert should preferably contain restriction sites, such as BamHI and XbaI, at the 5' end of the primers in order to clone the amplified product into the expression vector. For example, BamHI and XbaI correspond to the restriction enzyme sites on the bacterial  
15 expression vector pQE-9. (Qiagen, Inc., Chatsworth, CA). This plasmid vector encodes antibiotic resistance (Amp<sup>r</sup>), a bacterial origin of replication (ori), an IPTG-regulatable promoter/operator (P/O), a ribosome binding site (RBS), a 6-histidine tag (6-His), and restriction enzyme cloning sites.

The pQE-9 vector is digested with BamHI and XbaI and the amplified fragment is  
20 ligated into the pQE-9 vector maintaining the reading frame initiated at the bacterial RBS. The ligation mixture is then used to transform the E. coli strain M15/rep4 (Qiagen, Inc.) which contains multiple copies of the plasmid pREP4, which expresses the lacI repressor and also confers kanamycin resistance (Kan<sup>r</sup>). Transformants are identified by their ability to grow on LB plates and ampicillin/kanamycin resistant colonies are selected. Plasmid DNA is  
25 isolated and confirmed by restriction analysis.

Clones containing the desired constructs are grown overnight (O/N) in liquid culture in LB media supplemented with both Amp (100 ug/ml) and Kan (25 ug/ml). The O/N culture is used to inoculate a large culture at a ratio of 1:100 to 1:250. The cells are grown to an optical density 600 (O.D.<sup>600</sup>) of between 0.4 and 0.6. IPTG (Isopropyl-B-D-thiogalacto  
30 pyranoside) is then added to a final concentration of 1 mM. IPTG induces by inactivating the lacI repressor, clearing the P/O leading to increased gene expression.

Cells are grown for an extra 3 to 4 hours. Cells are then harvested by centrifugation (20 mins at 6000Xg). The cell pellet is solubilized in the chaotropic agent 6 Molar Guanidine HCl by stirring for 3-4 hours at 4°C. The cell debris is removed by centrifugation, and the supernatant containing the polypeptide is loaded onto a nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin column (available from QIAGEN, Inc., *supra*). Proteins with a 6 x His tag bind to the Ni-NTA resin with high affinity and can be purified in a simple one-step procedure (for details see: The QIAexpressionist (1995) QIAGEN, Inc., *supra*).

Briefly, the supernatant is loaded onto the column in 6 M guanidine-HCl, pH 8. the column is first washed with 10 volumes of 6 M guanidine-HCl, pH 8. then washed with 10 volumes of 6 M guanidine-HCl pH 6, and finally the polypeptide is eluted with 6 M guanidine-HCl, pH 5.

The purified protein is then renatured by dialyzing it against phosphate-buffered saline (PBS) or 50 mM Na-acetate, pH 6 buffer plus 200 mM NaCl. Alternatively, the protein can be successfully refolded while immobilized on the Ni-NTA column. The recommended conditions are as follows: renature using a linear 6M-1M urea gradient in 500 mM NaCl, 20% glycerol, 20 mM Tris/HCl pH 7.4, containing protease inhibitors. The renaturation should be performed over a period of 1.5 hours or more. After renaturation the proteins are eluted by the addition of 250 mM imidazole. Imidazole is removed by a final dialyzing step against PBS or 50 mM sodium acetate pH 6 buffer plus 200 mM NaCl. The purified protein is stored at 4°C or frozen at -80°C.

In addition to the above expression vector, the present invention further includes an expression vector comprising phage operator and promoter elements operatively linked to a polynucleotide of the present invention, called pHE4a. (ATCC Accession Number 209645, deposited on February 25, 1998.) This vector contains: 1) a neomycinphosphotransferase gene as a selection marker, 2) an E. coli origin of replication, 3) a T5 phage promoter sequence, 4) two lac operator sequences, 5) a Shine-Delgarno sequence, and 6) the lactose operon repressor gene (lacIq). The origin of replication (oriC) is derived from pUC19 (LTI, Gaithersburg, MD). The promoter sequence and operator sequences are made synthetically.

DNA can be inserted into the pHEa by restricting the vector with NdeI and XbaI, BamHI, XhoI, or Asp718, running the restricted product on a gel, and isolating the larger fragment (the stuffer fragment should be about 310 base pairs). The DNA insert is generated according to the PCR protocol described in Example 1, using PCR primers having restriction

sites for NdeI (5' primer) and XbaI, BamHI, XhoI, or Asp718 (3' primer). The PCR insert is gel purified and restricted with compatible enzymes. The insert and vector are ligated according to standard protocols.

The engineered vector could easily be substituted in the above protocol to express  
5 protein in a bacterial system.

***Example 6: Purification of a Polypeptide from an Inclusion Body***

The following alternative method can be used to purify a polypeptide expressed in *E*  
10 *coli* when it is present in the form of inclusion bodies. Unless otherwise specified, all of the following steps are conducted at 4-10°C.

Upon completion of the production phase of the *E. coli* fermentation, the cell culture is cooled to 4-10°C and the cells harvested by continuous centrifugation at 15,000 rpm (Heraeus Sepatech). On the basis of the expected yield of protein per unit weight of cell  
15 paste and the amount of purified protein required, an appropriate amount of cell paste, by weight, is suspended in a buffer solution containing 100 mM Tris, 50 mM EDTA, pH 7.4. The cells are dispersed to a homogeneous suspension using a high shear mixer.

The cells are then lysed by passing the solution through a microfluidizer (Microfluidics, Corp. or APV Gaulin, Inc.) twice at 4000-6000 psi. The homogenate is then  
20 mixed with NaCl solution to a final concentration of 0.5 M NaCl, followed by centrifugation at 7000 xg for 15 min. The resultant pellet is washed again using 0.5M NaCl, 100 mM Tris, 50 mM EDTA, pH 7.4.

The resulting washed inclusion bodies are solubilized with 1.5 M guanidine hydrochloride (GuHCl) for 2-4 hours. After 7000 xg centrifugation for 15 min., the pellet is  
25 discarded and the polypeptide containing supernatant is incubated at 4°C overnight to allow further GuHCl extraction.

Following high speed centrifugation (30,000 xg) to remove insoluble particles, the GuHCl solubilized protein is refolded by quickly mixing the GuHCl extract with 20 volumes of buffer containing 50 mM sodium, pH 4.5, 150 mM NaCl, 2 mM EDTA by vigorous  
30 stirring. The refolded diluted protein solution is kept at 4°C without mixing for 12 hours prior to further purification steps.

To clarify the refolded polypeptide solution, a previously prepared tangential filtration unit equipped with 0.16  $\mu\text{m}$  membrane filter with appropriate surface area (e.g., Filtron), equilibrated with 40 mM sodium acetate, pH 6.0 is employed. The filtered sample is loaded onto a cation exchange resin (e.g., Poros HS-50, Perseptive Biosystems). The column is washed with 40 mM sodium acetate, pH 6.0 and eluted with 250 mM, 500 mM, 1000 mM, and 1500 mM NaCl in the same buffer, in a stepwise manner. The absorbance at 280 nm of the effluent is continuously monitored. Fractions are collected and further analyzed by SDS-PAGE.

Fractions containing the polypeptide are then pooled and mixed with 4 volumes of water. The diluted sample is then loaded onto a previously prepared set of tandem columns of strong anion (Poros HQ-50, Perseptive Biosystems) and weak anion (Poros CM-20, Perseptive Biosystems) exchange resins. The columns are equilibrated with 40 mM sodium acetate, pH 6.0. Both columns are washed with 40 mM sodium acetate, pH 6.0, 200 mM NaCl. The CM-20 column is then eluted using a 10 column volume linear gradient ranging from 0.2 M NaCl, 50 mM sodium acetate, pH 6.0 to 1.0 M NaCl, 50 mM sodium acetate, pH 6.5. Fractions are collected under constant  $A_{280}$  monitoring of the effluent. Fractions containing the polypeptide (determined, for instance, by 16% SDS-PAGE) are then pooled.

The resultant polypeptide should exhibit greater than 95% purity after the above refolding and purification steps. No major contaminant bands should be observed from Commassie blue stained 16% SDS-PAGE gel when 5  $\mu\text{g}$  of purified protein is loaded. The purified protein can also be tested for endotoxin/LPS contamination, and typically the LPS content is less than 0.1 ng/ml according to LAL assays.

*Example 7: Cloning and Expression of a Polypeptide in a Baculovirus Expression System*

25

In this example, the plasmid shuttle vector pA2 is used to insert a polynucleotide into a baculovirus to express a polypeptide. This expression vector contains the strong polyhedrin promoter of the *Autographa californica* nuclear polyhedrosis virus (AcMNPV) followed by convenient restriction sites such as BamHI, Xba I and Asp718. The polyadenylation site of the simian virus 40 ("SV40") is used for efficient polyadenylation. For easy selection of recombinant virus, the plasmid contains the beta-galactosidase gene from *E. coli* under control of a weak *Drosophila* promoter in the same orientation, followed by the

polyadenylation signal of the polyhedrin gene. The inserted genes are flanked on both sides by viral sequences for cell-mediated homologous recombination with wild-type viral DNA to generate a viable virus that express the cloned polynucleotide.

Many other baculovirus vectors can be used in place of the vector above, such as pAc373, pVL941, and pAcIM1, as one skilled in the art would readily appreciate, as long as the construct provides appropriately located signals for transcription, translation, secretion and the like, including a signal peptide and an in-frame AUG as required. Such vectors are described, for instance, in Luckow et al., *Virology* 170:31-39 (1989).

Specifically, the cDNA sequence contained in the deposited clone, including the AUG initiation codon, is amplified using the PCR protocol described in Example 1. If a naturally occurring signal sequence is used to produce the polypeptide of the present invention, the pA2 vector does not need a second signal peptide. Alternatively, the vector can be modified (pA2 GP) to include a baculovirus leader sequence, using the standard methods described in Summers et al., "A Manual of Methods for Baculovirus Vectors and Insect Cell Culture Procedures," Texas Agricultural Experimental Station Bulletin No. 1555 (1987).

The amplified fragment is isolated from a 1% agarose gel using a commercially available kit ("GeneClean," BIO 101 Inc., La Jolla, Ca.). The fragment then is digested with appropriate restriction enzymes and again purified on a 1% agarose gel.

The plasmid is digested with the corresponding restriction enzymes and optionally, can be dephosphorylated using calf intestinal phosphatase, using routine procedures known in the art. The DNA is then isolated from a 1% agarose gel using a commercially available kit ("GeneClean" BIO 101 Inc., La Jolla, Ca.).

The fragment and the dephosphorylated plasmid are ligated together with T4 DNA ligase. *E. coli* HB101 or other suitable *E. coli* hosts such as XL-1 Blue (Stratagene Cloning Systems, La Jolla, CA) cells are transformed with the ligation mixture and spread on culture plates. Bacteria containing the plasmid are identified by digesting DNA from individual colonies and analyzing the digestion product by gel electrophoresis. The sequence of the cloned fragment is confirmed by DNA sequencing.

Five µg of a plasmid containing the polynucleotide is co-transfected with 1.0 µg of a commercially available linearized baculovirus DNA ("BaculoGold™ baculovirus DNA", Pharmingen, San Diego, CA), using the lipofection method described by Felgner et al., *Proc.*



Natl. Acad. Sci. USA 84:7413-7417 (1987). One  $\mu\text{g}$  of BaculoGold™ virus DNA and 5  $\mu\text{g}$  of the plasmid are mixed in a sterile well of a microtiter plate containing 50  $\mu\text{l}$  of serum-free Grace's medium (Life Technologies Inc., Gaithersburg, MD). Afterwards, 10  $\mu\text{l}$  Lipofectin plus 90  $\mu\text{l}$  Grace's medium are added, mixed and incubated for 15 minutes at room temperature. Then the transfection mixture is added drop-wise to Sf9 insect cells (ATCC CRL 1711) seeded in a 35 mm tissue culture plate with 1 ml Grace's medium without serum. The plate is then incubated for 5 hours at 27° C. The transfection solution is then removed from the plate and 1 ml of Grace's insect medium supplemented with 10% fetal calf serum is added. Cultivation is then continued at 27° C for four days.

After four days the supernatant is collected and a plaque assay is performed, as described by Summers and Smith, *supra*. An agarose gel with "Blue Gal" (Life Technologies Inc., Gaithersburg) is used to allow easy identification and isolation of gal-expressing clones, which produce blue-stained plaques. (A detailed description of a "plaque assay" of this type can also be found in the user's guide for insect cell culture and baculovirology distributed by Life Technologies Inc., Gaithersburg, page 9-10.) After appropriate incubation, blue stained plaques are picked with the tip of a micropipettor (e.g., Eppendorf). The agar containing the recombinant viruses is then resuspended in a microcentrifuge tube containing 200  $\mu\text{l}$  of Grace's medium and the suspension containing the recombinant baculovirus is used to infect Sf9 cells seeded in 35 mm dishes. Four days later the supernatants of these culture dishes are harvested and then they are stored at 4° C.

To verify the expression of the polypeptide, Sf9 cells are grown in Grace's medium supplemented with 10% heat-inactivated FBS. The cells are infected with the recombinant baculovirus containing the polynucleotide at a multiplicity of infection ("MOI") of about 2. If radiolabeled proteins are desired, 6 hours later the medium is removed and is replaced with SF900 II medium minus methionine and cysteine (available from Life Technologies Inc., Rockville, MD). After 42 hours, 5  $\mu\text{Ci}$  of  $^{35}\text{S}$ -methionine and 5  $\mu\text{Ci}$   $^{35}\text{S}$ -cysteine (available from Amersham) are added. The cells are further incubated for 16 hours and then are harvested by centrifugation. The proteins in the supernatant as well as the intracellular proteins are analyzed by SDS-PAGE followed by autoradiography (if radiolabeled).

Microsequencing of the amino acid sequence of the amino terminus of purified protein may be used to determine the amino terminal sequence of the produced protein.

*Example 8: Expression of a Polypeptide in Mammalian Cells*

The polypeptide of the present invention can be expressed in a mammalian cell. A typical mammalian expression vector contains a promoter element, which mediates the initiation of transcription of mRNA, a protein coding sequence, and signals required for the termination of transcription and polyadenylation of the transcript. Additional elements include enhancers, Kozak sequences and intervening sequences flanked by donor and acceptor sites for RNA splicing. Highly efficient transcription is achieved with the early and late promoters from SV40, the long terminal repeats (LTRs) from Retroviruses, e.g., RSV, HTLV, HIV and the early promoter of the cytomegalovirus (CMV). However, cellular elements can also be used (e.g., the human actin promoter).

Suitable expression vectors for use in practicing the present invention include, for example, vectors such as pSVL and pMSG (Pharmacia, Uppsala, Sweden), pRSVcat (ATCC 37152), pSV2dhfr (ATCC 37146), pBC12MI (ATCC 67109), pCMVSPORT 2.0, and pCMVSPORT 3.0. Mammalian host cells that could be used include, human Hela, 293, H9 and Jurkat cells, mouse NIH3T3 and C127 cells, Cos 1, Cos 7 and CV1, quail QC1-3 cells, mouse L cells and Chinese hamster ovary (CHO) cells.

Alternatively, the polypeptide can be expressed in stable cell lines containing the polynucleotide integrated into a chromosome. The co-transfection with a selectable marker such as DHFR, gpt, neomycin, hygromycin allows the identification and isolation of the transfected cells.

The transfected gene can also be amplified to express large amounts of the encoded protein. The DHFR (dihydrofolate reductase) marker is useful in developing cell lines that carry several hundred or even several thousand copies of the gene of interest. (See, e.g., Alt, F. W., et al., J. Biol. Chem. 253:1357-1370 (1978); Hamlin, J. L. and Ma, C., Biochem. et Biophys. Acta, 1097:107-143 (1990); Page, M. J. and Sydenham, M. A., Biotechnology 9:64-68 (1991).) Another useful selection marker is the enzyme glutamine synthase (GS) (Murphy et al., Biochem J. 227:277-279 (1991); Bebbington et al., Bio/Technology 10:169-175 (1992). Using these markers, the mammalian cells are grown in selective medium and the cells with the highest resistance are selected. These cell lines contain the amplified gene(s) integrated into a chromosome. Chinese hamster ovary (CHO) and NSO cells are often used for the production of proteins.

Derivatives of the plasmid pSV2-dhfr (ATCC Accession No. 37146), the expression vectors pC4 (ATCC Accession No. 209646) and pC6 (ATCC Accession No. 209647) contain the strong promoter (LTR) of the Rous Sarcoma Virus (Cullen et al., Molecular and Cellular Biology, 438-447 (March, 1985)) plus a fragment of the CMV-enhancer (Boshart et al., Cell 5 41:521-530 (1985).) Multiple cloning sites, e.g., with the restriction enzyme cleavage sites BamHI, XbaI and Asp718, facilitate the cloning of the gene of interest. The vectors also contain the 3' intron, the polyadenylation and termination signal of the rat preproinsulin gene, and the mouse DHFR gene under control of the SV40 early promoter.

Specifically, the plasmid pC6, for example, is digested with appropriate restriction 10 enzymes and then dephosphorylated using calf intestinal phosphates by procedures known in the art. The vector is then isolated from a 1% agarose gel.

A polynucleotide of the present invention is amplified according to the protocol outlined in Example 1. If a naturally occurring signal sequence is used to produce the polypeptide of the present invention, the vector does not need a second signal peptide. 15 Alternatively, if a naturally occurring signal sequence is not used, the vector can be modified to include a heterologous signal sequence. (See, e.g., WO 96/34891.)

The amplified fragment is isolated from a 1% agarose gel using a commercially available kit ("GeneClean," BIO 101 Inc., La Jolla, Ca.). The fragment then is digested with appropriate restriction enzymes and again purified on a 1% agarose gel.

20 The amplified fragment is then digested with the same restriction enzyme and purified on a 1% agarose gel. The isolated fragment and the dephosphorylated vector are then ligated with T4 DNA ligase. *E. coli* HB101 or XL-1 Blue cells are then transformed and bacteria are identified that contain the fragment inserted into plasmid pC6 using, for instance, restriction enzyme analysis.

25 Chinese hamster ovary cells lacking an active DHFR gene is used for transfection. Five  $\mu$ g of the expression plasmid pC6 or pC4 is cotransfected with 0.5  $\mu$ g of the plasmid pSVneo using lipofectin (Felgner et al., *supra*). The plasmid pSV2-neo contains a dominant selectable marker, the *neo* gene from Tn5 encoding an enzyme that confers resistance to a group of antibiotics including G418. The cells are seeded in alpha minus MEM 30 supplemented with 1 mg/ml G418. After 2 days, the cells are trypsinized and seeded in hybridoma cloning plates (Greiner, Germany) in alpha minus MEM supplemented with 10, 25, or 50 ng/ml of methotrexate plus 1 mg/ml G418. After about 10-14 days single clones

are trypsinized and then seeded in 6-well petri dishes or 10 ml flasks using different concentrations of methotrexate (50 nM, 100 nM, 200 nM, 400 nM, 800 nM). Clones growing at the highest concentrations of methotrexate are then transferred to new 6-well plates containing even higher concentrations of methotrexate (1  $\mu$ M, 2  $\mu$ M, 5  $\mu$ M, 10 mM, 20 mM). The same procedure is repeated until clones are obtained which grow at a concentration of 100 - 200  $\mu$ M. Expression of the desired gene product is analyzed, for instance, by SDS-PAGE and Western blot or by reversed phase HPLC analysis.

*Example 9: Protein Fusions*

10

The polypeptides of the present invention are preferably fused to other proteins. These fusion proteins can be used for a variety of applications. For example, fusion of the present polypeptides to His-tag, HA-tag, protein A, IgG domains, and maltose binding protein facilitates purification. (See Example 5; see also EP A 394,827; Traunecker, et al., Nature 331:84-86 (1988).) Similarly, fusion to IgG-1, IgG-3, and albumin increases the half-life time in vivo. Nuclear localization signals fused to the polypeptides of the present invention can target the protein to a specific subcellular localization, while covalent heterodimer or homodimers can increase or decrease the activity of a fusion protein. Fusion proteins can also create chimeric molecules having more than one function. Finally, fusion proteins can increase solubility and/or stability of the fused protein compared to the non-fused protein. All of the types of fusion proteins described above can be made by modifying the following protocol, which outlines the fusion of a polypeptide to an IgG molecule, or the protocol described in Example 5.

20

Briefly, the human Fc portion of the IgG molecule can be PCR amplified, using primers that span the 5' and 3' ends of the sequence described below. These primers also should have convenient restriction enzyme sites that will facilitate cloning into an expression vector, preferably a mammalian expression vector.

25

For example, if pC4 (Accession No. 209646) is used, the human Fc portion can be ligated into the BamHI cloning site. Note that the 3' BamHI site should be destroyed. Next, the vector containing the human Fc portion is re-restricted with BamHI, linearizing the vector, and a polynucleotide of the present invention, isolated by the PCR protocol described in Example 1, is ligated into this BamHI site. Note that the polynucleotide is cloned without

30

a stop codon, otherwise a fusion protein will not be produced.

If the naturally occurring signal sequence is used to produce the polypeptide of the present invention, pC4 does not need a second signal peptide. Alternatively, if the naturally occurring signal sequence is not used, the vector can be modified to include a heterologous signal sequence. (See, e.g., WO 96/34891.)

Human IgG Fc region:

```
GGGATCCGGAGCCCAAATCTTCTGACAAACTCACACATGCCCACCGTGCCCAG
CACCTGAATTCGAGGGTGCACCGTCAGTCTTCTCTTCCCCCAAAACCCAAGGA
10 CACCTCATGATCTCCCGGACTCCTGAGGTACATGCGTGGTGGTGGACGTAAGC
CACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCAT
AATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTC
AGCGTCTCACCCTGCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGC
AAGGTCTCCAACAAAGCCCTCCCAACCCCCATCGAGAAAACCATCTCCAAAGCC
15 AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAG
CTGACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCAAGC
GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGAC
CACGCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACC
GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT
20 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAT
GAGTGCGACGGCCGCGACTCTAGAGGAT (SEQ ID NO:1547)
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*Example 10: Production of an Antibody from a Polypeptide*

**25 a) Hybridoma Technology**

The antibodies of the present invention can be prepared by a variety of methods. (See, Current Protocols, Chapter 2.) As one example of such methods, cells expressing polypeptide of the present invention are administered to an animal to induce the production of sera containing polyclonal antibodies. In a preferred method, a preparation of polypeptide of the present invention is prepared and purified to render it substantially free of natural contaminants. Such a preparation is then introduced into an animal in order to produce polyclonal antisera of greater specific activity.

Monoclonal antibodies specific for polypeptide of the present invention are prepared using hybridoma technology. (Kohler et al., *Nature* 256:495 (1975); Kohler et al., *Eur. J. Immunol.* 6:511 (1976); Kohler et al., *Eur. J. Immunol.* 6:292 (1976); Hammerling et al., in: *Monoclonal Antibodies and T-Cell Hybridomas*, Elsevier, N.Y., pp. 563-681 (1981)). In  
5 general, an animal (preferably a mouse) is immunized with polypeptide of the present invention or, more preferably, with a secreted polypeptide of the present invention-expressing cell. Such polypeptide-expressing cells are cultured in any suitable tissue culture medium, preferably in Earle's modified Eagle's medium supplemented with 10% fetal bovine serum (inactivated at about 56°C), and supplemented with about 10 g/l of nonessential amino  
10 acids, about 1,000 U/ml of penicillin, and about 100 µg/ml of streptomycin.

The splenocytes of such mice are extracted and fused with a suitable myeloma cell line. Any suitable myeloma cell line may be employed in accordance with the present invention; however, it is preferable to employ the parent myeloma cell line (SP2O), available from the ATCC. After fusion, the resulting hybridoma cells are selectively maintained in  
15 HAT medium, and then cloned by limiting dilution as described by Wands et al. (*Gastroenterology* 80:225-232 (1981)). The hybridoma cells obtained through such a selection are then assayed to identify clones which secrete antibodies capable of binding the polypeptide of the present invention.

Alternatively, additional antibodies capable of binding to polypeptide of the present  
20 invention can be produced in a two-step procedure using anti-idiotypic antibodies. Such a method makes use of the fact that antibodies are themselves antigens, and therefore, it is possible to obtain an antibody which binds to a second antibody. In accordance with this method, protein specific antibodies are used to immunize an animal, preferably a mouse. The splenocytes of such an animal are then used to produce hybridoma cells, and the hybridoma  
25 cells are screened to identify clones which produce an antibody whose ability to bind to the polypeptide of the present invention-specific antibody can be blocked by polypeptide of the present invention. Such antibodies comprise anti-idiotypic antibodies to the polypeptide of the present invention-specific antibody and are used to immunize an animal to induce formation of further polypeptide of the present invention-specific antibodies.

30 For in vivo use of antibodies in humans, an antibody is "humanized". Such antibodies can be produced using genetic constructs derived from hybridoma cells producing the monoclonal antibodies described above. Methods for producing chimeric and humanized

antibodies are known in the art and are discussed herein. (See, for review, Morrison. Science 229:1202 (1985); Oi et al., BioTechniques 4:214 (1986); Cabilly et al., U.S. Patent No. 4,816,567; Taniguchi et al., EP 171496; Morrison et al., EP 173494; Neuberger et al., WO 8601533; Robinson et al., WO 8702671; Boulianne et al., Nature 312:643 (1984); Neuberger et al., Nature 314:268 (1985).)

**b) Isolation Of Antibody Fragments Directed Against Polypeptide of the Present Invention From A Library Of scFvs**

Naturally occurring V-genes isolated from human PBLs are constructed into a library of antibody fragments which contain reactivities against polypeptide of the present invention to which the donor may or may not have been exposed (see e.g., U.S. Patent 5,885,793 incorporated herein by reference in its entirety).

*Rescue of the Library.* A library of scFvs is constructed from the RNA of human PBLs as described in PCT publication WO 92/01047. To rescue phage displaying antibody fragments, approximately 10<sup>9</sup> E. coli harboring the phagemid are used to inoculate 50 ml of 2xTY containing 1% glucose and 100 µg/ml of ampicillin (2xTY-AMP-GLU) and grown to an O.D. of 0.8 with shaking. Five ml of this culture is used to inoculate 50 ml of 2xTY-AMP-GLU, 2 x 10<sup>8</sup> TU of delta gene 3 helper (M13 delta gene III, see PCT publication WO 92/01047) are added and the culture incubated at 37°C for 45 minutes without shaking and then at 37°C for 45 minutes with shaking. The culture is centrifuged at 4000 r.p.m. for 10 min. and the pellet resuspended in 2 liters of 2xTY containing 100 µg/ml ampicillin and 50 µg/ml kanamycin and grown overnight. Phage are prepared as described in PCT publication WO 92/01047.

M13 delta gene III is prepared as follows: M13 delta gene III helper phage does not encode gene III protein, hence the phage(mid) displaying antibody fragments have a greater avidity of binding to antigen. Infectious M13 delta gene III particles are made by growing the helper phage in cells harboring a pUC19 derivative supplying the wild type gene III protein during phage morphogenesis. The culture is incubated for 1 hour at 37° C without shaking and then for a further hour at 37°C with shaking. Cells are spun down (IEC-Centra 8,400 r.p.m. for 10 min), resuspended in 300 ml 2xTY broth containing 100 µg ampicillin/ml and 25 µg kanamycin/ml (2xTY-AMP-KAN) and grown overnight, shaking at 37°C. Phage particles are purified and concentrated from the culture medium by two PEG-precipitations

(Sambrook et al., 1990), resuspended in 2 ml PBS and passed through a 0.45  $\mu$ m filter (Minisart NML; Sartorius) to give a final concentration of approximately 10<sup>13</sup> transducing units/ml (ampicillin-resistant clones).

*Panning of the Library.* Immunotubes (Nunc) are coated overnight in PBS with 4 ml of either 100  $\mu$ g/ml or 10  $\mu$ g/ml of a polypeptide of the present invention. Tubes are blocked with 2% Marvel-PBS for 2 hours at 37°C and then washed 3 times in PBS. Approximately 10<sup>13</sup> TU of phage is applied to the tube and incubated for 30 minutes at room temperature tumbling on an over and under turntable and then left to stand for another 1.5 hours. Tubes are washed 10 times with PBS 0.1% Tween-20 and 10 times with PBS. Phage are eluted by adding 1 ml of 100 mM triethylamine and rotating 15 minutes on an under and over turntable after which the solution is immediately neutralized with 0.5 ml of 1.0M Tris-HCl, pH 7.4. Phage are then used to infect 10 ml of mid-log E. coli TG1 by incubating eluted phage with bacteria for 30 minutes at 37°C. The E. coli are then plated on TYE plates containing 1% glucose and 100  $\mu$ g/ml ampicillin. The resulting bacterial library is then rescued with delta gene 3 helper phage as described above to prepare phage for a subsequent round of selection. This process is then repeated for a total of 4 rounds of affinity purification with tube-washing increased to 20 times with PBS, 0.1% Tween-20 and 20 times with PBS for rounds 3 and 4.

*Characterization of Binders.* Eluted phage from the 3rd and 4th rounds of selection are used to infect E. coli HB 2151 and soluble scFv is produced (Marks, et al., 1991) from single colonies for assay. ELISAs are performed with microtitre plates coated with either 10  $\mu$ g/ml of the polypeptide of the present invention in 50 mM bicarbonate pH 9.6. Clones positive in ELISA are further characterized by PCR fingerprinting (see, e.g., PCT publication WO 92/01047) and then by sequencing. These ELISA positive clones may also be further characterized by techniques known in the art, such as, for example, epitope mapping, binding affinity, receptor signal transduction, ability to block or competitively inhibit antibody/antigen binding, and competitive agonistic or antagonistic activity.

*Example 11: Method of Determining Alterations in a Gene Corresponding to a Polynucleotide*

30

RNA isolated from entire families or individual patients presenting with a phenotype of interest (such as a disease) is isolated. cDNA is then generated from these RNA



samples using protocols known in the art. (See, Sambrook.) The cDNA is then used as a template for PCR, employing primers surrounding regions of interest in SEQ ID NO:X; and/or the nucleotide sequence of the related cDNA in the cDNA clone contained in a deposited library. Suggested PCR conditions consist of 35 cycles at 95 degrees C for 30  
5 seconds; 60-120 seconds at 52-58 degrees C; and 60-120 seconds at 70 degrees C, using buffer solutions described in Sidransky et al., Science 252:706 (1991).

PCR products are then sequenced using primers labeled at their 5' end with T4 polynucleotide kinase, employing SequiTherm Polymerase. (Epicentre Technologies). The intron-exon borders of selected exons is also determined and genomic PCR products  
10 analyzed to confirm the results. PCR products harboring suspected mutations is then cloned and sequenced to validate the results of the direct sequencing.

PCR products is cloned into T-tailed vectors as described in Holton et al., Nucleic Acids Research, 19:1156 (1991) and sequenced with T7 polymerase (United States Biochemical). Affected individuals are identified by mutations not present in unaffected  
15 individuals.

Genomic rearrangements are also observed as a method of determining alterations in a gene corresponding to a polynucleotide. Genomic clones isolated according to Example 2 are nick-translated with digoxigenin deoxy-uridine 5'-triphosphate (Boehringer Mannheim), and FISH performed as described in Johnson et al., Methods Cell Biol. 35:73-99 (1991).  
20 Hybridization with the labeled probe is carried out using a vast excess of human cot-1 DNA for specific hybridization to the corresponding genomic locus.

Chromosomes are counterstained with 4,6-diamino-2-phenylidole and propidium iodide, producing a combination of C- and R-bands. Aligned images for precise mapping are obtained using a triple-band filter set (Chroma Technology, Brattleboro, VT) in combination  
25 with a cooled charge-coupled device camera (Photometrics, Tucson, AZ) and variable excitation wavelength filters. (Johnson et al., Genet. Anal. Tech. Appl., 8:75 (1991).) Image collection, analysis and chromosomal fractional length measurements are performed using the ISee Graphical Program System. (Inovision Corporation, Durham, NC.) Chromosome alterations of the genomic region hybridized by the probe are identified as insertions,  
30 deletions, and translocations. These alterations are used as a diagnostic marker for an associated disease.

*Example 12: Method of Detecting Abnormal Levels of a Polypeptide in a Biological Sample*

A polypeptide of the present invention can be detected in a biological sample, and if an increased or decreased level of the polypeptide is detected, this polypeptide is a marker for a particular phenotype. Methods of detection are numerous, and thus, it is understood that one skilled in the art can modify the following assay to fit their particular needs.

For example, antibody-sandwich ELISAs are used to detect polypeptides in a sample, preferably a biological sample. Wells of a microtiter plate are coated with specific antibodies, at a final concentration of 0.2 to 10 ug/ml. The antibodies are either monoclonal or polyclonal and are produced by the method described in Example 10. The wells are blocked so that non-specific binding of the polypeptide to the well is reduced.

The coated wells are then incubated for > 2 hours at RT with a sample containing the polypeptide. Preferably, serial dilutions of the sample should be used to validate results. The plates are then washed three times with deionized or distilled water to remove unbounded polypeptide.

Next, 50 ul of specific antibody-alkaline phosphatase conjugate, at a concentration of 25-400 ng, is added and incubated for 2 hours at room temperature. The plates are again washed three times with deionized or distilled water to remove unbounded conjugate.

Add 75 ul of 4-methylumbelliferyl phosphate (MUP) or p-nitrophenyl phosphate (NPP) substrate solution to each well and incubate 1 hour at room temperature. Measure the reaction by a microtiter plate reader. Prepare a standard curve, using serial dilutions of a control sample, and plot polypeptide concentration on the X-axis (log scale) and fluorescence or absorbance of the Y-axis (linear scale). Interpolate the concentration of the polypeptide in the sample using the standard curve.

*Example 13: Formulation*

The invention also provides methods of treatment and/or prevention of diseases or disorders (such as, for example, any one or more of the diseases or disorders disclosed herein) by administration to a subject of an effective amount of a Therapeutic. By therapeutic is meant a polynucleotides or polypeptides of the invention (including fragments and variants), agonists or antagonists thereof, and/or antibodies thereto, in combination with

a pharmaceutically acceptable carrier type (e.g., a sterile carrier).

The Therapeutic will be formulated and dosed in a fashion consistent with good medical practice, taking into account the clinical condition of the individual patient (especially the side effects of treatment with the Therapeutic alone), the site of delivery, the method of administration, the scheduling of administration, and other factors known to practitioners. The "effective amount" for purposes herein is thus determined by such considerations.

As a general proposition, the total pharmaceutically effective amount of the Therapeutic administered parenterally per dose will be in the range of about 1 µg/kg/day to 10 mg/kg/day of patient body weight, although, as noted above, this will be subject to therapeutic discretion. More preferably, this dose is at least 0.01 mg/kg/day, and most preferably for humans between about 0.01 and 1 mg/kg/day for the hormone. If given continuously, the Therapeutic is typically administered at a dose rate of about 1 µg/kg/hour to about 50 µg/kg/hour, either by 1-4 injections per day or by continuous subcutaneous infusions, for example, using a mini-pump. An intravenous bag solution may also be employed. The length of treatment needed to observe changes and the interval following treatment for responses to occur appears to vary depending on the desired effect.

Therapeutics can be administered orally, rectally, parenterally, intracisternally, intravaginally, intraperitoneally, topically (as by powders, ointments, gels, drops or transdermal patch), buccally, or as an oral or nasal spray. "Pharmaceutically acceptable carrier" refers to a non-toxic solid, semisolid or liquid filler, diluent, encapsulating material or formulation auxiliary of any. The term "parenteral" as used herein refers to modes of administration which include intravenous, intramuscular, intraperitoneal, intrasternal, subcutaneous and intraarticular injection and infusion.

Therapeutics of the invention are also suitably administered by sustained-release systems. Suitable examples of sustained-release Therapeutics are administered orally, rectally, parenterally, intracisternally, intravaginally, intraperitoneally, topically (as by powders, ointments, gels, drops or transdermal patch), buccally, or as an oral or nasal spray. "Pharmaceutically acceptable carrier" refers to a non-toxic solid, semisolid or liquid filler, diluent, encapsulating material or formulation auxiliary of any type. The term "parenteral" as used herein refers to modes of administration which include intravenous, intramuscular, intraperitoneal, intrasternal, subcutaneous and intraarticular injection and infusion.

Therapeutics of the invention are also suitably administered by sustained-release systems. Suitable examples of sustained-release Therapeutics include suitable polymeric materials (such as, for example, semi-permeable polymer matrices in the form of shaped articles, e.g., films, or microcapsules), suitable hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, and sparingly soluble derivatives (such as, for example, a sparingly soluble salt).

Sustained-release matrices include polylactides (U.S. Pat. No. 3,773,919, EP 58,481), copolymers of L-glutamic acid and gamma-ethyl-L-glutamate (Sidman et al., *Biopolymers* 22:547-556 (1983)), poly (2- hydroxyethyl methacrylate) (Langer et al., *J. Biomed. Mater. Res.* 15:167-277 (1981), and Langer, *Chem. Tech.* 12:98-105 (1982)), ethylene vinyl acetate (Langer et al., *Id.*) or poly-D- (-)-3-hydroxybutyric acid (EP 133,988).

Sustained-release Therapeutics also include liposomally entrapped Therapeutics of the invention (*see generally*, Langer, *Science* 249:1527-1533 (1990); Treat et al., in *Liposomes in the Therapy of Infectious Disease and Cancer*, Lopez-Berestein and Fidler (eds.), Liss, New York, pp. 317 -327 and 353-365 (1989)). Liposomes containing the Therapeutic are prepared by methods known per se: DE 3,218,121; Epstein et al., *Proc. Natl. Acad. Sci. (USA)* 82:3688-3692 (1985); Hwang et al., *Proc. Natl. Acad. Sci.(USA)* 77:4030-4034 (1980); EP 52,322; EP 36,676; EP 88,046; EP 143,949; EP 142,641; Japanese Pat. Appl. 83-118008; U.S. Pat. Nos. 4,485,045 and 4,544,545; and EP 102,324. Ordinarily, the liposomes are of the small (about 200-800 Angstroms) unilamellar type in which the lipid content is greater than about 30 mol. percent cholesterol, the selected proportion being adjusted for the optimal Therapeutic.

In yet an additional embodiment, the Therapeutics of the invention are delivered by way of a pump (*see* Langer, *supra*; Sefton, *CRC Crit. Ref. Biomed. Eng.* 14:201 (1987); Buchwald et al., *Surgery* 88:507 (1980); Saudek et al., *N. Engl. J. Med.* 321:574 (1989)).

Other controlled release systems are discussed in the review by Langer (*Science* 249:1527-1533 (1990)).

For parenteral administration, in one embodiment, the Therapeutic is formulated generally by mixing it at the desired degree of purity, in a unit dosage injectable form (solution, suspension, or emulsion), with a pharmaceutically acceptable carrier, i.e., one that is non-toxic to recipients at the dosages and concentrations employed and is compatible with other ingredients of the formulation. For example, the formulation preferably does not

include oxidizing agents and other compounds that are known to be deleterious to the Therapeutic.

Generally, the formulations are prepared by contacting the Therapeutic uniformly and intimately with liquid carriers or finely divided solid carriers or both. Then, if necessary, the product is shaped into the desired formulation. Preferably the carrier is a parenteral carrier, more preferably a solution that is isotonic with the blood of the recipient. Examples of such carrier vehicles include water, saline, Ringer's solution, and dextrose solution. Non-aqueous vehicles such as fixed oils and ethyl oleate are also useful herein, as well as liposomes.

The carrier suitably contains minor amounts of additives such as substances that enhance isotonicity and chemical stability. Such materials are non-toxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, succinate, acetic acid, and other organic acids or their salts; antioxidants such as ascorbic acid; low molecular weight (less than about ten residues) polypeptides, e.g., polyarginine or tripeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids, such as glycine, glutamic acid, aspartic acid, or arginine; monosaccharides, disaccharides, and other carbohydrates including cellulose or its derivatives, glucose, manose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; counterions such as sodium; and/or nonionic surfactants such as polysorbates, poloxamers, or PEG.

The Therapeutic is typically formulated in such vehicles at a concentration of about 0.1 mg/ml to 100 mg/ml, preferably 1-10 mg/ml, at a pH of about 3 to 8. It will be understood that the use of certain of the foregoing excipients, carriers, or stabilizers will result in the formation of polypeptide salts.

Any pharmaceutical used for therapeutic administration can be sterile. Sterility is readily accomplished by filtration through sterile filtration membranes (e.g., 0.2 micron membranes). Therapeutics generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

Therapeutics ordinarily will be stored in unit or multi-dose containers, for example, sealed ampoules or vials, as an aqueous solution or as a lyophilized formulation for reconstitution. As an example of a lyophilized formulation, 10-ml vials are filled with 5 ml of sterile-filtered 1% (w/v) aqueous Therapeutic solution, and the resulting mixture is

lyophilized. The infusion solution is prepared by reconstituting the lyophilized Therapeutic using bacteriostatic Water-for-Injection.

The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the Therapeutics of the invention.

5 Associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration. In addition, the Therapeutics may be employed in conjunction with other therapeutic compounds.

10 The Therapeutics of the invention may be administered alone or in combination with adjuvants. Adjuvants that may be administered with the Therapeutics of the invention include, but are not limited to, alum, alum plus deoxycholate (ImmunoAg), MTP-PE (Biocine Corp.), QS21 (Genentech, Inc.), BCG, and MPL. In a specific embodiment, Therapeutics of the invention are administered in combination with alum. In another specific  
15 embodiment, Therapeutics of the invention are administered in combination with QS-21. Further adjuvants that may be administered with the Therapeutics of the invention include, but are not limited to, Monophosphoryl lipid immunomodulator, AdjuVax 100a, QS-21, QS-18, CRL1005, Aluminum salts, MF-59, and Virosomal adjuvant technology. Vaccines that may be administered with the Therapeutics of the invention include, but are not limited to,  
20 vaccines directed toward protection against MMR (measles, mumps, rubella), polio, varicella, tetanus/diphtheria, hepatitis A, hepatitis B, haemophilus influenzae B, whooping cough, pneumonia, influenza, Lyme's Disease, rotavirus, cholera, yellow fever, Japanese encephalitis, poliomyelitis, rabies, typhoid fever, and pertussis. Combinations may be administered either concomitantly, e.g., as an admixture, separately but simultaneously or  
25 concurrently; or sequentially. This includes presentations in which the combined agents are administered together as a therapeutic mixture, and also procedures in which the combined agents are administered separately but simultaneously, e.g., as through separate intravenous lines into the same individual. Administration "in combination" further includes the separate administration of one of the compounds or agents given first, followed by the second.

30 The Therapeutics of the invention may be administered alone or in combination with other therapeutic agents. Therapeutic agents that may be administered in combination with the Therapeutics of the invention, include but not limited to, other members of the TNF

family, chemotherapeutic agents, antibiotics, steroidal and non-steroidal anti-inflammatories, conventional immunotherapeutic agents, cytokines and/or growth factors. Combinations may be administered either concomitantly, e.g., as an admixture, separately but simultaneously or concurrently; or sequentially. This includes presentations in which the combined agents are administered together as a therapeutic mixture, and also procedures in which the combined agents are administered separately but simultaneously, e.g., as through separate intravenous lines into the same individual. Administration "in combination" further includes the separate administration of one of the compounds or agents given first, followed by the second.

In one embodiment, the Therapeutics of the invention are administered in combination with members of the TNF family. TNF, TNF-related or TNF-like molecules that may be administered with the Therapeutics of the invention include, but are not limited to, soluble forms of TNF-alpha, lymphotoxin-alpha (LT-alpha, also known as TNF-beta), LT-beta (found in complex heterotrimer LT-alpha2-beta), OPGL, FasL, CD27L, CD30L, CD40L, 4-1BBL, DcR3, OX40L, TNF-gamma (International Publication No. WO 96/14328), AIM-1 (International Publication No. WO 97/33899), endokine-alpha (International Publication No. WO 98/07880), TR6 (International Publication No. WO 98/30694), OPG, and neutrokin-alpha (International Publication No. WO 98/18921, OX40, and nerve growth factor (NGF), and soluble forms of Fas, CD30, CD27, CD40 and 4-1BB, TR2 (International Publication No. WO 96/34095), DR3 (International Publication No. WO 97/33904), DR4 (International Publication No. WO 98/32856), TR5 (International Publication No. WO 98/30693), TR6 (International Publication No. WO 98/30694), TR7 (International Publication No. WO 98/41629), TRANK, TR9 (International Publication No. WO 98/56892), TR10 (International Publication No. WO 98/54202), 312C2 (International Publication No. WO 98/06842), and TR12, and soluble forms CD154, CD70, and CD153.

In certain embodiments, Therapeutics of the invention are administered in combination with antiretroviral agents, nucleoside reverse transcriptase inhibitors, non-nucleoside reverse transcriptase inhibitors, and/or protease inhibitors. Nucleoside reverse transcriptase inhibitors that may be administered in combination with the Therapeutics of the invention, include, but are not limited to, RETROVIR™ (zidovudine/AZT), VIDEX™ (didanosine/ddI), HIVID™ (zalcitabine/ddC), ZERIT™ (stavudine/d4T), EPIVIR™ (lamivudine/3TC), and COMBIVIR™ (zidovudine/lamivudine). Non-nucleoside reverse transcriptase inhibitors that may be administered in combination with the Therapeutics of the

invention. include, but are not limited to, VIRAMUNE™ (nevirapine), RESCRIPTOR™ (delavirdine), and SUSTIVA™ (efavirenz). Protease inhibitors that may be administered in combination with the Therapeutics of the invention, include, but are not limited to, CRIXIVAN™ (indinavir), NORVIR™ (ritonavir), INVIRASE™ (saquinavir), and  
5 VIRACEPT™ (nelfinavir). In a specific embodiment, antiretroviral agents, nucleoside reverse transcriptase inhibitors, non-nucleoside reverse transcriptase inhibitors, and/or protease inhibitors may be used in any combination with Therapeutics of the invention to treat AIDS and/or to prevent or treat HIV infection.

In other embodiments, Therapeutics of the invention may be administered in  
10 combination with anti-opportunistic infection agents. Anti-opportunistic agents that may be administered in combination with the Therapeutics of the invention, include, but are not limited to, TRIMETHOPRIM-SULFAMETHOXAZOLE™, DAPSONE™, PENTAMIDINE™, ATOVAQUONE™, ISONIAZID™, RIFAMPIN™, PYRAZINAMIDE™, ETHAMBUTOL™, RIFABUTIN™, CLARITHROMYCIN™, AZITHROMYCIN™,  
15 GANCICLOVIR™, FOSCARNET™, CIDOFOVIR™, FLUCONAZOLE™, ITRACONAZOLE™, KETOCONAZOLE™, ACYCLOVIR™, FAMCICOLVIR™, PYRIMETHAMINE™, LEUCOVORIN™, NEUPOGEN™ (filgrastim/G-CSF), and LEUKINE™ (sargramostim/GM-CSF). In a specific embodiment, Therapeutics of the invention are used in any combination with TRIMETHOPRIM-SULFAMETHOXAZOLE™,  
20 DAPSONE™, PENTAMIDINE™, and/or ATOVAQUONE™ to prophylactically treat or prevent an opportunistic *Pneumocystis carinii* pneumonia infection. In another specific embodiment, Therapeutics of the invention are used in any combination with ISONIAZID™, RIFAMPIN™, PYRAZINAMIDE™, and/or ETHAMBUTOL™ to prophylactically treat or prevent an opportunistic *Mycobacterium avium* complex infection. In another specific  
25 embodiment, Therapeutics of the invention are used in any combination with RIFABUTIN™, CLARITHROMYCIN™, and/or AZITHROMYCIN™ to prophylactically treat or prevent an opportunistic *Mycobacterium tuberculosis* infection. In another specific embodiment, Therapeutics of the invention are used in any combination with GANCICLOVIR™, FOSCARNET™, and/or CIDOFOVIR™ to prophylactically treat or prevent an opportunistic  
30 cytomegalovirus infection. In another specific embodiment, Therapeutics of the invention are used in any combination with FLUCONAZOLE™, ITRACONAZOLE™, and/or



KETOCONAZOLE™ to prophylactically treat or prevent an opportunistic fungal infection. In another specific embodiment, Therapeutics of the invention are used in any combination with ACYCLOVIR™ and/or FAMCICOLVIR™ to prophylactically treat or prevent an opportunistic herpes simplex virus type I and/or type II infection. In another specific  
5 embodiment, Therapeutics of the invention are used in any combination with PYRIMETHAMINE™ and/or LEUCOVORIN™ to prophylactically treat or prevent an opportunistic *Toxoplasma gondii* infection. In another specific embodiment, Therapeutics of the invention are used in any combination with LEUCOVORIN™ and/or NEUPOGEN™ to prophylactically treat or prevent an opportunistic bacterial infection.

10 In a further embodiment, the Therapeutics of the invention are administered in combination with an antiviral agent. Antiviral agents that may be administered with the Therapeutics of the invention include, but are not limited to, acyclovir, ribavirin, amantadine, and remantidine.

In a further embodiment, the Therapeutics of the invention are administered in  
15 combination with an antibiotic agent. Antibiotic agents that may be administered with the Therapeutics of the invention include, but are not limited to, amoxicillin, beta-lactamases, aminoglycosides, beta-lactam (glycopeptide), beta-lactamases, Clindamycin, chloramphenicol, cephalosporins, ciprofloxacin, ciprofloxacin, erythromycin, fluoroquinolones, macrolides, metronidazole, penicillins, quinolones, rifampin, streptomycin,  
20 sulfonamide, tetracyclines, trimethoprim, trimethoprim-sulfamthoxazole, and vancomycin.

Conventional nonspecific immunosuppressive agents, that may be administered in combination with the Therapeutics of the invention include, but are not limited to, steroids, cyclosporine, cyclosporine analogs, cyclophosphamide methylprednisone, prednisone, azathioprine, FK-506, 15-deoxyspergualin, and other immunosuppressive agents that act by  
25 suppressing the function of responding T cells.

In specific embodiments, Therapeutics of the invention are administered in combination with immunosuppressants. Immunosuppressants preparations that may be administered with the Therapeutics of the invention include, but are not limited to, ORTHOCLONE™ (OKT3), SANDIMMUNE™/NEORAL™/SANGDYA™ (cyclosporin),  
30 PROGRAF™ (tacrolimus), CELLCEPT™ (mycophenolate), Azathioprine, glucocorticosteroids, and RAPAMUNE™ (sirolimus). In a specific embodiment, immunosuppressants may be

used to prevent rejection of organ or bone marrow transplantation.

In an additional embodiment, Therapeutics of the invention are administered alone or in combination with one or more intravenous immune globulin preparations. Intravenous immune globulin preparations that may be administered with the Therapeutics of the invention include, but not limited to, GAMMAR™, IVEEGAM™, SANDOGLOBULIN™, 5 GAMMAGARD S/D™, and GAMIMUNE™. In a specific embodiment, Therapeutics of the invention are administered in combination with intravenous immune globulin preparations in transplantation therapy (e.g., bone marrow transplant).

In an additional embodiment, the Therapeutics of the invention are administered alone 10 or in combination with an anti-inflammatory agent. Anti-inflammatory agents that may be administered with the Therapeutics of the invention include, but are not limited to, glucocorticoids and the nonsteroidal anti-inflammatories, aminoarylcarboxylic acid derivatives, arylacetic acid derivatives, arylbutyric acid derivatives, arylcarboxylic acids, arylpropionic acid derivatives, pyrazoles, pyrazolones, salicylic acid derivatives, 15 thiazinecarboxamides, e-acetamidocaproic acid, S-adenosylmethionine, 3-amino-4-hydroxybutyric acid, amixetrine, bendazac, benzydamine, bucolome, difenpiramide, ditazol, emorfazone, guaiazulene, nabumetone, nimesulide, orgotein, oxaceprol, paranyline, perisoxal, pifoxime, proquazone, proxazole, and tenidap.

In another embodiment, compositions of the invention are administered in 20 combination with a chemotherapeutic agent. Chemotherapeutic agents that may be administered with the Therapeutics of the invention include, but are not limited to, antibiotic derivatives (e.g., doxorubicin, bleomycin, daunorubicin, and dactinomycin); antiestrogens (e.g., tamoxifen); antimetabolites (e.g., fluorouracil, 5-FU, methotrexate, floxuridine, interferon alpha-2b, glutamic acid, plicamycin, mercaptopurine, and 6-thioguanine); 25 cytotoxic agents (e.g., carmustine, BCNU, lomustine, CCNU, cytosine arabinoside, cyclophosphamide, estramustine, hydroxyurea, procarbazine, mitomycin, busulfan, cis-platin, and vincristine sulfate); hormones (e.g., medroxyprogesterone, estramustine phosphate sodium, ethinyl estradiol, estradiol, megestrol acetate, methyltestosterone, diethylstilbestrol diphosphate, chlorotrianisene, and testolactone); nitrogen mustard derivatives (e.g., 30 mephalen, chorambucil, mechlorethamine (nitrogen mustard) and thiotepa); steroids and combinations (e.g., bethamethasone sodium phosphate); and others (e.g., dicarbazine, asparaginase, mitotane, vincristine sulfate, vinblastine sulfate, and etoposide).

In a specific embodiment, Therapeutics of the invention are administered in combination with CHOP (cyclophosphamide, doxorubicin, vincristine, and prednisone) or any combination of the components of CHOP. In another embodiment, Therapeutics of the invention are administered in combination with Rituximab. In a further embodiment, 5 Therapeutics of the invention are administered with Rituximab and CHOP, or Rituximab and any combination of the components of CHOP.

In an additional embodiment, the Therapeutics of the invention are administered in combination with cytokines. Cytokines that may be administered with the Therapeutics of the invention include, but are not limited to, IL2, IL3, IL4, IL5, IL6, IL7, IL10, IL12, IL13, 10 IL15, anti-CD40, CD40L, IFN-gamma and TNF-alpha. In another embodiment, Therapeutics of the invention may be administered with any interleukin, including, but not limited to, IL-1alpha, IL-1beta, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IL-16, IL-17, IL-18, IL-19, IL-20, and IL-21.

In an additional embodiment, the Therapeutics of the invention are administered in 15 combination with angiogenic proteins. Angiogenic proteins that may be administered with the Therapeutics of the invention include, but are not limited to, Glioma Derived Growth Factor (GDGF), as disclosed in European Patent Number EP-399816; Platelet Derived Growth Factor-A (PDGF-A), as disclosed in European Patent Number EP-682110; Platelet Derived Growth Factor-B (PDGF-B), as disclosed in European Patent Number EP-282317; 20 Placental Growth Factor (PlGF), as disclosed in International Publication Number WO 92/06194; Placental Growth Factor-2 (PlGF-2), as disclosed in Hauser et al., Growth Factors, 4:259-268 (1993); Vascular Endothelial Growth Factor (VEGF), as disclosed in International Publication Number WO 90/13649; Vascular Endothelial Growth Factor-A (VEGF-A), as disclosed in European Patent Number EP-506477; Vascular Endothelial Growth Factor-2 25 (VEGF-2), as disclosed in International Publication Number WO 96/39515; Vascular Endothelial Growth Factor B (VEGF-3); Vascular Endothelial Growth Factor B-186 (VEGF-B186), as disclosed in International Publication Number WO 96/26736; Vascular Endothelial Growth Factor-D (VEGF-D), as disclosed in International Publication Number WO 98/02543; Vascular Endothelial Growth Factor-D (VEGF-D), as disclosed in International 30 Publication Number WO 98/07832; and Vascular Endothelial Growth Factor-E (VEGF-E), as disclosed in German Patent Number DE19639601. The above mentioned references are incorporated herein by reference herein.

In an additional embodiment, the Therapeutics of the invention are administered in combination with hematopoietic growth factors. Hematopoietic growth factors that may be administered with the Therapeutics of the invention include, but are not limited to, LEUKINE™ (SARGRAMOSTIM™) and NEUPOGEN™ (FILGRASTIM™).

5 In an additional embodiment, the Therapeutics of the invention are administered in combination with Fibroblast Growth Factors. Fibroblast Growth Factors that may be administered with the Therapeutics of the invention include, but are not limited to, FGF-1, FGF-2, FGF-3, FGF-4, FGF-5, FGF-6, FGF-7, FGF-8, FGF-9, FGF-10, FGF-11, FGF-12, FGF-13, FGF-14, and FGF-15.

10 In additional embodiments, the Therapeutics of the invention are administered in combination with other therapeutic or prophylactic regimens, such as, for example, radiation therapy.

*Example 14: Method of Treating Decreased Levels of the Polypeptide*

15

The present invention relates to a method for treating an individual in need of an increased level of a polypeptide of the invention in the body comprising administering to such an individual a composition comprising a therapeutically effective amount of an agonist of the invention (including polypeptides of the invention). Moreover, it will be appreciated that conditions caused by a decrease in the standard or normal expression level of a polypeptide of the present invention in an individual can be treated by administering the agonist or antagonist of the present invention. Thus, the invention also provides a method of treatment of an individual in need of an increased level of the polypeptide comprising administering to such an individual a Therapeutic comprising an amount of the agonist or antagonist to increase the activity level of the polypeptide in such an individual.

20 25 For example, a patient with decreased levels of a polypeptide receives a daily dose 0.1-100 ug/kg of the agonist or antagonist for six consecutive days. The exact details of the dosing scheme, based on administration and formulation, are provided in Example 13.

30 *Example 15: Method of Treating Increased Levels of the Polypeptide*

The present invention also relates to a method of treating an individual in need of a

decreased level of a polypeptide of the invention in the body comprising administering to such an individual a composition comprising a therapeutically effective amount of an antagonist of the invention (including polypeptides and antibodies of the invention).

5 In one example, antisense technology is used to inhibit production of a polypeptide of the present invention. This technology is one example of a method of decreasing levels of a polypeptide, due to a variety of etiologies, such as cancer.

For example, a patient diagnosed with abnormally increased levels of a polypeptide is administered intravenously antisense polynucleotides at 0.5, 1.0, 1.5, 2.0 and 3.0 mg/kg day for 21 days. This treatment is repeated after a 7-day rest period if the treatment was well  
10 tolerated. The formulation of the antisense polynucleotide is provided in Example 13.

*Example 16: Method of Treatment Using Gene Therapy-Ex Vivo*

One method of gene therapy transplants fibroblasts, which are capable of expressing a  
15 polypeptide, onto a patient. Generally, fibroblasts are obtained from a subject by skin biopsy. The resulting tissue is placed in tissue-culture medium and separated into small pieces. Small chunks of the tissue are placed on a wet surface of a tissue culture flask, approximately ten pieces are placed in each flask. The flask is turned upside down, closed tight and left at room temperature over night. After 24 hours at room temperature, the flask is inverted and  
20 the chunks of tissue remain fixed to the bottom of the flask and fresh media (e.g., Ham's F12 media, with 10% FBS, penicillin and streptomycin) is added. The flasks are then incubated at 37 degree C for approximately one week.

At this time, fresh media is added and subsequently changed every several days. After an additional two weeks in culture, a monolayer of fibroblasts emerge. The monolayer  
25 is trypsinized and scaled into larger flasks.

pMV-7 (Kirschmeier, P.T. et al., DNA, 7:219-25 (1988)), flanked by the long terminal repeats of the Moloney murine sarcoma virus, is digested with EcoRI and HindIII and subsequently treated with calf intestinal phosphatase. The linear vector is fractionated on agarose gel and purified, using glass beads.

30 The cDNA encoding a polypeptide of the present invention can be amplified using PCR primers which correspond to the 5' and 3' end sequences respectively as set forth in Example 1 using primers and having appropriate restriction sites and initiation/stop codons, if

necessary. Preferably, the 5' primer contains an EcoRI site and the 3' primer includes a HindIII site. Equal quantities of the Moloney murine sarcoma virus linear backbone and the amplified EcoRI and HindIII fragment are added together, in the presence of T4 DNA ligase. The resulting mixture is maintained under conditions appropriate for ligation of the two fragments. The ligation mixture is then used to transform bacteria HB101, which are then plated onto agar containing kanamycin for the purpose of confirming that the vector has the gene of interest properly inserted.

The amphotropic pA317 or GP+am12 packaging cells are grown in tissue culture to confluent density in Dulbecco's Modified Eagles Medium (DMEM) with 10% calf serum (CS), penicillin and streptomycin. The MSV vector containing the gene is then added to the media and the packaging cells transduced with the vector. The packaging cells now produce infectious viral particles containing the gene (the packaging cells are now referred to as producer cells).

Fresh media is added to the transduced producer cells, and subsequently, the media is harvested from a 10 cm plate of confluent producer cells. The spent media, containing the infectious viral particles, is filtered through a millipore filter to remove detached producer cells and this media is then used to infect fibroblast cells. Media is removed from a sub-confluent plate of fibroblasts and quickly replaced with the media from the producer cells. This media is removed and replaced with fresh media. If the titer of virus is high, then virtually all fibroblasts will be infected and no selection is required. If the titer is very low, then it is necessary to use a retroviral vector that has a selectable marker, such as neo or his. Once the fibroblasts have been efficiently infected, the fibroblasts are analyzed to determine whether protein is produced.

The engineered fibroblasts are then transplanted onto the host, either alone or after having been grown to confluence on cytodex 3 microcarrier beads.

*Example 17: Gene Therapy Using Endogenous Genes Corresponding To Polynucleotides of the Invention*

Another method of gene therapy according to the present invention involves operably associating the endogenous polynucleotide sequence of the invention with a promoter via homologous recombination as described, for example, in U.S. Patent NO: 5,641,670, issued

June 24, 1997; International Publication NO: WO 96/29411, published September 26, 1996; International Publication NO: WO 94/12650, published August 4, 1994; Koller et al., *Proc. Natl. Acad. Sci. USA*, 86:8932-8935 (1989); and Zijlstra et al., *Nature*, 342:435-438 (1989).

This method involves the activation of a gene which is present in the target cells, but which is  
5 not expressed in the cells, or is expressed at a lower level than desired.

Polynucleotide constructs are made which contain a promoter and targeting sequences, which are homologous to the 5' non-coding sequence of endogenous polynucleotide sequence, flanking the promoter. The targeting sequence will be sufficiently near the 5' end of the polynucleotide sequence so the promoter will be operably linked to the  
10 endogenous sequence upon homologous recombination. The promoter and the targeting sequences can be amplified using PCR. Preferably, the amplified promoter contains distinct restriction enzyme sites on the 5' and 3' ends. Preferably, the 3' end of the first targeting sequence contains the same restriction enzyme site as the 5' end of the amplified promoter and the 5' end of the second targeting sequence contains the same restriction site as the 3' end  
15 of the amplified promoter.

The amplified promoter and the amplified targeting sequences are digested with the appropriate restriction enzymes and subsequently treated with calf intestinal phosphatase. The digested promoter and digested targeting sequences are added together in the presence of T4 DNA ligase. The resulting mixture is maintained under conditions appropriate for  
20 ligation of the two fragments. The construct is size fractionated on an agarose gel then purified by phenol extraction and ethanol precipitation.

In this Example, the polynucleotide constructs are administered as naked polynucleotides via electroporation. However, the polynucleotide constructs may also be administered with transfection-facilitating agents, such as liposomes, viral sequences, viral  
25 particles, precipitating agents, etc. Such methods of delivery are known in the art.

Once the cells are transfected, homologous recombination will take place which results in the promoter being operably linked to the endogenous polynucleotide sequence. This results in the expression of polynucleotide corresponding to the polynucleotide in the cell. Expression may be detected by immunological staining, or any other method known in  
30 the art.

Fibroblasts are obtained from a subject by skin biopsy. The resulting tissue is placed in DMEM + 10% fetal calf serum. Exponentially growing or early stationary phase

fibroblasts are trypsinized and rinsed from the plastic surface with nutrient medium. An aliquot of the cell suspension is removed for counting, and the remaining cells are subjected to centrifugation. The supernatant is aspirated and the pellet is resuspended in 5 ml of electroporation buffer (20 mM HEPES pH 7.3, 137 mM NaCl, 5 mM KCl, 0.7 mM Na<sub>2</sub>HPO<sub>4</sub>, 6 mM dextrose). The cells are recentrifuged, the supernatant aspirated, and the cells resuspended in electroporation buffer containing 1 mg/ml acetylated bovine serum albumin. The final cell suspension contains approximately  $3 \times 10^6$  cells/ml. Electroporation should be performed immediately following resuspension.

Plasmid DNA is prepared according to standard techniques. For example, to construct a plasmid for targeting to the locus corresponding to the polynucleotide of the invention, plasmid pUC18 (MBI Fermentas, Amherst, NY) is digested with HindIII. The CMV promoter is amplified by PCR with an XbaI site on the 5' end and a BamHI site on the 3' end. Two non-coding sequences are amplified via PCR: one non-coding sequence (fragment 1) is amplified with a HindIII site at the 5' end and an Xba site at the 3' end; the other non-coding sequence (fragment 2) is amplified with a BamHI site at the 5' end and a HindIII site at the 3' end. The CMV promoter and the fragments (1 and 2) are digested with the appropriate enzymes (CMV promoter - XbaI and BamHI; fragment 1 - XbaI; fragment 2 - BamHI) and ligated together. The resulting ligation product is digested with HindIII, and ligated with the HindIII-digested pUC18 plasmid.

Plasmid DNA is added to a sterile cuvette with a 0.4 cm electrode gap (Bio-Rad). The final DNA concentration is generally at least 120 µg/ml. 0.5 ml of the cell suspension (containing approximately  $1.5 \times 10^6$  cells) is then added to the cuvette, and the cell suspension and DNA solutions are gently mixed. Electroporation is performed with a Gene-Pulser apparatus (Bio-Rad). Capacitance and voltage are set at 960 µF and 250-300 V, respectively. As voltage increases, cell survival decreases, but the percentage of surviving cells that stably incorporate the introduced DNA into their genome increases dramatically. Given these parameters, a pulse time of approximately 14-20 mSec should be observed.

Electroporated cells are maintained at room temperature for approximately 5 min, and the contents of the cuvette are then gently removed with a sterile transfer pipette. The cells are added directly to 10 ml of prewarmed nutrient media (DMEM with 15% calf serum) in a 10 cm dish and incubated at 37 degree C. The following day, the media is aspirated and replaced with 10 ml of fresh media and incubated for a further 16-24 hours.



The engineered fibroblasts are then injected into the host, either alone or after having been grown to confluence on cytodex 3 microcarrier beads. The fibroblasts now produce the protein product. The fibroblasts can then be introduced into a patient as described above.

5    *Example 18: Method of Treatment Using Gene Therapy - In Vivo*

Another aspect of the present invention is using *in vivo* gene therapy methods to treat disorders, diseases and conditions. The gene therapy method relates to the introduction of naked nucleic acid (DNA, RNA, and antisense DNA or RNA) sequences into an animal to  
10    increase or decrease the expression of the polypeptide. The polynucleotide of the present invention may be operatively linked to a promoter or any other genetic elements necessary for the expression of the polypeptide by the target tissue. Such gene therapy and delivery techniques and methods are known in the art, see, for example, WO90/11092, WO98/11779; U.S. Patent NO. 5693622, 5705151, 5580859; Tabata et al., *Cardiovasc. Res.* 35(3):470-479  
15    (1997); Chao et al., *Pharmacol. Res.* 35(6):517-522 (1997); Wolff, *Neuromuscul. Disord.* 7(5):314-318 (1997); Schwartz et al., *Gene Ther.* 3(5):405-411 (1996); Tsurumi et al., *Circulation* 94(12):3281-3290 (1996) (incorporated herein by reference).

The polynucleotide constructs may be delivered by any method that delivers injectable materials to the cells of an animal, such as, injection into the interstitial space of  
20    tissues (heart, muscle, skin, lung, liver, intestine and the like). The polynucleotide constructs can be delivered in a pharmaceutically acceptable liquid or aqueous carrier.

The term "naked" polynucleotide, DNA or RNA, refers to sequences that are free from any delivery vehicle that acts to assist, promote, or facilitate entry into the cell, including viral sequences, viral particles, liposome formulations, lipofectin or precipitating  
25    agents and the like. However, the polynucleotides of the present invention may also be delivered in liposome formulations (such as those taught in Felgner P.L. et al. (1995) *Ann. NY Acad. Sci.* 772:126-139 and Abdallah B. et al. (1995) *Biol. Cell* 85(1):1-7) which can be prepared by methods well known to those skilled in the art.

The polynucleotide vector constructs used in the gene therapy method are preferably  
30    constructs that will not integrate into the host genome nor will they contain sequences that allow for replication. Any strong promoter known to those skilled in the art can be used for driving the expression of DNA. Unlike other gene therapies techniques, one major advantage

of introducing naked nucleic acid sequences into target cells is the transitory nature of the polynucleotide synthesis in the cells. Studies have shown that non-replicating DNA sequences can be introduced into cells to provide production of the desired polypeptide for periods of up to six months.

5       The polynucleotide construct can be delivered to the interstitial space of tissues within the an animal, including of muscle, skin, brain, lung, liver, spleen, bone marrow, thymus, heart, lymph, blood, bone, cartilage, pancreas, kidney, gall bladder, stomach, intestine, testis, ovary, uterus, rectum, nervous system, eye, gland, and connective tissue. Interstitial space of the tissues comprises the intercellular fluid, mucopolysaccharide matrix among the reticular  
10   fibers of organ tissues, elastic fibers in the walls of vessels or chambers, collagen fibers of fibrous tissues, or that same matrix within connective tissue ensheathing muscle cells or in the lacunae of bone. It is similarly the space occupied by the plasma of the circulation and the lymph fluid of the lymphatic channels. Delivery to the interstitial space of muscle tissue is preferred for the reasons discussed below. They may be conveniently delivered by  
15   injection into the tissues comprising these cells. They are preferably delivered to and expressed in persistent, non-dividing cells which are differentiated, although delivery and expression may be achieved in non-differentiated or less completely differentiated cells, such as, for example, stem cells of blood or skin fibroblasts. *In vivo* muscle cells are particularly competent in their ability to take up and express polynucleotides.

20       For the naked polynucleotide injection, an effective dosage amount of DNA or RNA will be in the range of from about 0.05 g/kg body weight to about 50 mg/kg body weight. Preferably the dosage will be from about 0.005 mg/kg to about 20 mg/kg and more preferably from about 0.05 mg/kg to about 5 mg/kg. Of course, as the artisan of ordinary skill will appreciate, this dosage will vary according to the tissue site of injection. The appropriate and  
25   effective dosage of nucleic acid sequence can readily be determined by those of ordinary skill in the art and may depend on the condition being treated and the route of administration. The preferred route of administration is by the parenteral route of injection into the interstitial space of tissues. However, other parenteral routes may also be used, such as, inhalation of an aerosol formulation particularly for delivery to lungs or bronchial tissues, throat or mucous  
30   membranes of the nose. In addition, naked polynucleotide constructs can be delivered to arteries during angioplasty by the catheter used in the procedure.

The dose response effects of injected polynucleotide in muscle *in vivo* is determined

as follows. Suitable template DNA for production of mRNA coding for polypeptide of the present invention is prepared in accordance with a standard recombinant DNA methodology. The template DNA, which may be either circular or linear, is either used as naked DNA or complexed with liposomes. The quadriceps muscles of mice are then injected with various amounts of the template DNA.

Five to six week old female and male Balb/C mice are anesthetized by intraperitoneal injection with 0.3 ml of 2.5% Avertin. A 1.5 cm incision is made on the anterior thigh, and the quadriceps muscle is directly visualized. The template DNA is injected in 0.1 ml of carrier in a 1 cc syringe through a 27 gauge needle over one minute, approximately 0.5 cm from the distal insertion site of the muscle into the knee and about 0.2 cm deep. A suture is placed over the injection site for future localization, and the skin is closed with stainless steel clips.

After an appropriate incubation time (e.g., 7 days) muscle extracts are prepared by excising the entire quadriceps. Every fifth 15 um cross-section of the individual quadriceps muscles is histochemically stained for protein expression. A time course for protein expression may be done in a similar fashion except that quadriceps from different mice are harvested at different times. Persistence of DNA in muscle following injection may be determined by Southern blot analysis after preparing total cellular DNA and HIRT supernatants from injected and control mice. The results of the above experimentation in mice can be use to extrapolate proper dosages and other treatment parameters in humans and other animals using naked DNA.

#### *Example 19: Transgenic Animals*

The polypeptides of the invention can also be expressed in transgenic animals. Animals of any species, including, but not limited to, mice, rats, rabbits, hamsters, guinea pigs, pigs, micro-pigs, goats, sheep, cows and non-human primates, e.g., baboons, monkeys, and chimpanzees may be used to generate transgenic animals. In a specific embodiment, techniques described herein or otherwise known in the art, are used to express polypeptides of the invention in humans, as part of a gene therapy protocol.

Any technique known in the art may be used to introduce the transgene (i.e., polynucleotides of the invention) into animals to produce the founder lines of transgenic

animals. Such techniques include, but are not limited to, pronuclear microinjection (Paterson et al., Appl. Microbiol. Biotechnol. 40:691-698 (1994); Carver et al., Biotechnology (NY) 11:1263-1270 (1993); Wright et al., Biotechnology (NY) 9:830-834 (1991); and Hoppe et al., U.S. Pat. No. 4,873,191 (1989)); retrovirus mediated gene transfer into germ lines (Van der Putten et al., Proc. Natl. Acad. Sci., USA 82:6148-6152 (1985)), blastocysts or embryos; gene targeting in embryonic stem cells (Thompson et al., Cell 56:313-321 (1989)); electroporation of cells or embryos (Lo, 1983, Mol Cell. Biol. 3:1803-1814 (1983)); introduction of the polynucleotides of the invention using a gene gun (see, e.g., Ulmer et al., Science 259:1745 (1993)); introducing nucleic acid constructs into embryonic pluripotent stem cells and transferring the stem cells back into the blastocyst; and sperm-mediated gene transfer (Lavitrano et al., Cell 57:717-723 (1989); etc. For a review of such techniques, see Gordon, "Transgenic Animals," Intl. Rev. Cytol. 115:171-229 (1989), which is incorporated by reference herein in its entirety.

Any technique known in the art may be used to produce transgenic clones containing polynucleotides of the invention, for example, nuclear transfer into enucleated oocytes of nuclei from cultured embryonic, fetal, or adult cells induced to quiescence (Campell et al., Nature 380:64-66 (1996); Wilmut et al., Nature 385:810-813 (1997)).

The present invention provides for transgenic animals that carry the transgene in all their cells, as well as animals which carry the transgene in some, but not all their cells, *i.e.*, mosaic animals or chimeric. The transgene may be integrated as a single transgene or as multiple copies such as in concatamers, *e.g.*, head-to-head tandems or head-to-tail tandems. The transgene may also be selectively introduced into and activated in a particular cell type by following, for example, the teaching of Lasko et al. (Lasko et al., Proc. Natl. Acad. Sci. USA 89:6232-6236 (1992)). The regulatory sequences required for such a cell-type specific activation will depend upon the particular cell type of interest, and will be apparent to those of skill in the art. When it is desired that the polynucleotide transgene be integrated into the chromosomal site of the endogenous gene, gene targeting is preferred. Briefly, when such a technique is to be utilized, vectors containing some nucleotide sequences homologous to the endogenous gene are designed for the purpose of integrating, via homologous recombination with chromosomal sequences, into and disrupting the function of the nucleotide sequence of the endogenous gene. The transgene may also be selectively introduced into a particular cell type, thus inactivating the endogenous gene in only that cell type, by following, for example,

the teaching of Gu et al. (Gu et al., Science 265:103-106 (1994)). The regulatory sequences required for such a cell-type specific inactivation will depend upon the particular cell type of interest, and will be apparent to those of skill in the art.

Once transgenic animals have been generated, the expression of the recombinant gene may be assayed utilizing standard techniques. Initial screening may be accomplished by Southern blot analysis or PCR techniques to analyze animal tissues to verify that integration of the transgene has taken place. The level of mRNA expression of the transgene in the tissues of the transgenic animals may also be assessed using techniques which include, but are not limited to, Northern blot analysis of tissue samples obtained from the animal, *in situ* hybridization analysis, and reverse transcriptase-PCR (rt-PCR). Samples of transgenic gene-expressing tissue may also be evaluated immunocytochemically or immunohistochemically using antibodies specific for the transgene product.

Once the founder animals are produced, they may be bred, inbred, outbred, or crossbred to produce colonies of the particular animal. Examples of such breeding strategies include, but are not limited to: outbreeding of founder animals with more than one integration site in order to establish separate lines; inbreeding of separate lines in order to produce compound transgenics that express the transgene at higher levels because of the effects of additive expression of each transgene; crossing of heterozygous transgenic animals to produce animals homozygous for a given integration site in order to both augment expression and eliminate the need for screening of animals by DNA analysis; crossing of separate homozygous lines to produce compound heterozygous or homozygous lines; and breeding to place the transgene on a distinct background that is appropriate for an experimental model of interest.

Transgenic animals of the invention have uses which include, but are not limited to, animal model systems useful in elaborating the biological function of polypeptides of the present invention, studying conditions and/or disorders associated with aberrant expression, and in screening for compounds effective in ameliorating such conditions and/or disorders.

#### *Example 20: Knock-Out Animals*

30

Endogenous gene expression can also be reduced by inactivating or "knocking out" the gene and/or its promoter using targeted homologous recombination. (E.g., see Smithies

et al., Nature 317:230-234 (1985); Thomas & Capecchi, Cell 51:503-512 (1987); Thompson et al., Cell 5:313-321 (1989); each of which is incorporated by reference herein in its entirety). For example, a mutant, non-functional polynucleotide of the invention (or a completely unrelated DNA sequence) flanked by DNA homologous to the endogenous polynucleotide sequence (either the coding regions or regulatory regions of the gene) can be used, with or without a selectable marker and/or a negative selectable marker, to transfect cells that express polypeptides of the invention *in vivo*. In another embodiment, techniques known in the art are used to generate knockouts in cells that contain, but do not express the gene of interest. Insertion of the DNA construct, via targeted homologous recombination, results in inactivation of the targeted gene. Such approaches are particularly suited in research and agricultural fields where modifications to embryonic stem cells can be used to generate animal offspring with an inactive targeted gene (*e.g.*, see Thomas & Capecchi 1987 and Thompson 1989, *supra*). However this approach can be routinely adapted for use in humans provided the recombinant DNA constructs are directly administered or targeted to the required site *in vivo* using appropriate viral vectors that will be apparent to those of skill in the art.

In further embodiments of the invention, cells that are genetically engineered to express the polypeptides of the invention, or alternatively, that are genetically engineered not to express the polypeptides of the invention (*e.g.*, knockouts) are administered to a patient *in vivo*. Such cells may be obtained from the patient (*i.e.*, animal, including human) or an MHC compatible donor and can include, but are not limited to fibroblasts, bone marrow cells, blood cells (*e.g.*, lymphocytes), adipocytes, muscle cells, endothelial cells etc. The cells are genetically engineered *in vitro* using recombinant DNA techniques to introduce the coding sequence of polypeptides of the invention into the cells, or alternatively, to disrupt the coding sequence and/or endogenous regulatory sequence associated with the polypeptides of the invention, *e.g.*, by transduction (using viral vectors, and preferably vectors that integrate the transgene into the cell genome) or transfection procedures, including, but not limited to, the use of plasmids, cosmids, YACs, naked DNA, electroporation, liposomes, etc. The coding sequence of the polypeptides of the invention can be placed under the control of a strong constitutive or inducible promoter or promoter/enhancer to achieve expression, and preferably secretion, of the polypeptides of the invention. The engineered cells which express and preferably secrete the polypeptides of the invention can be introduced into the

patient systemically. e.g., in the circulation, or intraperitoneally.

Alternatively, the cells can be incorporated into a matrix and implanted in the body, e.g., genetically engineered fibroblasts can be implanted as part of a skin graft; genetically engineered endothelial cells can be implanted as part of a lymphatic or vascular graft. (See, 5 for example, Anderson et al. U.S. Patent No. 5,399,349; and Mulligan & Wilson, U.S. Patent No. 5,460,959 each of which is incorporated by reference herein in its entirety).

When the cells to be administered are non-autologous or non-MHC compatible cells, they can be administered using well known techniques which prevent the development of a host immune response against the introduced cells. For example, the cells may be introduced 10 in an encapsulated form which, while allowing for an exchange of components with the immediate extracellular environment, does not allow the introduced cells to be recognized by the host immune system.

Transgenic and "knock-out" animals of the invention have uses which include, but are not limited to, animal model systems useful in elaborating the biological function of 15 polypeptides of the present invention, studying conditions and/or disorders associated with aberrant expression, and in screening for compounds effective in ameliorating such conditions and/or disorders.

20 *Example 22: Assays Detecting Stimulation or Inhibition of B cell Proliferation and Differentiation*

Generation of functional humoral immune responses requires both soluble and cognate signaling between B-lineage cells and their microenvironment. Signals may impart a positive stimulus that allows a B-lineage cell to continue its programmed development, or a 25 negative stimulus that instructs the cell to arrest its current developmental pathway. To date, numerous stimulatory and inhibitory signals have been found to influence B cell responsiveness including IL-2, IL-4, IL-5, IL-6, IL-7, IL10, IL-13, IL-14 and IL-15. Interestingly, these signals are by themselves weak effectors but can, in combination with various co-stimulatory proteins, induce activation, proliferation, differentiation, homing, 30 tolerance and death among B cell populations.

One of the best studied classes of B-cell co-stimulatory proteins is the TNF-superfamily. Within this family CD40, CD27, and CD30 along with their respective ligands

CD154, CD70, and CD153 have been found to regulate a variety of immune responses. Assays which allow for the detection and/or observation of the proliferation and differentiation of these B-cell populations and their precursors are valuable tools in determining the effects various proteins may have on these B-cell populations in terms of proliferation and differentiation. Listed below are two assays designed to allow for the detection of the differentiation, proliferation, or inhibition of B-cell populations and their precursors.

**In Vitro Assay-** Agonists or antagonists of the invention can be assessed for its ability to induce activation, proliferation, differentiation or inhibition and/or death in B-cell populations and their precursors. The activity of the agonists or antagonists of the invention on purified human tonsillar B cells, measured qualitatively over the dose range from 0.1 to 10,000 ng/mL, is assessed in a standard B-lymphocyte co-stimulation assay in which purified tonsillar B cells are cultured in the presence of either formalin-fixed *Staphylococcus aureus* Cowan I (SAC) or immobilized anti-human IgM antibody as the priming agent. Second signals such as IL-2 and IL-15 synergize with SAC and IgM crosslinking to elicit B cell proliferation as measured by tritiated-thymidine incorporation. Novel synergizing agents can be readily identified using this assay. The assay involves isolating human tonsillar B cells by magnetic bead (MACS) depletion of CD3-positive cells. The resulting cell population is greater than 95% B cells as assessed by expression of CD45R(B220).

Various dilutions of each sample are placed into individual wells of a 96-well plate to which are added  $10^5$  B-cells suspended in culture medium (RPMI 1640 containing 10% FBS,  $5 \times 10^{-5}$ M 2ME, 100U/ml penicillin, 10ug/ml streptomycin, and  $10^{-5}$  dilution of SAC) in a total volume of 150ul. Proliferation or inhibition is quantitated by a 20h pulse (1uCi/well) with  $^3$ H-thymidine (6.7 Ci/mM) beginning 72h post factor addition. The positive and negative controls are IL2 and medium respectively.

**In Vivo Assay-** BALB/c mice are injected (i.p.) twice per day with buffer only, or 2 mg/Kg of agonists or antagonists of the invention, or truncated forms thereof. Mice receive this treatment for 4 consecutive days, at which time they are sacrificed and various tissues and serum collected for analyses. Comparison of H&E sections from normal spleens and spleens treated with agonists or antagonists of the invention identify the results of the activity of the agonists or antagonists on spleen cells, such as the diffusion of peri-arterial lymphatic sheaths, and/or significant increases in the nucleated cellularity of the red pulp regions, which



may indicate the activation of the differentiation and proliferation of B-cell populations. Immunohistochemical studies using a B cell marker, anti-CD45R(B220), are used to determine whether any physiological changes to splenic cells, such as splenic disorganization, are due to increased B-cell representation within loosely defined B-cell zones that infiltrate established T-cell regions.

Flow cytometric analyses of the spleens from mice treated with agonist or antagonist is used to indicate whether the agonists or antagonists specifically increases the proportion of ThB+, CD45R(B220)dull B cells over that which is observed in control mice.

Likewise, a predicted consequence of increased mature B-cell representation in vivo is a relative increase in serum Ig titers. Accordingly, serum IgM and IgA levels are compared between buffer and agonists or antagonists-treated mice.

The studies described in this example tested activity of agonists or antagonists of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides or polypeptides of the invention (e.g., gene therapy).

#### *Example 23: T Cell Proliferation Assay*

A CD3-induced proliferation assay is performed on PBMCs and is measured by the uptake of <sup>3</sup>H-thymidine. The assay is performed as follows. Ninety-six well plates are coated with 100 µl/well of mAb to CD3 (HIT3a, Pharmingen) or isotype-matched control mAb (B33.1) overnight at 4 degrees C (1 µg/ml in .05M bicarbonate buffer, pH 9.5), then washed three times with PBS. PBMC are isolated by F/H gradient centrifugation from human peripheral blood and added to quadruplicate wells (5 x 10<sup>4</sup>/well) of mAb coated plates in RPMI containing 10% FCS and P/S in the presence of varying concentrations of agonists or antagonists of the invention (total volume 200 µl). Relevant protein buffer and medium alone are controls. After 48 hr. culture at 37 degrees C, plates are spun for 2 min. at 1000 rpm and 100 µl of supernatant is removed and stored -20 degrees C for measurement of IL-2 (or other cytokines) if effect on proliferation is observed. Wells are supplemented with 100 µl of medium containing 0.5 uCi of <sup>3</sup>H-thymidine and cultured at 37 degrees C for 18-24 hr. Wells are harvested and incorporation of <sup>3</sup>H-thymidine used as a measure of proliferation. Anti-CD3 alone is the positive control for proliferation. IL-2 (100 U/ml) is also used as a control which enhances proliferation. Control antibody which does not induce proliferation

of T cells is used as the negative controls for the effects of agonists or antagonists of the invention.

The studies described in this example tested activity of agonists or antagonists of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides or polypeptides of the invention (e.g., gene therapy).

*Example 24: Effect of Agonists or Antagonists of the Invention on the Expression of MHC Class II, Costimulatory and Adhesion Molecules and Cell Differentiation of Monocytes and Monocyte-Derived Human Dendritic Cells*

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Dendritic cells are generated by the expansion of proliferating precursors found in the peripheral blood: adherent PBMC or elutriated monocytic fractions are cultured for 7-10 days with GM-CSF (50 ng/ml) and IL-4 (20 ng/ml). These dendritic cells have the characteristic phenotype of immature cells (expression of CD1, CD80, CD86, CD40 and MHC class II antigens). Treatment with activating factors, such as TNF- $\alpha$ , causes a rapid change in surface phenotype (increased expression of MHC class I and II, costimulatory and adhesion molecules, downregulation of FC $\gamma$ RII, upregulation of CD83). These changes correlate with increased antigen-presenting capacity and with functional maturation of the dendritic cells.

15

FACS analysis of surface antigens is performed as follows. Cells are treated 1-3 days with increasing concentrations of agonist or antagonist of the invention or LPS (positive control), washed with PBS containing 1% BSA and 0.02 mM sodium azide, and then incubated with 1:20 dilution of appropriate FITC- or PE-labeled monoclonal antibodies for 30 minutes at 4 degrees C. After an additional wash, the labeled cells are analyzed by flow cytometry on a FACScan (Becton Dickinson).

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Effect on the production of cytokines. Cytokines generated by dendritic cells, in particular IL-12, are important in the initiation of T-cell dependent immune responses. IL-12 strongly influences the development of Th1 helper T-cell immune response, and induces cytotoxic T and NK cell function. An ELISA is used to measure the IL-12 release as follows. Dendritic cells ( $10^6$ /ml) are treated with increasing concentrations of agonists or antagonists of the invention for 24 hours. LPS (100 ng/ml) is added to the cell culture as positive control. Supernatants from the cell cultures are then collected and analyzed for IL-12 content using

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commercial ELISA kit (e.g., R & D Systems (Minneapolis, MN)). The standard protocols provided with the kits are used.

Effect on the expression of MHC Class II, costimulatory and adhesion molecules. Three major families of cell surface antigens can be identified on monocytes: adhesion molecules, molecules involved in antigen presentation, and Fc receptor. Modulation of the expression of MHC class II antigens and other costimulatory molecules, such as B7 and ICAM-1, may result in changes in the antigen presenting capacity of monocytes and ability to induce T cell activation. Increase expression of Fc receptors may correlate with improved monocyte cytotoxic activity, cytokine release and phagocytosis.

FACS analysis is used to examine the surface antigens as follows. Monocytes are treated 1-5 days with increasing concentrations of agonists or antagonists of the invention or LPS (positive control), washed with PBS containing 1% BSA and 0.02 mM sodium azide, and then incubated with 1:20 dilution of appropriate FITC- or PE-labeled monoclonal antibodies for 30 minutes at 4 degreesC. After an additional wash, the labeled cells are analyzed by flow cytometry on a FACScan (Becton Dickinson).

Monocyte activation and/or increased survival. Assays for molecules that activate (or alternatively, inactivate) monocytes and/or increase monocyte survival (or alternatively, decrease monocyte survival) are known in the art and may routinely be applied to determine whether a molecule of the invention functions as an inhibitor or activator of monocytes. Agonists or antagonists of the invention can be screened using the three assays described below. For each of these assays, Peripheral blood mononuclear cells (PBMC) are purified from single donor leukopacks (American Red Cross, Baltimore, MD) by centrifugation through a Histopaque gradient (Sigma). Monocytes are isolated from PBMC by counterflow centrifugal elutriation.

Monocyte Survival Assay. Human peripheral blood monocytes progressively lose viability when cultured in absence of serum or other stimuli. Their death results from internally regulated process (apoptosis). Addition to the culture of activating factors, such as TNF-alpha dramatically improves cell survival and prevents DNA fragmentation. Propidium iodide (PI) staining is used to measure apoptosis as follows. Monocytes are cultured for 48 hours in

- polypropylene tubes in serum-free medium (positive control), in the presence of 100 ng/ml TNF-alpha (negative control), and in the presence of varying concentrations of the compound to be tested. Cells are suspended at a concentration of  $2 \times 10^6$ /ml in PBS containing PI at a final concentration of 5  $\mu$ g/ml, and then incubated at room temperature for 5 minutes before
- 5 FACSscan analysis. PI uptake has been demonstrated to correlate with DNA fragmentation in this experimental paradigm.

- Effect on cytokine release. An important function of monocytes/macrophages is their regulatory activity on other cellular populations of the immune system through the release of
- 10 cytokines after stimulation. An ELISA to measure cytokine release is performed as follows. Human monocytes are incubated at a density of  $5 \times 10^5$  cells/ml with increasing concentrations of agonists or antagonists of the invention and under the same conditions, but in the absence of agonists or antagonists. For IL-12 production, the cells are primed overnight with IFN (100 U/ml) in presence of agonist or antagonist of the invention. LPS (10
- 15 ng/ml) is then added. Conditioned media are collected after 24h and kept frozen until use. Measurement of TNF-alpha, IL-10, MCP-1 and IL-8 is then performed using a commercially available ELISA kit (e. g, R & D Systems (Minneapolis, MN)) and applying the standard protocols provided with the kit.

- 20 Oxidative burst. Purified monocytes are plated in 96-w plate at  $2 \times 10^5$  cell/well. Increasing concentrations of agonists or antagonists of the invention are added to the wells in a total volume of 0.2 ml culture medium (RPMI 1640 + 10% FCS, glutamine and antibiotics). After 3 days incubation, the plates are centrifuged and the medium is removed from the wells. To the macrophage monolayers, 0.2 ml per well of phenol red solution (140 mM NaCl, 10 mM
- 25 potassium phosphate buffer pH 7.0, 5.5 mM dextrose, 0.56 mM phenol red and 19 U/ml of HRPO) is added, together with the stimulant (200 nM PMA). The plates are incubated at 37°C for 2 hours and the reaction is stopped by adding 20  $\mu$ l 1N NaOH per well. The absorbance is read at 610 nm. To calculate the amount of  $H_2O_2$  produced by the macrophages, a standard curve of a  $H_2O_2$  solution of known molarity is performed for each
- 30 experiment.

The studies described in this example tested activity of agonists or antagonists of the invention. However, one skilled in the art could easily modify the exemplified studies to test

the activity of polynucleotides or polypeptides of the invention (e.g., gene therapy).

*Example 25: Biological Effects of Agonists or Antagonists of the Invention*

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Astrocyte and Neuronal Assays.

Agonists or antagonists of the invention, expressed in *Escherichia coli* and purified as described above, can be tested for activity in promoting the survival, neurite outgrowth, or phenotypic differentiation of cortical neuronal cells and for inducing the proliferation of glial fibrillary acidic protein immunopositive cells, astrocytes. The selection of cortical cells for the bioassay is based on the prevalent expression of FGF-1 and FGF-2 in cortical structures and on the previously reported enhancement of cortical neuronal survival resulting from FGF-2 treatment. A thymidine incorporation assay, for example, can be used to elucidate an agonist or antagonist of the invention's activity on these cells.

Moreover, previous reports describing the biological effects of FGF-2 (basic FGF) on cortical or hippocampal neurons *in vitro* have demonstrated increases in both neuron survival and neurite outgrowth (Walicke et al., "Fibroblast growth factor promotes survival of dissociated hippocampal neurons and enhances neurite extension." *Proc. Natl. Acad. Sci. USA* 83:3012-3016. (1986), assay herein incorporated by reference in its entirety). However, reports from experiments done on PC-12 cells suggest that these two responses are not necessarily synonymous and may depend on not only which FGF is being tested but also on which receptor(s) are expressed on the target cells. Using the primary cortical neuronal culture paradigm, the ability of an agonist or antagonist of the invention to induce neurite outgrowth can be compared to the response achieved with FGF-2 using, for example, a thymidine incorporation assay.

Fibroblast and endothelial cell assays.

Human lung fibroblasts are obtained from Clonetics (San Diego, CA) and maintained in growth media from Clonetics. Dermal microvascular endothelial cells are obtained from Cell Applications (San Diego, CA). For proliferation assays, the human lung fibroblasts and

dermal microvascular endothelial cells can be cultured at 5,000 cells/well in a 96-well plate for one day in growth medium. The cells are then incubated for one day in 0.1% BSA basal medium. After replacing the medium with fresh 0.1% BSA medium, the cells are incubated with the test proteins for 3 days. Alamar Blue (Alamar Biosciences, Sacramento, CA) is added to each well to a final concentration of 10%. The cells are incubated for 4 hr. Cell viability is measured by reading in a CytoFluor fluorescence reader. For the PGE<sub>2</sub> assays, the human lung fibroblasts are cultured at 5,000 cells/well in a 96-well plate for one day. After a medium change to 0.1% BSA basal medium, the cells are incubated with FGF-2 or agonists or antagonists of the invention with or without IL-1 $\alpha$  for 24 hours. The supernatants are collected and assayed for PGE<sub>2</sub> by EIA kit (Cayman, Ann Arbor, MI). For the IL-6 assays, the human lung fibroblasts are cultured at 5,000 cells/well in a 96-well plate for one day. After a medium change to 0.1% BSA basal medium, the cells are incubated with FGF-2 or with or without agonists or antagonists of the invention IL-1 $\alpha$  for 24 hours. The supernatants are collected and assayed for IL-6 by ELISA kit (Endogen, Cambridge, MA).

Human lung fibroblasts are cultured with FGF-2 or agonists or antagonists of the invention for 3 days in basal medium before the addition of Alamar Blue to assess effects on growth of the fibroblasts. FGF-2 should show a stimulation at 10 - 2500 ng/ml which can be used to compare stimulation with agonists or antagonists of the invention.

#### 20 Parkinson Models.

The loss of motor function in Parkinson's disease is attributed to a deficiency of striatal dopamine resulting from the degeneration of the nigrostriatal dopaminergic projection neurons. An animal model for Parkinson's that has been extensively characterized involves the systemic administration of 1-methyl-4 phenyl 1,2,3,6-tetrahydropyridine (MPTP). In the CNS, MPTP is taken-up by astrocytes and catabolized by monoamine oxidase B to 1-methyl-4-phenyl pyridine (MPP<sup>+</sup>) and released. Subsequently, MPP<sup>+</sup> is actively accumulated in dopaminergic neurons by the high-affinity reuptake transporter for dopamine. MPP<sup>+</sup> is then concentrated in mitochondria by the electrochemical gradient and selectively inhibits nicotinamide adenine disphosphate: ubiquinone oxidoreductionase (complex I), thereby interfering with electron transport and eventually generating oxygen radicals.

It has been demonstrated in tissue culture paradigms that FGF-2 (basic FGF) has

trophic activity towards nigral dopaminergic neurons (Ferrari et al., Dev. Biol. 1989). Recently, Dr. Unsicker's group has demonstrated that administering FGF-2 in gel foam implants in the striatum results in the near complete protection of nigral dopaminergic neurons from the toxicity associated with MPTP exposure (Otto and Unsicker, J. Neuroscience, 1990).

Based on the data with FGF-2, agonists or antagonists of the invention can be evaluated to determine whether it has an action similar to that of FGF-2 in enhancing dopaminergic neuronal survival *in vitro* and it can also be tested *in vivo* for protection of dopaminergic neurons in the striatum from the damage associated with MPTP treatment. The potential effect of an agonist or antagonist of the invention is first examined *in vitro* in a dopaminergic neuronal cell culture paradigm. The cultures are prepared by dissecting the midbrain floor plate from gestation day 14 Wistar rat embryos. The tissue is dissociated with trypsin and seeded at a density of 200,000 cells/cm<sup>2</sup> on polyorthinine-laminin coated glass coverslips. The cells are maintained in Dulbecco's Modified Eagle's medium and F12 medium containing hormonal supplements (N1). The cultures are fixed with paraformaldehyde after 8 days *in vitro* and are processed for tyrosine hydroxylase, a specific marker for dopaminergic neurons, immunohistochemical staining. Dissociated cell cultures are prepared from embryonic rats. The culture medium is changed every third day and the factors are also added at that time.

Since the dopaminergic neurons are isolated from animals at gestation day 14, a developmental time which is past the stage when the dopaminergic precursor cells are proliferating, an increase in the number of tyrosine hydroxylase immunopositive neurons would represent an increase in the number of dopaminergic neurons surviving *in vitro*. Therefore, if an agonist or antagonist of the invention acts to prolong the survival of dopaminergic neurons, it would suggest that the agonist or antagonist may be involved in Parkinson's Disease.

The studies described in this example tested activity of agonists or antagonists of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides or polypeptides of the invention (e.g., gene therapy).

*Example 26: The Effect of Agonists or Antagonists of the Invention on the Growth of*

*Vascular Endothelial Cells*

On day 1, human umbilical vein endothelial cells (HUVEC) are seeded at  $2.5 \times 10^4$  cells/35 mm dish density in M199 medium containing 4% fetal bovine serum (FBS), 16 units/ml heparin, and 50 units/ml endothelial cell growth supplements (ECGS, Biotechnology, Inc.). On day 2, the medium is replaced with M199 containing 10% FBS, 8 units/ml heparin. An agonist or antagonist of the invention, and positive controls, such as VEGF and basic FGF (bFGF) are added, at varying concentrations. On days 4 and 6, the medium is replaced. On day 8, cell number is determined with a Coulter Counter.

10 An increase in the number of HUVEC cells indicates that the compound of the invention may proliferate vascular endothelial cells, while a decrease in the number of HUVEC cell indicates that the compound of the invention inhibits vascular endothelial cells.

The studies described in this example tested activity of a polypeptide of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity  
15 of polynucleotides (e.g., gene therapy), agonists, and/or antagonists of the invention.

*Example 27: Rat Corneal Wound Healing Model*

This animal model shows the effect of an agonist or antagonist of the invention on  
20 neovascularization. The experimental protocol includes:

- a) Making a 1-1.5 mm long incision from the center of cornea into the stromal layer.
- b) Inserting a spatula below the lip of the incision facing the outer corner of the eye.
- 25 c) Making a pocket (its base is 1-1.5 mm from the edge of the eye).
- d) Positioning a pellet, containing 50ng- 5ug of an agonist or antagonist of the invention, within the pocket.
- e) Treatment with an agonist or antagonist of the invention can also be applied topically to the corneal wounds in a dosage range of 20mg - 500mg (daily treatment for five  
30 days).

The studies described in this example tested activity of agonists or antagonists of the invention. However, one skilled in the art could easily modify the exemplified studies to test



the activity of polynucleotides or polypeptides of the invention (e.g., gene therapy).

*Example 28: Diabetic Mouse and Glucocorticoid-Impaired Wound Healing Models*

5           A.       *Diabetic db+/db+ Mouse Model.*

To demonstrate that an agonist or antagonist of the invention accelerates the healing process, the genetically diabetic mouse model of wound healing is used. The full thickness wound healing model in the db+/db+ mouse is a well characterized, clinically relevant and reproducible model of impaired wound healing. Healing of the diabetic wound is dependent  
10 on formation of granulation tissue and re-epithelialization rather than contraction (Gartner, M.H. *et al.*, *J. Surg. Res.* 52:389 (1992); Greenhalgh, D.G. *et al.*, *Am. J. Pathol.* 136:1235 (1990)).

The diabetic animals have many of the characteristic features observed in Type II diabetes mellitus. Homozygous (db+/db+) mice are obese in comparison to their normal  
15 heterozygous (db+/+m) littermates. Mutant diabetic (db+/db+) mice have a single autosomal recessive mutation on chromosome 4 (db+) (Coleman *et al.* *Proc. Natl. Acad. Sci. USA* 77:283-293 (1982)). Animals show polyphagia, polydipsia and polyuria. Mutant diabetic mice (db+/db+) have elevated blood glucose, increased or normal insulin levels, and suppressed cell-mediated immunity (Mandel *et al.*, *J. Immunol.* 120:1375 (1978); Debray-  
20 Sachs, M. *et al.*, *Clin. Exp. Immunol.* 51(1):1-7 (1983); Leiter *et al.*, *Am. J. of Pathol.* 114:46-55 (1985)). Peripheral neuropathy, myocardial complications, and microvascular lesions, basement membrane thickening and glomerular filtration abnormalities have been described in these animals (Norido, F. *et al.*, *Exp. Neurol.* 83(2):221-232 (1984); Robertson *et al.*, *Diabetes* 29(1):60-67 (1980); Giacomelli *et al.*, *Lab Invest.* 40(4):460-473 (1979); Coleman,  
25 D.L., *Diabetes* 31 (Suppl):1-6 (1982)). These homozygous diabetic mice develop hyperglycemia that is resistant to insulin analogous to human type II diabetes (Mandel *et al.*, *J. Immunol.* 120:1375-1377 (1978)).

The characteristics observed in these animals suggests that healing in this model may be similar to the healing observed in human diabetes (Greenhalgh, *et al.*, *Am. J. of Pathol.*  
30 136:1235-1246 (1990)).

Genetically diabetic female C57BL/KsJ (db+/db+) mice and their non-diabetic (db+/+m) heterozygous littermates are used in this study (Jackson Laboratories). The

animals are purchased at 6 weeks of age and are 8 weeks old at the beginning of the study. Animals are individually housed and received food and water ad libitum. All manipulations are performed using aseptic techniques. The experiments are conducted according to the rules and guidelines of Human Genome Sciences, Inc. Institutional Animal Care and Use Committee and the Guidelines for the Care and Use of Laboratory Animals.

Wounding protocol is performed according to previously reported methods (Tsuboi, R. and Rifkin, D.B., *J. Exp. Med.* 172:245-251 (1990)). Briefly, on the day of wounding, animals are anesthetized with an intraperitoneal injection of Avertin (0.01 mg/mL), 2,2,2-tribromoethanol and 2-methyl-2-butanol dissolved in deionized water. The dorsal region of the animal is shaved and the skin washed with 70% ethanol solution and iodine. The surgical area is dried with sterile gauze prior to wounding. An 8 mm full-thickness wound is then created using a Keyes tissue punch. Immediately following wounding, the surrounding skin is gently stretched to eliminate wound expansion. The wounds are left open for the duration of the experiment. Application of the treatment is given topically for 5 consecutive days commencing on the day of wounding. Prior to treatment, wounds are gently cleansed with sterile saline and gauze sponges.

Wounds are visually examined and photographed at a fixed distance at the day of surgery and at two day intervals thereafter. Wound closure is determined by daily measurement on days 1-5 and on day 8. Wounds are measured horizontally and vertically using a calibrated Jameson caliper. Wounds are considered healed if granulation tissue is no longer visible and the wound is covered by a continuous epithelium.

An agonist or antagonist of the invention is administered using at a range different doses, from 4mg to 500mg per wound per day for 8 days in vehicle. Vehicle control groups received 50mL of vehicle solution.

Animals are euthanized on day 8 with an intraperitoneal injection of sodium pentobarbital (300mg/kg). The wounds and surrounding skin are then harvested for histology and immunohistochemistry. Tissue specimens are placed in 10% neutral buffered formalin in tissue cassettes between biopsy sponges for further processing.

Three groups of 10 animals each (5 diabetic and 5 non-diabetic controls) are evaluated: 1) Vehicle placebo control, 2) untreated group, and 3) treated group.

Wound closure is analyzed by measuring the area in the vertical and horizontal axis and obtaining the total square area of the wound. Contraction is then estimated by establishing

the differences between the initial wound area (day 0) and that of post treatment (day 8). The wound area on day 1 is 64mm<sup>2</sup>, the corresponding size of the dermal punch. Calculations are made using the following formula:

5            
$$[\text{Open area on day 8}] - [\text{Open area on day 1}] / [\text{Open area on day 1}]$$

Specimens are fixed in 10% buffered formalin and paraffin embedded blocks are sectioned perpendicular to the wound surface (5mm) and cut using a Reichert-Jung microtome. Routine hematoxylin-eosin (H&E) staining is performed on cross-sections of bisected  
10    wounds. Histologic examination of the wounds are used to assess whether the healing process and the morphologic appearance of the repaired skin is altered by treatment with an agonist or antagonist of the invention. This assessment included verification of the presence of cell accumulation, inflammatory cells, capillaries, fibroblasts, re-epithelialization and epidermal maturity (Greenhalgh, D.G. *et al.*, *Am. J. Pathol.* 136:1235 (1990)). A calibrated  
15    lens micrometer is used by a blinded observer.

Tissue sections are also stained immunohistochemically with a polyclonal rabbit anti-human keratin antibody using ABC Elite detection system. Human skin is used as a positive tissue control while non-immune IgG is used as a negative control. Keratinocyte growth is determined by evaluating the extent of reepithelialization of the wound using a calibrated  
20    lens micrometer.

Proliferating cell nuclear antigen/cyclin (PCNA) in skin specimens is demonstrated by using anti-PCNA antibody (1:50) with an ABC Elite detection system. Human colon cancer served as a positive tissue control and human brain tissue is used as a negative tissue control. Each specimen included a section with omission of the primary antibody and  
25    substitution with non-immune mouse IgG. Ranking of these sections is based on the extent of proliferation on a scale of 0-8, the lower side of the scale reflecting slight proliferation to the higher side reflecting intense proliferation.

Experimental data are analyzed using an unpaired t test. A p value of < 0.05 is considered significant.

30

#### *B. Steroid Impaired Rat Model*

The inhibition of wound healing by steroids has been well documented in various *in vitro* and

*in vivo* systems (Wahl, Glucocorticoids and Wound healing. In: Anti-Inflammatory Steroid Action: Basic and Clinical Aspects. 280-302 (1989); Wahl *et al.*, *J. Immunol.* 115: 476-481 (1975); Werb *et al.*, *J. Exp. Med.* 147:1684-1694 (1978)). Glucocorticoids retard wound healing by inhibiting angiogenesis, decreasing vascular permeability (Ebert *et al.*, *An. Intern. Med.* 37:701-705 (1952)), fibroblast proliferation, and collagen synthesis (Beck *et al.*, *Growth Factors.* 5: 295-304 (1991); Haynes *et al.*, *J. Clin. Invest.* 61: 703-797 (1978)) and producing a transient reduction of circulating monocytes (Haynes *et al.*, *J. Clin. Invest.* 61: 703-797 (1978); Wahl, "Glucocorticoids and wound healing", In: Antiinflammatory Steroid Action: Basic and Clinical Aspects, Academic Press, New York, pp. 280-302 (1989)). The systemic administration of steroids to impaired wound healing is a well establish phenomenon in rats (Beck *et al.*, *Growth Factors.* 5: 295-304 (1991); Haynes *et al.*, *J. Clin. Invest.* 61: 703-797 (1978); Wahl, "Glucocorticoids and wound healing", In: Antiinflammatory Steroid Action: Basic and Clinical Aspects, Academic Press, New York, pp. 280-302 (1989); Pierce *et al.*, *Proc. Natl. Acad. Sci. USA* 86: 2229-2233 (1989)).

To demonstrate that an agonist or antagonist of the invention can accelerate the healing process, the effects of multiple topical applications of the agonist or antagonist on full thickness excisional skin wounds in rats in which healing has been impaired by the systemic administration of methylprednisolone is assessed.

Young adult male Sprague Dawley rats weighing 250-300 g (Charles River Laboratories) are used in this example. The animals are purchased at 8 weeks of age and are 9 weeks old at the beginning of the study. The healing response of rats is impaired by the systemic administration of methylprednisolone (17mg/kg/rat intramuscularly) at the time of wounding. Animals are individually housed and received food and water *ad libitum*. All manipulations are performed using aseptic techniques. This study is conducted according to the rules and guidelines of Human Genome Sciences, Inc. Institutional Animal Care and Use Committee and the Guidelines for the Care and Use of Laboratory Animals.

The wounding protocol is followed according to section A, above. On the day of wounding, animals are anesthetized with an intramuscular injection of ketamine (50 mg/kg) and xylazine (5 mg/kg). The dorsal region of the animal is shaved and the skin washed with 70% ethanol and iodine solutions. The surgical area is dried with sterile gauze prior to wounding. An 8 mm full-thickness wound is created using a Keyes tissue punch. The wounds are left open for the duration of the experiment. Applications of the testing materials

are given topically once a day for 7 consecutive days commencing on the day of wounding and subsequent to methylprednisolone administration. Prior to treatment, wounds are gently cleansed with sterile saline and gauze sponges.

Wounds are visually examined and photographed at a fixed distance at the day of  
5 wounding and at the end of treatment. Wound closure is determined by daily measurement on days 1-5 and on day 8. Wounds are measured horizontally and vertically using a calibrated Jameson caliper. Wounds are considered healed if granulation tissue is no longer visible and the wound is covered by a continuous epithelium.

The agonist or antagonist of the invention is administered using at a range different  
10 doses, from 4mg to 500mg per wound per day for 8 days in vehicle. Vehicle control groups received 50mL of vehicle solution.

Animals are euthanized on day 8 with an intraperitoneal injection of sodium  
pentobarbital (300mg/kg). The wounds and surrounding skin are then harvested for  
histology. Tissue specimens are placed in 10% neutral buffered formalin in tissue cassettes  
15 between biopsy sponges for further processing.

Four groups of 10 animals each (5 with methylprednisolone and 5 without  
glucocorticoid) are evaluated: 1) Untreated group 2) Vehicle placebo control 3) treated  
groups.

Wound closure is analyzed by measuring the area in the vertical and horizontal axis  
20 and obtaining the total area of the wound. Closure is then estimated by establishing the differences between the initial wound area (day 0) and that of post treatment (day 8). The wound area on day 1 is 64mm<sup>2</sup>, the corresponding size of the dermal punch. Calculations are made using the following formula:

25 
$$[\text{Open area on day 8}] - [\text{Open area on day 1}] / [\text{Open area on day 1}]$$

Specimens are fixed in 10% buffered formalin and paraffin embedded blocks are sectioned  
perpendicular to the wound surface (5mm) and cut using an Olympus microtome. Routine  
hematoxylin-eosin (H&E) staining is performed on cross-sections of bisected wounds.  
30 Histologic examination of the wounds allows assessment of whether the healing process and the morphologic appearance of the repaired skin is improved by treatment with an agonist or antagonist of the invention. A calibrated lens micrometer is used by a blinded observer to

determine the distance of the wound gap.

Experimental data are analyzed using an unpaired t test. A p value of  $< 0.05$  is considered significant.

The studies described in this example tested activity of agonists or antagonists of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides or polypeptides of the invention (e.g., gene therapy).

*Example 29: Lymphadema Animal Model*

The purpose of this experimental approach is to create an appropriate and consistent lymphedema model for testing the therapeutic effects of an agonist or antagonist of the invention in lymphangiogenesis and re-establishment of the lymphatic circulatory system in the rat hind limb. Effectiveness is measured by swelling volume of the affected limb, quantification of the amount of lymphatic vasculature, total blood plasma protein, and histopathology. Acute lymphedema is observed for 7-10 days. Perhaps more importantly, the chronic progress of the edema is followed for up to 3-4 weeks.

Prior to beginning surgery, blood sample is drawn for protein concentration analysis. Male rats weighing approximately ~350g are dosed with Pentobarbital. Subsequently, the right legs are shaved from knee to hip. The shaved area is swabbed with gauze soaked in 70% EtOH. Blood is drawn for serum total protein testing. Circumference and volumetric measurements are made prior to injecting dye into paws after marking 2 measurement levels (0.5 cm above heel, at mid-pt of dorsal paw). The intradermal dorsum of both right and left paws are injected with 0.05 ml of 1% Evan's Blue. Circumference and volumetric measurements are then made following injection of dye into paws.

Using the knee joint as a landmark, a mid-leg inguinal incision is made circumferentially allowing the femoral vessels to be located. Forceps and hemostats are used to dissect and separate the skin flaps. After locating the femoral vessels, the lymphatic vessel that runs along side and underneath the vessel(s) is located. The main lymphatic vessels in this area are then electrically coagulated or suture ligated.

Using a microscope, muscles in back of the leg (near the semitendinosus and adductors) are bluntly dissected. The popliteal lymph node is then located. The 2 proximal and 2 distal lymphatic vessels and distal blood supply of the popliteal node are then and

ligated by suturing. The popliteal lymph node, and any accompanying adipose tissue, is then removed by cutting connective tissues.

Care is taken to control any mild bleeding resulting from this procedure. After lymphatics are occluded, the skin flaps are sealed by using liquid skin (Vetbond) (AJ Buck).

- 5 The separated skin edges are sealed to the underlying muscle tissue while leaving a gap of ~0.5 cm around the leg. Skin also may be anchored by suturing to underlying muscle when necessary.

- To avoid infection, animals are housed individually with mesh (no bedding). Recovering animals are checked daily through the optimal edematous peak, which typically occurred by day 5-7. The plateau edematous peak are then observed. To evaluate the intensity of the lymphedema, the circumference and volumes of 2 designated places on each paw before operation and daily for 7 days are measured. The effect plasma proteins on lymphedema is determined and whether protein analysis is a useful testing perimeter is also investigated. The weights of both control and edematous limbs are evaluated at 2 places.
- 15 Analysis is performed in a blind manner.

Circumference Measurements: Under brief gas anesthetic to prevent limb movement, a cloth tape is used to measure limb circumference. Measurements are done at the ankle bone and dorsal paw by 2 different people then those 2 readings are averaged. Readings are taken from both control and edematous limbs.

- 20 Volumetric Measurements: On the day of surgery, animals are anesthetized with Pentobarbital and are tested prior to surgery. For daily volumetrics animals are under brief halothane anesthetic (rapid immobilization and quick recovery), both legs are shaved and equally marked using waterproof marker on legs. Legs are first dipped in water, then dipped into instrument to each marked level then measured by Buxco edema software(Chen/Victor).
- 25 Data is recorded by one person, while the other is dipping the limb to marked area.

Blood-plasma protein measurements: Blood is drawn, spun, and serum separated prior to surgery and then at conclusion for total protein and Ca<sup>2+</sup> comparison.

- Limb Weight Comparison: After drawing blood, the animal is prepared for tissue collection. The limbs are amputated using a quillitine, then both experimental and control legs are cut at the ligature and weighed. A second weighing is done as the tibio-cacaneal joint is disarticulated and the foot is weighed.
- 30

Histological Preparations: The transverse muscle located behind the knee (popliteal)

area is dissected and arranged in a metal mold. filled with freezeGel, dipped into cold methylbutane, placed into labeled sample bags at - 80EC until sectioning. Upon sectioning, the muscle is observed under fluorescent microscopy for lymphatics..

The studies described in this example tested activity of agonists or antagonists of the invention. However, one skilled in the art could easily modify the exemplified studies to test  
5 the activity of polynucleotides or polypeptides of the invention (e.g., gene therapy).

*Example 30: Suppression of TNF alpha-induced adhesion molecule expression by a Agonist or Antagonist of the Invention*

10

The recruitment of lymphocytes to areas of inflammation and angiogenesis involves specific receptor-ligand interactions between cell surface adhesion molecules (CAMs) on lymphocytes and the vascular endothelium. The adhesion process, in both normal and pathological settings, follows a multi-step cascade that involves intercellular adhesion  
15 molecule-1 (ICAM-1), vascular cell adhesion molecule-1 (VCAM-1), and endothelial leukocyte adhesion molecule-1 (E-selectin) expression on endothelial cells (EC). The expression of these molecules and others on the vascular endothelium determines the efficiency with which leukocytes may adhere to the local vasculature and extravasate into the local tissue during the development of an inflammatory response. The local concentration of  
20 cytokines and growth factor participate in the modulation of the expression of these CAMs.

Tumor necrosis factor alpha (TNF-a), a potent proinflammatory cytokine, is a stimulator of all three CAMs on endothelial cells and may be involved in a wide variety of inflammatory responses, often resulting in a pathological outcome.

The potential of an agonist or antagonist of the invention to mediate a suppression of TNF-a  
25 induced CAM expression can be examined. A modified ELISA assay which uses ECs as a solid phase absorbent is employed to measure the amount of CAM expression on TNF-a treated ECs when co-stimulated with a member of the FGF family of proteins.

To perform the experiment, human umbilical vein endothelial cell (HUVEC) cultures are obtained from pooled cord harvests and maintained in growth medium (EGM-2; Clonetics. San Diego, CA) supplemented with 10% FCS and 1% penicillin/streptomycin in a  
30 37 degree C humidified incubator containing 5% CO<sub>2</sub>. HUVECs are seeded in 96-well plates at concentrations of  $1 \times 10^4$  cells/well in EGM medium at 37 degree C for 18-24 hrs or



until confluent. The monolayers are subsequently washed 3 times with a serum-free solution of RPMI-1640 supplemented with 100 U/ml penicillin and 100 mg/ml streptomycin, and treated with a given cytokine and/or growth factor(s) for 24 h at 37 degree C. Following incubation, the cells are then evaluated for CAM expression.

- 5 Human Umbilical Vein Endothelial cells (HUVECs) are grown in a standard 96 well plate to confluence. Growth medium is removed from the cells and replaced with 90 ul of 199 Medium (10% FBS). Samples for testing and positive or negative controls are added to the plate in triplicate (in 10 ul volumes). Plates are incubated at 37 degree C for either 5 h (selectin and integrin expression) or 24 h (integrin expression only). Plates are aspirated to  
10 remove medium and 100 µl of 0.1% paraformaldehyde-PBS(with Ca++ and Mg++) is added to each well. Plates are held at 4°C for 30 min.

- Fixative is then removed from the wells and wells are washed 1X with PBS(+Ca,Mg)+0.5% BSA and drained. Do not allow the wells to dry. Add 10 µl of diluted primary antibody to the test and control wells. Anti-ICAM-1-Biotin, Anti-VCAM-1-Biotin  
15 and Anti-E-selectin-Biotin are used at a concentration of 10 µg/ml (1:10 dilution of 0.1 mg/ml stock antibody). Cells are incubated at 37°C for 30 min. in a humidified environment. Wells are washed X3 with PBS(+Ca,Mg)+0.5% BSA.

- Then add 20 µl of diluted ExtrAvidin-Alkaline Phosphatase (1:5,000 dilution) to each well and incubated at 37°C for 30 min. Wells are washed X3 with PBS(+Ca,Mg)+0.5%  
20 BSA. 1 tablet of p-Nitrophenol Phosphate pNPP is dissolved in 5 ml of glycine buffer (pH 10.4). 100 µl of pNPP substrate in glycine buffer is added to each test well. Standard wells in triplicate are prepared from the working dilution of the ExtrAvidin-Alkaline Phosphatase in glycine buffer: 1:5,000 ( $10^0$ ) >  $10^{0.5}$  >  $10^{-1}$  >  $10^{-1.5}$ . 5 µl of each dilution is added to triplicate wells and the resulting AP content in each well is 5.50 ng, 1.74 ng, 0.55 ng, 0.18 ng. 100 µl  
25 of pNPP reagent must then be added to each of the standard wells. The plate must be incubated at 37°C for 4h. A volume of 50 µl of 3M NaOH is added to all wells. The results are quantified on a plate reader at 405 nm. The background subtraction option is used on blank wells filled with glycine buffer only. The template is set up to indicate the concentration of AP-conjugate in each standard well [ 5.50 ng; 1.74 ng; 0.55 ng; 0.18 ng].  
30 Results are indicated as amount of bound AP-conjugate in each sample.

The studies described in this example tested activity of agonists or antagonists of the invention. However, one skilled in the art could easily modify the exemplified studies to test

the activity of polynucleotides or polypeptides of the invention (e.g., gene therapy).

*Example 31: Production Of Polypeptide of the Invention For High-Throughput Screening Assays*

5

The following protocol produces a supernatant containing polypeptide of the present invention to be tested. This supernatant can then be used in the Screening Assays described in Examples 33-42.

10 First, dilute Poly-D-Lysine (644 587 Boehringer-Mannheim) stock solution (1mg/ml in PBS) 1:20 in PBS (w/o calcium or magnesium 17-516F Biowhittaker) for a working solution of 50ug/ml. Add 200 ul of this solution to each well (24 well plates) and incubate at RT for 20 minutes. Be sure to distribute the solution over each well (note: a 12-channel pipetter may be used with tips on every other channel). Aspirate off the Poly-D-Lysine solution and rinse with 1ml PBS (Phosphate Buffered Saline). The PBS should remain in the well until just prior to plating the cells and plates may be poly-lysine coated in advance for up to two weeks.

20 Plate 293T cells (do not carry cells past P+20) at  $2 \times 10^5$  cells/well in .5ml DMEM(Dulbecco's Modified Eagle Medium)(with 4.5 G/L glucose and L-glutamine (12-604F Biowhittaker))/10% heat inactivated FBS(14-503F Biowhittaker)/1x Penstrep(17-602E Biowhittaker). Let the cells grow overnight.

25 The next day, mix together in a sterile solution basin: 300 ul Lipofectamine (18324-012 Gibco/BRL) and 5ml Optimem I (31985070 Gibco/BRL)/96-well plate. With a small volume multi-channel pipetter, aliquot approximately 2ug of an expression vector containing a polynucleotide insert, produced by the methods described in Examples 8-10, into an appropriately labeled 96-well round bottom plate. With a multi-channel pipetter, add 50ul of the Lipofectamine/Optimem I mixture to each well. Pipette up and down gently to mix. Incubate at RT 15-45 minutes. After about 20 minutes, use a multi-channel pipetter to add 150ul Optimem I to each well. As a control, one plate of vector DNA lacking an insert should be transfected with each set of transfections.

30 Preferably, the transfection should be performed by tag-teaming the following tasks. By tag-teaming, hands on time is cut in half, and the cells do not spend too much time on PBS. First, person A aspirates off the media from four 24-well plates of cells, and then

person B rinses each well with .5-1ml PBS. Person A then aspirates off PBS rinse, and person B, using a12-channel pipetter with tips on every other channel, adds the 200ul of DNA/Lipofectamine/Optimem I complex to the odd wells first, then to the even wells, to each row on the 24-well plates. Incubate at 37 degree C for 6 hours.

- 5 While cells are incubating, prepare appropriate media, either 1%BSA in DMEM with 1x penstrep, or HGS CHO-5 media (116.6 mg/L of CaCl<sub>2</sub> (anhyd); 0.00130 mg/L CuSO<sub>4</sub>-5H<sub>2</sub>O; 0.050 mg/L of Fe(NO<sub>3</sub>)<sub>3</sub>-9H<sub>2</sub>O; 0.417 mg/L of FeSO<sub>4</sub>-7H<sub>2</sub>O; 311.80 mg/L of Kcl; 28.64 mg/L of MgCl<sub>2</sub>; 48.84 mg/L of MgSO<sub>4</sub>; 6995.50 mg/L of NaCl; 2400.0 mg/L of NaHCO<sub>3</sub>; 62.50 mg/L of NaH<sub>2</sub>PO<sub>4</sub>-H<sub>2</sub>O; 71.02 mg/L of Na<sub>2</sub>HPO<sub>4</sub>; .4320 mg/L of ZnSO<sub>4</sub>-10 7H<sub>2</sub>O; .002 mg/L of Arachidonic Acid ; 1.022 mg/L of Cholesterol; .070 mg/L of DL-alpha-Tocopherol-Acetate; 0.0520 mg/L of Linoleic Acid; 0.010 mg/L of Linolenic Acid; 0.010 mg/L of Myristic Acid; 0.010 mg/L of Oleic Acid; 0.010 mg/L of Palmitric Acid; 0.010 mg/L of Palmitic Acid; 100 mg/L of Pluronic F-68; 0.010 mg/L of Stearic Acid; 2.20 mg/L of Tween 80; 4551 mg/L of D-Glucose; 130.85 mg/ml of L- Alanine; 147.50 mg/ml of L-Arginine-HCL; 7.50 mg/ml of L-Asparagine-H<sub>2</sub>O; 6.65 mg/ml of L-Aspartic Acid; 29.56 15 mg/ml of L-Cystine-2HCL-H<sub>2</sub>O; 31.29 mg/ml of L-Cystine-2HCL; 7.35 mg/ml of L-Glutamic Acid; 365.0 mg/ml of L-Glutamine; 18.75 mg/ml of Glycine; 52.48 mg/ml of L-Histidine-HCL-H<sub>2</sub>O; 106.97 mg/ml of L-Isoleucine; 111.45 mg/ml of L-Leucine; 163.75 mg/ml of L-Lysine HCL; 32.34 mg/ml of L-Methionine; 68.48 mg/ml of L-Phenylalanine; 20 40.0 mg/ml of L-Proline; 26.25 mg/ml of L-Serine; 101.05 mg/ml of L-Threonine; 19.22 mg/ml of L-Tryptophan; 91.79 mg/ml of L-Tyrosine-2Na-2H<sub>2</sub>O; and 99.65 mg/ml of L-Valine; 0.0035 mg/L of Biotin; 3.24 mg/L of D-Ca Pantothenate; 11.78 mg/L of Choline Chloride; 4.65 mg/L of Folic Acid; 15.60 mg/L of i-Inositol; 3.02 mg/L of Niacinamide; 3.00 mg/L of Pyridoxal HCL; 0.031 mg/L of Pyridoxine HCL; 0.319 mg/L of Riboflavin; 3.17 25 mg/L of Thiamine HCL; 0.365 mg/L of Thymidine; 0.680 mg/L of Vitamin B<sub>12</sub>; 25 mM of HEPES Buffer; 2.39 mg/L of Na Hypoxanthine; 0.105 mg/L of Lipoic Acid; 0.081 mg/L of Sodium Putrescine-2HCL; 55.0 mg/L of Sodium Pyruvate; 0.0067 mg/L of Sodium Selenite; 20uM of Ethanolamine; 0.122 mg/L of Ferric Citrate; 41.70 mg/L of Methyl-B-Cyclodextrin complexed with Linoleic Acid; 33.33 mg/L of Methyl-B-Cyclodextrin complexed with Oleic 30 Acid; 10 mg/L of Methyl-B-Cyclodextrin complexed with Retinal Acetate. Adjust

osmolarity to 327 mOsm) with 2mm glutamine and 1x penstrep. (BSA (81-068-3 Bayer) 100gm dissolved in 1L DMEM for a 10% BSA stock solution). Filter the media and collect 50 ul for endotoxin assay in 15ml polystyrene conical.

5 The transfection reaction is terminated, preferably by tag-teaming, at the end of the incubation period. Person A aspirates off the transfection media, while person B adds 1.5ml appropriate media to each well. Incubate at 37 degree C for 45 or 72 hours depending on the media used: 1%BSA for 45 hours or CHO-5 for 72 hours.

10 On day four, using a 300ul multichannel pipetter, aliquot 600ul in one 1ml deep well plate and the remaining supernatant into a 2ml deep well. The supernatants from each well can then be used in the assays described in Examples 33-40.

It is specifically understood that when activity is obtained in any of the assays described below using a supernatant, the activity originates from either the polypeptide of the present invention directly (e.g., as a secreted protein) or by polypeptide of the present invention inducing expression of other proteins, which are then secreted into the supernatant.

15 Thus, the invention further provides a method of identifying the protein in the supernatant characterized by an activity in a particular assay.

*Example 32: Construction of GAS Reporter Construct*

20 One signal transduction pathway involved in the differentiation and proliferation of cells is called the Jaks-STATs pathway. Activated proteins in the Jaks-STATs pathway bind to gamma activation site "GAS" elements or interferon-sensitive responsive element ("ISRE"), located in the promoter of many genes. The binding of a protein to these elements alter the expression of the associated gene.

25 GAS and ISRE elements are recognized by a class of transcription factors called Signal Transducers and Activators of Transcription, or "STATs." There are six members of the STATs family. Stat1 and Stat3 are present in many cell types, as is Stat2 (as response to IFN-alpha is widespread). Stat4 is more restricted and is not in many cell types though it has been found in T helper class 1, cells after treatment with IL-12. Stat5 was originally called

30 mammary growth factor, but has been found at higher concentrations in other cells including myeloid cells. It can be activated in tissue culture cells by many cytokines.

The STATs are activated to translocate from the cytoplasm to the nucleus upon

tyrosine phosphorylation by a set of kinases known as the Janus Kinase ("Jaks") family. Jaks represent a distinct family of soluble tyrosine kinases and include Tyk2, Jak1, Jak2, and Jak3. These kinases display significant sequence similarity and are generally catalytically inactive in resting cells.

5       The Jaks are activated by a wide range of receptors summarized in the Table below. (Adapted from review by Schidler and Damell, *Ann. Rev. Biochem.* 64:621-51 (1995).) A cytokine receptor family, capable of activating Jaks, is divided into two groups: (a) Class 1 includes receptors for IL-2, IL-3, IL-4, IL-6, IL-7, IL-9, IL-11, IL-12, IL-15, Epo, PRL, GH, G-CSF, GM-CSF, LIF, CNTF, and thrombopoietin; and (b) Class 2 includes IFN- $\alpha$ , IFN- $\gamma$ ,  
10   and IL-10. The Class 1 receptors share a conserved cysteine motif (a set of four conserved cysteines and one tryptophan) and a WSXWS motif (a membrane proximal region encoding Trp-Ser-Xxx-Trp-Ser (SEQ ID NO:1548)).

      Thus, on binding of a ligand to a receptor, Jaks are activated, which in turn activate STATs, which then translocate and bind to GAS elements. This entire process is  
15   encompassed in the Jaks-STATs signal transduction pathway.

      Therefore, activation of the Jaks-STATs pathway, reflected by the binding of the GAS or the ISRE element, can be used to indicate proteins involved in the proliferation and differentiation of cells. For example, growth factors and cytokines are known to activate the Jaks-STATs pathway. (See Table below.) Thus, by using GAS elements linked to reporter  
20   molecules, activators of the Jaks-STATs pathway can be identified.

	<u>Ligand</u>	<u>JAKs</u>				<u>STATS GAS(elements) or ISRE</u>	
		<u>tyk2</u>	<u>Jak1</u>	<u>Jak2</u>	<u>Jak3</u>		
	<u>IFN family</u>						
5	IFN-a/B	+	+	-	-	1,2,3	ISRE
	IFN-g		+	+	-	1	GAS
	(IRF1>Lys6>IFP)						
	IL-10	+	?	?	-	1,3	
10	<u>gp130 family</u>						
	IL-6 (Pleiotrohic)	+	+	+	?	1,3	GAS
	(IRF1>Lys6>IFP)						
	IL-11(Pleiotrohic)	?	+	?	?	1,3	
	OnM(Pleiotrohic)	?	+	+	?	1,3	
15	LIF(Pleiotrohic)	?	+	+	?	1,3	
	CNTF(Pleiotrohic)	-/+	+	+	?	1,3	
	G-CSF(Pleiotrohic)	?	+	?	?	1,3	
	IL-12(Pleiotrohic)	+	-	+	+	1,3	
20	<u>g-C family</u>						
	IL-2 (lymphocytes)	-	+	-	+	1,3,5	GAS
	IL-4 (lymph/myeloid)	-	+	-	+	6	GAS (IRF1 = IFP
	>>Ly6)(IgH)						
	IL-7 (lymphocytes)	-	+	-	+	5	GAS
25	IL-9 (lymphocytes)	-	+	-	+	5	GAS
	IL-13 (lymphocyte)	-	+	?	?	6	GAS
	IL-15	?	+	?	+	5	GAS
	<u>gp140 family</u>						
30	IL-3 (myeloid)	-	-	+	-	5	GAS
	(IRF1>IFP>>Ly6)						
	IL-5 (myeloid)	-	-	+	-	5	GAS
	GM-CSF (myeloid)	-	-	+	-	5	GAS

Growth hormone family

	GH	?	-	+	-	5	
	PRL	?	+/-	+	-	1,3,5	
5	EPO	?	-	+	-	5	GAS(B-
	CAS>IRF1=IFP>>Ly6)						

Receptor Tyrosine Kinases

	EGF	?	+	+	-	1,3	GAS (IRF1)
10	PDGF	?	+	+	-	1,3	
	CSF-1	?	+	+	-	1,3	GAS (not IRF1)

To construct a synthetic GAS containing promoter element, which is used in the Biological Assays described in Examples 33-34, a PCR based strategy is employed to generate a GAS-SV40 promoter sequence. The 5' primer contains four tandem copies of the GAS binding site found in the IRF1 promoter and previously demonstrated to bind STATs upon induction with a range of cytokines (Rothman et al., Immunity 1:457-468 (1994).), although other GAS or ISRE elements can be used instead. The 5' primer also contains 18bp of sequence complementary to the SV40 early promoter sequence and is flanked with an XhoI site. The sequence of the 5' primer is:

5' GCGCCTCGAGATTTCCTCCGAAATCTAGATTTCCTCCGAAATGATTTCCTCCGAAATGATTTCCTCCGAAATATCTGCCATCTCAATTAG:3' (SEQ ID NO:1549)

The downstream primer is complementary to the SV40 promoter and is flanked with a Hind III site: 5' GCGGCAAGCTTTTGGCAAAGCCTAGGC:3' (SEQ ID NO:1550)

PCR amplification is performed using the SV40 promoter template present in the B-gal:promoter plasmid obtained from Clontech. The resulting PCR fragment is digested with XhoI/Hind III and subcloned into BLSK2-. (Stratagene.) Sequencing with forward and reverse primers confirms that the insert contains the following sequence:

5' CTCGAGATTTCCTCCGAAATCTAGATTTCCTCCGAAATGATTTCCTCCGAAATGATTTCCTCCGAAATATCTGCCATCTCAATTAGTCAGCAACCATAGTCCCGCCCTAACTCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTGGAGGCCTAGGCTTTGCAAAAAGCTT:3' (SEQ ID NO:1551)

With this GAS promoter element linked to the SV40 promoter, a GAS:SEAP2 reporter construct is next engineered. Here, the reporter molecule is a secreted alkaline phosphatase, or "SEAP." Clearly, however, any reporter molecule can be instead of SEAP, in this or in any of the other Examples. Well known reporter molecules that can be used instead of SEAP include chloramphenicol



acetyltransferase (CAT), luciferase, alkaline phosphatase, B-galactosidase, green fluorescent protein (GFP), or any protein detectable by an antibody.

The above sequence confirmed synthetic GAS-SV40 promoter element is subcloned into the pSEAP-Promoter vector obtained from Clontech using HindIII and XhoI, effectively replacing the SV40 promoter with the amplified GAS:SV40 promoter element, to create the GAS-SEAP vector. However, this vector does not contain a neomycin resistance gene, and therefore, is not preferred for mammalian expression systems.

Thus, in order to generate mammalian stable cell lines expressing the GAS-SEAP reporter, the GAS-SEAP cassette is removed from the GAS-SEAP vector using SalI and NotI, and inserted into a backbone vector containing the neomycin resistance gene, such as pGFP-1 (Clontech), using these restriction sites in the multiple cloning site, to create the GAS-SEAP/Neo vector. Once this vector is transfected into mammalian cells, this vector can then be used as a reporter molecule for GAS binding as described in Examples 33-34.

Other constructs can be made using the above description and replacing GAS with a different promoter sequence. For example, construction of reporter molecules containing NFK-B and EGR promoter sequences are described in Examples 35 and 36. However, many other promoters can be substituted using the protocols described in these Examples. For instance, SRE, IL-2, NFAT, or Osteocalcin promoters can be substituted, alone or in combination (e.g., GAS/NF-KB/EGR, GAS/NF-KB, IL-2/NFAT, or NF-KB/GAS). Similarly, other cell lines can be used to test reporter construct activity, such as HELA (epithelial), HUVEC (endothelial), Reh (B-cell), Saos-2 (osteoblast), HUVAC (aortic), or Cardiomyocyte.

*Example 33: High-Throughput Screening Assay for T-cell Activity.*

The following protocol is used to assess T-cell activity by identifying factors, and determining whether supernate containing a polypeptide of the invention proliferates and/or differentiates T-cells. T-cell activity is assessed using the

GAS/SEAP/Neo construct produced in Example 32. Thus, factors that increase SEAP activity indicate the ability to activate the Jaks-STATS signal transduction pathway. The T-cell used in this assay is Jurkat T-cells (ATCC Accession No. TIB-152), although Molt-3 cells (ATCC Accession No. CRL-1552) and Molt-4 cells (ATCC  
5 Accession No. CRL-1582) cells can also be used.

Jurkat T-cells are lymphoblastic CD4<sup>+</sup> Th1 helper cells. In order to generate stable cell lines, approximately 2 million Jurkat cells are transfected with the GAS-SEAP/neo vector using DMRIE-C (Life Technologies)(transfection procedure described below). The transfected cells are seeded to a density of approximately  
10 20,000 cells per well and transfectants resistant to 1 mg/ml gentamicin selected. Resistant colonies are expanded and then tested for their response to increasing concentrations of interferon gamma. The dose response of a selected clone is demonstrated.

Specifically, the following protocol will yield sufficient cells for 75 wells  
15 containing 200 ul of cells. Thus, it is either scaled up, or performed in multiple to generate sufficient cells for multiple 96 well plates. Jurkat cells are maintained in RPMI + 10% serum with 1%Pen-Strep. Combine 2.5 mls of OPTI-MEM (Life Technologies) with 10 ug of plasmid DNA in a T25 flask. Add 2.5 ml OPTI-MEM containing 50 ul of DMRIE-C and incubate at room temperature for 15-45 mins.

20 During the incubation period, count cell concentration, spin down the required number of cells ( $10^7$  per transfection), and resuspend in OPTI-MEM to a final concentration of  $10^7$  cells/ml. Then add 1ml of  $1 \times 10^7$  cells in OPTI-MEM to T25 flask and incubate at 37 degree C for 6 hrs. After the incubation, add 10 ml of RPMI + 15% serum.

25 The Jurkat:GAS-SEAP stable reporter lines are maintained in RPMI + 10% serum, 1 mg/ml Gentamicin, and 1% Pen-Strep. These cells are treated with supernatants containing polypeptide of the present invention or polypeptide of the present invention induced polypeptides as produced by the protocol described in Example 31.

30 On the day of treatment with the supernatant, the cells should be washed and

resuspended in fresh RPMI + 10% serum to a density of 500,000 cells per ml. The exact number of cells required will depend on the number of supernatants being screened. For one 96 well plate, approximately 10 million cells (for 10 plates, 100 million cells) are required.

5           Transfer the cells to a triangular reservoir boat, in order to dispense the cells into a 96 well dish, using a 12 channel pipette. Using a 12 channel pipette, transfer 200 ul of cells into each well (therefore adding 100,000 cells per well).

          After all the plates have been seeded, 50 ul of the supernatants are transferred directly from the 96 well plate containing the supernatants into each well using a 12  
10   channel pipette. In addition, a dose of exogenous interferon gamma (0.1, 1.0, 10 ng) is added to wells H9, H10, and H11 to serve as additional positive controls for the assay.

          The 96 well dishes containing Jurkat cells treated with supernatants are placed in an incubator for 48 hrs (note: this time is variable between 48-72 hrs). 35 ul  
15   samples from each well are then transferred to an opaque 96 well plate using a 12 channel pipette. The opaque plates should be covered (using sellophene covers) and stored at -20 degree C until SEAP assays are performed according to Example 37. The plates containing the remaining treated cells are placed at 4 degree C and serve as a source of material for repeating the assay on a specific well if desired.

20           As a positive control, 100 Unit/ml interferon gamma can be used which is known to activate Jurkat T cells. Over 30 fold induction is typically observed in the positive control wells.

          The above protocol may be used in the generation of both transient, as well as, stable transfected cells, which would be apparent to those of skill in the art.

25

*Example 34: High-Throughput Screening Assay Identifying Myeloid Activity*

          The following protocol is used to assess myeloid activity of polypeptide of the present invention by determining whether polypeptide of the present invention  
30   proliferates and/or differentiates myeloid cells. Myeloid cell activity is assessed using

the GAS/SEAP/Neo construct produced in Example 32. Thus, factors that increase SEAP activity indicate the ability to activate the Jaks-STATS signal transduction pathway. The myeloid cell used in this assay is U937, a pre-monocyte cell line, although TF-1, HL60, or KG1 can be used.

- 5 To transiently transfect U937 cells with the GAS/SEAP/Neo construct produced in Example 32, a DEAE-Dextran method (Kharbanda et. al., 1994, Cell Growth & Differentiation, 5:259-265) is used. First, harvest  $2 \times 10^7$  U937 cells and wash with PBS. The U937 cells are usually grown in RPMI 1640 medium containing 10% heat-inactivated fetal bovine serum (FBS) supplemented with 100 units/ml  
10 penicillin and 100 mg/ml streptomycin.

Next, suspend the cells in 1 ml of 20 mM Tris-HCl (pH 7.4) buffer containing 0.5 mg/ml DEAE-Dextran, 8 ug GAS-SEAP2 plasmid DNA, 140 mM NaCl, 5 mM KCl, 375 uM  $\text{Na}_2\text{HPO}_4 \cdot 7\text{H}_2\text{O}$ , 1 mM  $\text{MgCl}_2$ , and 675 uM  $\text{CaCl}_2$ . Incubate at 37 degrees C for 45 min.

- 15 Wash the cells with RPMI 1640 medium containing 10% FBS and then resuspend in 10 ml complete medium and incubate at 37 degree C for 36 hr.

The GAS-SEAP/U937 stable cells are obtained by growing the cells in 400 ug/ml G418. The G418-free medium is used for routine growth but every one to two months, the cells should be re-grown in 400 ug/ml G418 for couple of passages.

- 20 These cells are tested by harvesting  $1 \times 10^8$  cells (this is enough for ten 96-well plates assay) and wash with PBS. Suspend the cells in 200 ml above described growth medium, with a final density of  $5 \times 10^5$  cells/ml. Plate 200 ul cells per well in the 96-well plate (or  $1 \times 10^5$  cells/well).

- Add 50 ul of the supernatant prepared by the protocol described in Example  
25 31. Incubate at 37 degree C for 48 to 72 hr. As a positive control, 100 Unit/ml interferon gamma can be used which is known to activate U937 cells. Over 30 fold induction is typically observed in the positive control wells. SEAP assay the supernatant according to the protocol described in Example 37.

- 30 *Example 35: High-Throughput Screening Assay Identifying Neuronal Activity.*

When cells undergo differentiation and proliferation, a group of genes are activated through many different signal transduction pathways. One of these genes, EGR1 (early growth response gene 1), is induced in various tissues and cell types upon activation. The promoter of EGR1 is responsible for such induction. Using the EGR1 promoter linked to reporter molecules, activation of cells can be assessed by polypeptide of the present invention.

Particularly, the following protocol is used to assess neuronal activity in PC12 cell lines. PC12 cells (rat phenochromocytoma cells) are known to proliferate and/or differentiate by activation with a number of mitogens, such as TPA (tetradecanoyl phorbol acetate), NGF (nerve growth factor), and EGF (epidermal growth factor). The EGR1 gene expression is activated during this treatment. Thus, by stably transfecting PC12 cells with a construct containing an EGR promoter linked to SEAP reporter, activation of PC12 cells by polypeptide of the present invention can be assessed.

The EGR/SEAP reporter construct can be assembled by the following protocol. The EGR-1 promoter sequence (-633 to +1)(Sakamoto K et al., Oncogene 6:867-871 (1991)) can be PCR amplified from human genomic DNA using the following primers:

20        5' GCGCTCGAGGGATGACAGCGATAGAACCCCGG -3' (SEQ ID NO: 1552)

5' GCGAAGCTTCGCGACTCCCCGGATCCGCCTC-3' (SEQ ID NO: 1553)

Using the GAS:SEAP/Neo vector produced in Example 32, EGR1 amplified product can then be inserted into this vector. Linearize the GAS:SEAP/Neo vector using restriction enzymes XhoI/HindIII, removing the GAS/SV40 stuffer. Restrict the EGR1 amplified product with these same enzymes. Ligate the vector and the EGR1 promoter.

To prepare 96 well-plates for cell culture, two mls of a coating solution (1:30 dilution of collagen type I (Upstate Biotech Inc. Cat#08-115) in 30% ethanol (filter

sterilized)) is added per one 10 cm plate or 50 ml per well of the 96-well plate, and allowed to air dry for 2 hr.

PC12 cells are routinely grown in RPMI-1640 medium (Bio Whittaker) containing 10% horse serum (JRH BIOSCIENCES, Cat. # 12449-78P), 5% heat-inactivated fetal bovine serum (FBS) supplemented with 100 units/ml penicillin and 100 ug/ml streptomycin on a precoated 10 cm tissue culture dish. One to four split is done every three to four days. Cells are removed from the plates by scraping and resuspended with pipetting up and down for more than 15 times.

Transfect the EGR/SEAP/Neo construct into PC12 using the Lipofectamine protocol described in Example 31. EGR-SEAP/PC12 stable cells are obtained by growing the cells in 300 ug/ml G418. The G418-free medium is used for routine growth but every one to two months, the cells should be re-grown in 300 ug/ml G418 for couple of passages.

To assay for neuronal activity, a 10 cm plate with cells around 70 to 80% confluent is screened by removing the old medium. Wash the cells once with PBS (Phosphate buffered saline). Then starve the cells in low serum medium (RPMI-1640 containing 1% horse serum and 0.5% FBS with antibiotics) overnight.

The next morning, remove the medium and wash the cells with PBS. Scrape off the cells from the plate, suspend the cells well in 2 ml low serum medium. Count the cell number and add more low serum medium to reach final cell density as  $5 \times 10^5$  cells/ml.

Add 200 ul of the cell suspension to each well of 96-well plate (equivalent to  $1 \times 10^5$  cells/well). Add 50 ul supernatant produced by Example 31, 37 degree C for 48 to 72 hr. As a positive control, a growth factor known to activate PC12 cells through EGR can be used, such as 50 ng/ul of Neuronal Growth Factor (NGF). Over fifty-fold induction of SEAP is typically seen in the positive control wells. SEAP assay the supernatant according to Example 37.

*Example 36: High-Throughput Screening Assay for T-cell Activity*

NF-KB (Nuclear Factor KB) is a transcription factor activated by a wide variety of agents including the inflammatory cytokines IL-1 and TNF. CD30 and CD40, lymphotoxin-alpha and lymphotoxin-beta, by exposure to LPS or thrombin, and by expression of certain viral gene products. As a transcription factor, NF-KB regulates the expression of genes involved in immune cell activation, control of apoptosis (NF- KB appears to shield cells from apoptosis), B and T-cell development, anti-viral and antimicrobial responses, and multiple stress responses.

In non-stimulated conditions, NF- KB is retained in the cytoplasm with I-KB (Inhibitor KB). However, upon stimulation, I- KB is phosphorylated and degraded, causing NF- KB to shuttle to the nucleus, thereby activating transcription of target genes. Target genes activated by NF- KB include IL-2, IL-6, GM-CSF, ICAM-1 and class I MHC.

Due to its central role and ability to respond to a range of stimuli, reporter constructs utilizing the NF-KB promoter element are used to screen the supernatants produced in Example 31. Activators or inhibitors of NF-KB would be useful in treating, preventing, and/or diagnosing diseases. For example, inhibitors of NF-KB could be used to treat those diseases related to the acute or chronic activation of NF-KB, such as rheumatoid arthritis.

To construct a vector containing the NF-KB promoter element, a PCR based strategy is employed. The upstream primer contains four tandem copies of the NF-KB binding site (GGGGACTTTCCC) (SEQ ID NO:1554), 18 bp of sequence complementary to the 5' end of the SV40 early promoter sequence, and is flanked with an XhoI site:

5':GCGGCCTCGAGGGGACTTTCCCGGGGACTTTCCGGGGACTTTCCGGGAC  
TTTCCATCCTGCCATCTCAATTAG:3' (SEQ ID NO:1555)

The downstream primer is complementary to the 3' end of the SV40 promoter and is flanked with a Hind III site:

5':GCGGCAAGCTTTTGGCAAAGCCTAGGC:3' (SEQ ID NO:1550)

PCR amplification is performed using the SV40 promoter template present in the pB-gal:promoter plasmid obtained from Clontech. The resulting PCR fragment is

digested with XhoI and Hind III and subcloned into BLSK2-. (Stratagene) Sequencing with the T7 and T3 primers confirms the insert contains the following sequence:

5':CTCGAGGGGACTTTCCCGGGGACTTTCCGGGGACTTTCCGGGACTTTCC  
 5 ATCTGCCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCC  
 ATCCCGCCCCTAACTCCGCCCAGTTCGCCCCATTCTCCGCCCCATGGCTGA  
 CTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCTCGGCCTCTGAGCTA  
 TTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAAA  
 GCTT:3' (SEQ ID NO:1556)

10 Next, replace the SV40 minimal promoter element present in the pSEAP2-promoter plasmid (Clontech) with this NF-KB/SV40 fragment using XhoI and HindIII. However, this vector does not contain a neomycin resistance gene, and therefore, is not preferred for mammalian expression systems.

In order to generate stable mammalian cell lines, the NF-KB/SV40/SEAP  
 15 cassette is removed from the above NF-KB/SEAP vector using restriction enzymes SalI and NotI, and inserted into a vector containing neomycin resistance. Particularly, the NF-KB/SV40/SEAP cassette was inserted into pGFP-1 (Clontech), replacing the GFP gene, after restricting pGFP-1 with SalI and NotI.

Once NF-KB/SV40/SEAP/Neo vector is created, stable Jurkat T-cells are  
 20 created and maintained according to the protocol described in Example 33. Similarly, the method for assaying supernatants with these stable Jurkat T-cells is also described in Example 33. As a positive control, exogenous TNF alpha (0.1, 1, 10 ng) is added to wells H9, H10, and H11, with a 5-10 fold activation typically observed.

#### 25 *Example 37: Assay for SEAP Activity*

As a reporter molecule for the assays described in Examples 33-36, SEAP activity is assayed using the Tropix Phospho-light Kit (Cat. BP-400) according to the following general procedure. The Tropix Phospho-light Kit supplies the Dilution,  
 30 Assay, and Reaction Buffers used below.



Prime a dispenser with the 2.5x Dilution Buffer and dispense 15 ul of 2.5x dilution buffer into Optiplates containing 35 ul of a supernatant. Seal the plates with a plastic sealer and incubate at 65 degree C for 30 min. Separate the Optiplates to avoid uneven heating.

- 5 Cool the samples to room temperature for 15 minutes. Empty the dispenser and prime with the Assay Buffer. Add 50 ml Assay Buffer and incubate at room temperature 5 min. Empty the dispenser and prime with the Reaction Buffer (see the table below). Add 50 ul Reaction Buffer and incubate at room temperature for 20 minutes. Since the intensity of the chemiluminescent signal is time dependent, and it
- 10 takes about 10 minutes to read 5 plates on luminometer, one should treat 5 plates at each time and start the second set 10 minutes later.

Read the relative light unit in the luminometer. Set H12 as blank, and print the results. An increase in chemiluminescence indicates reporter activity.

#### 15 Reaction Buffer Formulation:

# of plates	Rxn buffer diluent (ml)	CSPD (ml)
10	60	3
11	65	3.25
12	70	3.5
13	75	3.75
14	80	4
15	85	4.25
16	90	4.5
17	95	4.75
18	100	5
19	105	5.25
20	110	5.5
21	115	5.75
22	120	6
23	125	6.25
24	130	6.5

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25	135	6.75
26	140	7
27	145	7.25
28	150	7.5
29	155	7.75
30	160	8
31	165	8.25
32	170	8.5
33	175	8.75
34	180	9
35	185	9.25
36	190	9.5
37	195	9.75
38	200	10
39	205	10.25
40	210	10.5
41	215	10.75
42	220	11
43	225	11.25
44	230	11.5
45	235	11.75
46	240	12
47	245	12.25
48	250	12.5
49	255	12.75
50	260	13

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*Example 38: High-Throughput Screening Assay Identifying Changes in Small Molecule Concentration and Membrane Permeability*

- 5 Binding of a ligand to a receptor is known to alter intracellular levels of small molecules, such as calcium, potassium, sodium, and pH, as well as alter membrane potential. These alterations can be measured in an assay to identify supernatants which bind to receptors of a particular cell. Although the following protocol

describes an assay for calcium, this protocol can easily be modified to detect changes in potassium, sodium, pH, membrane potential, or any other small molecule which is detectable by a fluorescent probe.

5 The following assay uses Fluorometric Imaging Plate Reader ("FLIPR") to measure changes in fluorescent molecules (Molecular Probes) that bind small molecules. Clearly, any fluorescent molecule detecting a small molecule can be used instead of the calcium fluorescent molecule, fluo-4 (Molecular Probes, Inc.; catalog no. F-14202), used here.

10 For adherent cells, seed the cells at 10,000 -20,000 cells/well in a Co-star black 96-well plate with clear bottom. The plate is incubated in a CO<sub>2</sub> incubator for 20 hours. The adherent cells are washed two times in Biotek washer with 200 ul of HBSS (Hank's Balanced Salt Solution) leaving 100 ul of buffer after the final wash.

15 A stock solution of 1 mg/ml fluo-4 is made in 10% pluronic acid DMSO. To load the cells with fluo-4, 50 ul of 12 ug/ml fluo-4 is added to each well. The plate is incubated at 37 degrees C in a CO<sub>2</sub> incubator for 60 min. The plate is washed four times in the Biotek washer with HBSS leaving 100 ul of buffer.

20 For non-adherent cells, the cells are spun down from culture media. Cells are re-suspended to  $2.5 \times 10^6$  cells/ml with HBSS in a 50-ml conical tube. 4 ul of 1 mg/ml fluo-4 solution in 10% pluronic acid DMSO is added to each ml of cell suspension. The tube is then placed in a 37 degrees C water bath for 30-60 min. The cells are washed twice with HBSS, resuspended to  $1 \times 10^6$  cells/ml, and dispensed into a microplate, 100 ul/well. The plate is centrifuged at 1000 rpm for 5 min. The plate is then washed once in Denley Cell Wash with 200 ul, followed by an aspiration step to 100 ul final volume.

25 For a non-cell based assay, each well contains a fluorescent molecule, such as fluo-4. The supernatant is added to the well, and a change in fluorescence is detected.

30 To measure the fluorescence of intracellular calcium, the FLIPR is set for the following parameters: (1) System gain is 300-800 mW; (2) Exposure time is 0.4 second; (3) Camera F/stop is F/2; (4) Excitation is 488 nm; (5) Emission is 530 nm;

and (6) Sample addition is 50 ul. Increased emission at 530 nm indicates an extracellular signaling event caused by the a molecule. either polypeptide of the present invention or a molecule induced by polypeptide of the present invention, which has resulted in an increase in the intracellular  $Ca^{++}$  concentration.

5

*Example 40: High-Throughput Screening Assay Identifying Tyrosine Kinase Activity*

The Protein Tyrosine Kinases (PTK) represent a diverse group of transmembrane and cytoplasmic kinases. Within the Receptor Protein Tyrosine  
10 Kinase RPTK) group are receptors for a range of mitogenic and metabolic growth factors including the PDGF, FGF, EGF, NGF, HGF and Insulin receptor subfamilies. In addition there are a large family of RPTKs for which the corresponding ligand is unknown. Ligands for RPTKs include mainly secreted small proteins, but also membrane-bound and extracellular matrix proteins.

15 Activation of RPTK by ligands involves ligand-mediated receptor dimerization, resulting in transphosphorylation of the receptor subunits and activation of the cytoplasmic tyrosine kinases. The cytoplasmic tyrosine kinases include receptor associated tyrosine kinases of the src-family (e.g., src, yes, lck, lyn, fyn) and non-receptor linked and cytosolic protein tyrosine kinases, such as the Jak family,  
20 members of which mediate signal transduction triggered by the cytokine superfamily of receptors (e.g., the Interleukins, Interferons, GM-CSF, and Leptin).

Because of the wide range of known factors capable of stimulating tyrosine kinase activity, identifying whether polypeptide of the present invention or a molecule induced by polypeptide of the present invention is capable of activating tyrosine  
25 kinase signal transduction pathways is of interest. Therefore, the following protocol is designed to identify such molecules capable of activating the tyrosine kinase signal transduction pathways.

Seed target cells (e.g., primary keratinocytes) at a density of approximately 25,000 cells per well in a 96 well Loprodyne Silent Screen Plates purchased from  
30 Nalge Nunc (Naperville, IL). The plates are sterilized with two 30 minute rinses with

100% ethanol, rinsed with water and dried overnight. Some plates are coated for 2 hr with 100 ml of cell culture grade type I collagen (50 mg/ml), gelatin (2%) or polylysine (50 mg/ml), all of which can be purchased from Sigma Chemicals (St. Louis, MO) or 10% Matrigel purchased from Becton Dickinson (Bedford, MA), or calf serum, rinsed with PBS and stored at 4 degree C. Cell growth on these plates is assayed by seeding 5,000 cells/well in growth medium and indirect quantitation of cell number through use of alamarBlue as described by the manufacturer Alamar Biosciences, Inc. (Sacramento, CA) after 48 hr. Falcon plate covers #3071 from Becton Dickinson (Bedford, MA) are used to cover the Loprodyne Silent Screen  
10 Plates. Falcon Microtest III cell culture plates can also be used in some proliferation experiments.

To prepare extracts, A431 cells are seeded onto the nylon membranes of Loprodyne plates (20,000/200ml/well) and cultured overnight in complete medium. Cells are quiesced by incubation in serum-free basal medium for 24 hr. After 5-20  
15 minutes treatment with EGF (60ng/ml) or 50 ul of the supernatant produced in Example 31, the medium was removed and 100 ml of extraction buffer ((20 mM HEPES pH 7.5, 0.15 M NaCl, 1% Triton X-100, 0.1% SDS, 2 mM Na<sub>3</sub>VO<sub>4</sub>, 2 mM Na<sub>4</sub>P<sub>2</sub>O<sub>7</sub> and a cocktail of protease inhibitors (# 1836170) obtained from Boehringer Mannheim (Indianapolis, IN) is added to each well and the plate is  
20 shaken on a rotating shaker for 5 minutes at 4°C. The plate is then placed in a vacuum transfer manifold and the extract filtered through the 0.45 mm membrane bottoms of each well using house vacuum. Extracts are collected in a 96-well catch/assay plate in the bottom of the vacuum manifold and immediately placed on ice. To obtain extracts clarified by centrifugation, the content of each well, after  
25 detergent solubilization for 5 minutes, is removed and centrifuged for 15 minutes at 4 degree C at 16,000 x g.

Test the filtered extracts for levels of tyrosine kinase activity. Although many methods of detecting tyrosine kinase activity are known, one method is described here.

30 Generally, the tyrosine kinase activity of a supernatant is evaluated by

determining its ability to phosphorylate a tyrosine residue on a specific substrate (a biotinylated peptide). Biotinylated peptides that can be used for this purpose include PSK1 (corresponding to amino acids 6-20 of the cell division kinase cdc2-p34) and PSK2 (corresponding to amino acids 1-17 of gastrin). Both peptides are substrates for a range of tyrosine kinases and are available from Boehringer Mannheim.

The tyrosine kinase reaction is set up by adding the following components in order. First, add 10ul of 5uM Biotinylated Peptide, then 10ul ATP/Mg<sub>2</sub><sup>+</sup> (5mM ATP/50mM MgCl<sub>2</sub>), then 10ul of 5x Assay Buffer (40mM imidazole hydrochloride, pH7.3, 40 mM beta-glycerophosphate, 1mM EGTA, 100mM MgCl<sub>2</sub>, 5 mM MnCl<sub>2</sub>, 0.5 mg/ml BSA); then 5ul of Sodium Vanadate(1mM), and then 5ul of water. Mix the components gently and preincubate the reaction mix at 30 degree C for 2 min. Initial the reaction by adding 10ul of the control enzyme or the filtered supernatant.

The tyrosine kinase assay reaction is then terminated by adding 10 ul of 120mM EDTA and place the reactions on ice.

Tyrosine kinase activity is determined by transferring 50 ul aliquot of reaction mixture to a microtiter plate (MTP) module and incubating at 37 degree C for 20 min. This allows the streptavidin coated 96 well plate to associate with the biotinylated peptide. Wash the MTP module with 300ul/well of PBS four times. Next add 75 ul of anti-phosphotyrosine antibody conjugated to horse radish peroxidase(anti-P-Tyr-POD(0.5u/ml)) to each well and incubate at 37 degree C for one hour. Wash the well as above.

Next add 100ul of peroxidase substrate solution (Boehringer Mannheim) and incubate at room temperature for at least 5 mins (up to 30 min). Measure the absorbance of the sample at 405 nm by using ELISA reader. The level of bound peroxidase activity is quantitated using an ELISA reader and reflects the level of tyrosine kinase activity.

*Example 41: High-Throughput Screening Assay Identifying Phosphorylation Activity*

As a potential alternative and/or compliment to the assay of protein tyrosine

kinase activity described in Example 40. an assay which detects activation (phosphorylation) of major intracellular signal transduction intermediates can also be used. For example, as described below one particular assay can detect tyrosine phosphorylation of the Erk-1 and Erk-2 kinases. However, phosphorylation of other molecules, such as Raf, JNK, p38 MAP. Map kinase kinase (MEK), MEK kinase, Src, 5 Muscle specific kinase (MuSK), IRAK, Tec, and Janus, as well as any other phosphoserine, phosphotyrosine, or phosphothreonine molecule, can be detected by substituting these molecules for Erk-1 or Erk-2 in the following assay.

Specifically, assay plates are made by coating the wells of a 96-well ELISA 10 plate with 0.1ml of protein G (1ug/ml) for 2 hr at room temp, (RT). The plates are then rinsed with PBS and blocked with 3% BSA/PBS for 1 hr at RT. The protein G plates are then treated with 2 commercial monoclonal antibodies (100ng/well) against Erk-1 and Erk-2 (1 hr at RT) (Santa Cruz Biotechnology). (To detect other molecules, this step can easily be modified by substituting a monoclonal antibody 15 detecting any of the above described molecules.) After 3-5 rinses with PBS, the plates are stored at 4 degree C until use.

A431 cells are seeded at 20,000/well in a 96-well Loprodyne filterplate and cultured overnight in growth medium. The cells are then starved for 48 hr in basal medium (DMEM) and then treated with EGF (6ng/well) or 50 ul of the supernatants 20 obtained in Example 31 for 5-20 minutes. The cells are then solubilized and extracts filtered directly into the assay plate.

After incubation with the extract for 1 hr at RT, the wells are again rinsed. As a positive control, a commercial preparation of MAP kinase (10ng/well) is used in place of A431 extract. Plates are then treated with a commercial polyclonal (rabbit) 25 antibody (1ug/ml) which specifically recognizes the phosphorylated epitope of the Erk-1 and Erk-2 kinases (1 hr at RT). This antibody is biotinylated by standard procedures. The bound polyclonal antibody is then quantitated by successive incubations with Europium-streptavidin and Europium fluorescence enhancing reagent in the Wallac DELFIA instrument (time-resolved fluorescence). An increased 30 fluorescent signal over background indicates a phosphorylation by polypeptide of the

present invention or a molecule induced by polypeptide of the present invention.

*Example 42: Assay for the Stimulation of Bone Marrow CD34+ Cell Proliferation*

5        This assay is based on the ability of human CD34+ to proliferate in the presence of hematopoietic growth factors and evaluates the ability of isolated polypeptides expressed in mammalian cells to stimulate proliferation of CD34+ cells.

         It has been previously shown that most mature precursors will respond to only a single signal. More immature precursors require at least two signals to respond.  
10       Therefore, to test the effect of polypeptides on hematopoietic activity of a wide range of progenitor cells, the assay contains a given polypeptide in the presence or absence of other hematopoietic growth factors. Isolated cells are cultured for 5 days in the presence of Stem Cell Factor (SCF) in combination with tested sample. SCF alone has a very limited effect on the proliferation of bone marrow (BM) cells, acting in  
15       such conditions only as a "survival" factor. However, combined with any factor exhibiting stimulatory effect on these cells (e.g., IL-3), SCF will cause a synergistic effect. Therefore, if the tested polypeptide has a stimulatory effect on a hematopoietic progenitors, such activity can be easily detected. Since normal BM cells have a low level of cycling cells, it is likely that any inhibitory effect of a given polypeptide, or  
20       agonists or antagonists thereof, might not be detected. Accordingly, assays for an inhibitory effect on progenitors is preferably tested in cells that are first subjected to *in vitro* stimulation with SCF+IL+3, and then contacted with the compound that is being evaluated for inhibition of such induced proliferation.

         Briefly, CD34+ cells are isolated using methods known in the art. The cells  
25       are thawed and resuspended in medium (QBSF 60 serum-free medium with 1% L-glutamine (500ml) Quality Biological, Inc., Gaithersburg, MD Cat# 160-204-101). After several gentle centrifugation steps at 200 x g, cells are allowed to rest for one hour. The cell count is adjusted to  $2.5 \times 10^5$  cells/ml. During this time, 100  $\mu$ l of sterile water is added to the peripheral wells of a 96-well plate. The cytokines that  
30       can be tested with a given polypeptide in this assay is rhSCF (R&D Systems,



Minneapolis, MN, Cat# 255-SC) at 50 ng/ml alone and in combination with rhSCF and rhIL-3 (R&D Systems, Minneapolis, MN, Cat# 203-ML) at 30 ng/ml. After one hour, 10  $\mu$ l of prepared cytokines, 50  $\mu$ l of the supernatants prepared in Example 31 (supernatants at 1:2 dilution = 50  $\mu$ l) and 20  $\mu$ l of diluted cells are added to the media  
5 which is already present in the wells to allow for a final total volume of 100  $\mu$ l. The plates are then placed in a 37°C/5% CO<sub>2</sub> incubator for five days.

Eighteen hours before the assay is harvested, 0.5  $\mu$ Ci/well of [3H] Thymidine is added in a 10  $\mu$ l volume to each well to determine the proliferation rate. The experiment is terminated by harvesting the cells from each 96-well plate to a filtermat  
10 using the Tomtec Harvester 96. After harvesting, the filtermats are dried, trimmed and placed into OmniFilter assemblies consisting of one OmniFilter plate and one OmniFilter Tray. 60  $\mu$ l Microscint is added to each well and the plate sealed with TopSeal-A press-on sealing film. A bar code 15 sticker is affixed to the first plate for counting. The sealed plates is then loaded and the level of radioactivity determined  
15 via the Packard Top Count and the printed data collected for analysis. The level of radioactivity reflects the amount of cell proliferation.

The studies described in this example test the activity of a given polypeptide to stimulate bone marrow CD34+ cell proliferation. One skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides (e.g., gene  
20 therapy), antibodies, agonists, and/or antagonists and fragments and variants thereof. As a nonlimiting example, potential antagonists tested in this assay would be expected to inhibit cell proliferation in the presence of cytokines and/or to increase the inhibition of cell proliferation in the presence of cytokines and a given polypeptide. In contrast, potential agonists tested in this assay would be expected to enhance cell  
25 proliferation and/or to decrease the inhibition of cell proliferation in the presence of cytokines and a given polypeptide.

The ability of a gene to stimulate the proliferation of bone marrow CD34+ cells indicates that polynucleotides and polypeptides corresponding to the gene are useful for the diagnosis and treatment of disorders affecting the immune system and  
30 hematopoiesis. Representative uses are described in the "Immune Activity" and

"Infectious Disease" sections above, and elsewhere herein.

*Example 43: Assay for Extracellular Matrix Enhanced Cell Response (EMECCR)*

5           The objective of the Extracellular Matrix Enhanced Cell Response (EMECCR) assay is to identify gene products (e.g., isolated polypeptides) that act on the hematopoietic stem cells in the context of the extracellular matrix (ECM) induced signal.

10           Cells respond to the regulatory factors in the context of signal(s) received from the surrounding microenvironment. For example, fibroblasts, and endothelial and epithelial stem cells fail to replicate in the absence of signals from the ECM. Hematopoietic stem cells can undergo self-renewal in the bone marrow, but not in *in vitro* suspension culture. The ability of stem cells to undergo self-renewal *in vitro* is dependent upon their interaction with the stromal cells and the ECM protein  
15           fibronectin (fn). Adhesion of cells to fn is mediated by the  $\alpha_3\beta_1$  and  $\alpha_4\beta_1$  integrin receptors, which are expressed by human and mouse hematopoietic stem cells. The factor(s) which integrate with the ECM environment and responsible for stimulating stem cell self-renewal has not yet been identified. Discovery of such factors should be of great interest in gene therapy and bone marrow transplant applications

20           Briefly, polystyrene, non tissue culture treated, 96-well plates are coated with fn fragment at a coating concentration of  $0.2 \mu\text{g}/\text{cm}^2$ . Mouse bone marrow cells are plated (1,000 cells/well) in 0.2 ml of serum-free medium. Cells cultured in the presence of IL-3 (5 ng/ml) + SCF (50 ng/ml) would serve as the positive control, conditions under which little self-renewal but pronounced differentiation of the stem  
25           cells is to be expected. Gene products of the invention (e.g., including, but not limited to, polynucleotides and polypeptides of the present invention, and supernatants produced in Example 31), are tested with appropriate negative controls in the presence and absence of SCF(5.0 ng/ml), where test factor supernates represent 10% of the total assay volume. The plated cells are then allowed to grow by incubating in  
30           a low oxygen environment (5%  $\text{CO}_2$ , 7%  $\text{O}_2$ , and 88%  $\text{N}_2$ ) tissue culture incubator

for 7 days. The number of proliferating cells within the wells is then quantitated by measuring thymidine incorporation into cellular DNA. Verification of the positive hits in the assay will require phenotypic characterization of the cells, which can be accomplished by scaling up of the culture system and using appropriate antibody  
5 reagents against cell surface antigens and FACScan.

One skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides (e.g., gene therapy), antibodies, agonists, and/or antagonists and fragments and variants thereof.

If a particular polypeptide of the present invention is found to be a stimulator  
10 of hematopoietic progenitors, polynucleotides and polypeptides corresponding to the gene encoding said polypeptide may be useful for the diagnosis and treatment of disorders affecting the immune system and hematopoiesis. Representative uses are described in the "Immune Activity" and "Infectious Disease" sections above, and elsewhere herein. The gene product may also be useful in the expansion of stem cells  
15 and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types.

Additionally, the polynucleotides and/or polypeptides of the gene of interest and/or agonists and/or antagonists thereof, may also be employed to inhibit the proliferation and differentiation of hematopoietic cells and therefore may be  
20 employed to protect bone marrow stem cells from chemotherapeutic agents during chemotherapy. This antiproliferative effect may allow administration of higher doses of chemotherapeutic agents and, therefore, more effective chemotherapeutic treatment.

Moreover, polynucleotides and polypeptides corresponding to the gene of  
25 interest may also be useful for the treatment and diagnosis of hematopoietic related disorders such as, for example, anemia, pancytopenia, leukopenia, thrombocytopenia or leukemia since stromal cells are important in the production of cells of hematopoietic lineages. The uses include bone marrow cell ex-vivo culture, bone marrow transplantation, bone marrow reconstitution, radiotherapy or chemotherapy of  
30 neoplasia.

*Example 44: Human Dermal Fibroblast and Aortic Smooth Muscle Cell Proliferation*

- The polypeptide of interest is added to cultures of normal human dermal fibroblasts (NHDF) and human aortic smooth muscle cells (AoSMC) and two co-assays are performed with each sample. The first assay examines the effect of the polypeptide of interest on the proliferation of normal human dermal fibroblasts (NHDF) or aortic smooth muscle cells (AoSMC). Aberrant growth of fibroblasts or smooth muscle cells is a part of several pathological processes, including fibrosis, and restenosis. The second assay examines IL6 production by both NHDF and SMC. IL6 production is an indication of functional activation. Activated cells will have increased production of a number of cytokines and other factors, which can result in a proinflammatory or immunomodulatory outcome. Assays are run with and without co-TNF $\alpha$  stimulation, in order to check for costimulatory or inhibitory activity.
- Briefly, on day 1, 96-well black plates are set up with 1000 cells/well (NHDF) or 2000 cells/well (AoSMC) in 100  $\mu$ l culture media. NHDF culture media contains: Clonetics FB basal media, 1mg/ml hFGF, 5mg/ml insulin, 50mg/ml gentamycin, 2%FBS, while AoSMC culture media contains Clonetics SM basal media, 0.5  $\mu$ g/ml hEGF, 5mg/ml insulin, 1 $\mu$ g/ml hFGF, 50mg/ml gentamycin, 50  $\mu$ g/ml Amphotericin B, 5%FBS. After incubation at 37°C for at least 4-5 hours, culture media is aspirated and replaced with growth arrest media. Growth arrest media for NHDF contains fibroblast basal media, 50mg/ml gentamycin, 2% FBS, while growth arrest media for AoSMC contains SM basal media, 50mg/ml gentamycin, 50 $\mu$ g/ml Amphotericin B, 0.4% FBS. Incubate at 37°C until day 2.
- On day 2, serial dilutions and templates of the polypeptide of interest are designed such that they always include media controls and known-protein controls. For both stimulation and inhibition experiments, proteins are diluted in growth arrest media. For inhibition experiments, TNF $\alpha$  is added to a final concentration of 2ng/ml (NHDF) or 5ng/ml (AoSMC). Add 1/3 vol media containing controls or polypeptides of the present invention and incubate at 37°C/5% CO<sub>2</sub> until day 5.

Transfer 60 $\mu$ l from each well to another labeled 96-well plate. cover with a plate-sealer. and store at 4°C until Day 6 (for IL6 ELISA). To the remaining 100  $\mu$ l in the cell culture plate, aseptically add Alamar Blue in an amount equal to 10% of the culture volume (10 $\mu$ l). Return plates to incubator for 3 to 4 hours. Then measure  
5 fluorescence with excitation at 530nm and emission at 590nm using the CytoFluor. This yields the growth stimulation/inhibition data.

On day 5, the IL6 ELISA is performed by coating a 96 well plate with 50-100  $\mu$ l/well of Anti-Human IL6 Monoclonal antibody diluted in PBS, pH 7.4, incubate ON at room temperature.

10 On day 6, empty the plates into the sink and blot on paper towels. Prepare Assay Buffer containing PBS with 4% BSA. Block the plates with 200  $\mu$ l/well of Pierce Super Block blocking buffer in PBS for 1-2 hr and then wash plates with wash buffer (PBS, 0.05% Tween-20). Blot plates on paper towels. Then add 50  $\mu$ l/well of diluted Anti-Human IL-6 Monoclonal, Biotin-labeled antibody at 0.50 mg/ml. Make  
15 dilutions of IL-6 stock in media (30, 10, 3, 1, 0.3, 0 ng/ml). Add duplicate samples to top row of plate. Cover the plates and incubate for 2 hours at RT on shaker. Plates are washed with wash buffer and blotted on paper towels. Dilute EU-labeled Streptavidin 1:1000 in Assay buffer, and add 100  $\mu$ l/well. Cover the plate and incubate 1 h at RT. Plates are again washed with wash buffer and blotted on paper towels. Add 100  
20  $\mu$ l/well of Enhancement Solution and shake for 5 minutes. Read the plate on the Wallac DELFIA Fluorometer. Readings from triplicate samples in each assay are tabulated and averaged.

A positive result in this assay suggests AoSMC cell proliferation and that the polypeptide of the present invention may be involved in dermal fibroblast  
25 proliferation and/or smooth muscle cell proliferation. A positive result also suggests many potential uses of polypeptides, polynucleotides, agonists and/or antagonists of the polynucleotide/polypeptide of the present invention which gives a positive result. For example, inflammation and immune responses, wound healing, and angiogenesis, as detailed throughout this specification. Particularly, polypeptides of the present  
30 invention and polynucleotides of the present invention may be used in wound healing

and dermal regeneration, as well as the promotion of vasculogenesis, both of the blood vessels and lymphatics. The growth of vessels can be used in the treatment of, for example, cardiovascular diseases. Additionally, antagonists of polypeptides and polynucleotides of the invention may be useful in treating diseases, disorders, and/or conditions which involve angiogenesis by acting as an anti-vascular (e.g., anti-angiogenesis). These diseases, disorders, and/or conditions are known in the art and/or are described herein, such as, for example, malignancies, solid tumors, benign tumors, for example hemangiomas, acoustic neuromas, neurofibromas, trachomas, and pyogenic granulomas; arteriosclerotic plaques; ocular angiogenic diseases, for example, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, retinoblastoma, uveitis and Pterygia (abnormal blood vessel growth) of the eye; rheumatoid arthritis; psoriasis; delayed wound healing; endometriosis; vasculogenesis; granulations; hypertrophic scars (keloids); nonunion fractures; scleroderma; trachoma; vascular adhesions; myocardial angiogenesis; coronary collaterals; cerebral collaterals; arteriovenous malformations; ischemic limb angiogenesis; Osler-Webber Syndrome; plaque neovascularization; telangiectasia; hemophilic joints; angiofibroma; fibromuscular dysplasia; wound granulation; Crohn's disease; and atherosclerosis. Moreover, antagonists of polypeptides and polynucleotides of the invention may be useful in treating anti-hyperproliferative diseases and/or anti-inflammatory known in the art and/or described herein.

One skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides (e.g., gene therapy), antibodies, agonists, and/or antagonists and fragments and variants thereof.

#### *Example 45: Cellular Adhesion Molecule (CAM) Expression on Endothelial Cells*

The recruitment of lymphocytes to areas of inflammation and angiogenesis involves specific receptor-ligand interactions between cell surface adhesion molecules

(CAMs) on lymphocytes and the vascular endothelium. The adhesion process, in both normal and pathological settings, follows a multi-step cascade that involves intercellular adhesion molecule-1 (ICAM-1), vascular cell adhesion molecule-1 (VCAM-1), and endothelial leukocyte adhesion molecule-1 (E-selectin) expression on endothelial cells (EC). The expression of these molecules and others on the vascular endothelium determines the efficiency with which leukocytes may adhere to the local vasculature and extravasate into the local tissue during the development of an inflammatory response. The local concentration of cytokines and growth factor participate in the modulation of the expression of these CAMs.

10 Briefly, endothelial cells (e.g., Human Umbilical Vein Endothelial cells (HUVECs)) are grown in a standard 96 well plate to confluence, growth medium is removed from the cells and replaced with 100  $\mu$ l of 199 Medium (10% fetal bovine serum (FBS)). Samples for testing and positive or negative controls are added to the plate in triplicate (in 10  $\mu$ l volumes). Plates are then incubated at 37°C for either 5 h  
15 (selectin and integrin expression) or 24 h (integrin expression only). Plates are aspirated to remove medium and 100  $\mu$ l of 0.1% paraformaldehyde-PBS(with Ca++ and Mg++) is added to each well. Plates are held at 4°C for 30 min. Fixative is removed from the wells and wells are washed 1X with PBS(+Ca,Mg) + 0.5% BSA and drained. 10  $\mu$ l of diluted primary antibody is added to the test and control wells.  
20 Anti-ICAM-1-Biotin, Anti-VCAM-1-Biotin and Anti-E-selectin-Biotin are used at a concentration of 10  $\mu$ g/ml (1:10 dilution of 0.1 mg/ml stock antibody). Cells are incubated at 37°C for 30 min. in a humidified environment. Wells are washed three times with PBS(+Ca,Mg) + 0.5% BSA. 20  $\mu$ l of diluted ExtrAvidin-Alkaline Phosphatase (1:5,000 dilution, referred to herein as the working dilution) are added to  
25 each well and incubated at 37°C for 30 min. Wells are washed three times with PBS(+Ca,Mg)+0.5% BSA. Dissolve 1 tablet of p-Nitrophenol Phosphate pNPP per 5 ml of glycine buffer (pH 10.4). 100  $\mu$ l of pNPP substrate in glycine buffer is added to each test well. Standard wells in triplicate are prepared from the working dilution of the ExtrAvidin-Alkaline Phosphatase in glycine buffer: 1:5,000 ( $10^0$ ) >  $10^{-0.5}$  >  $10^{-1}$  >  
30  $10^{-1.5}$ . 5  $\mu$ l of each dilution is added to triplicate wells and the resulting AP content in

each well is 5.50 ng, 1.74 ng, 0.55 ng, 0.18 ng. 100 µl of pNPN reagent is then added to each of the standard wells. The plate is incubated at 37°C for 4h. A volume of 50 µl of 3M NaOH is added to all wells. The plate is read on a plate reader at 405 nm using the background subtraction option on blank wells filled with glycine buffer only. Additionally, the template is set up to indicate the concentration of AP-conjugate in each standard well [ 5.50 ng; 1.74 ng; 0.55 ng; 0.18 ng]. Results are indicated as amount of bound AP-conjugate in each sample.

*Example 46: Alamar Blue Endothelial Cells Proliferation Assay*

10

This assay may be used to quantitatively determine protein mediated inhibition of bFGF-induced proliferation of Bovine Lymphatic Endothelial Cells (LECs), Bovine Aortic Endothelial Cells (BAECs) or Human Microvascular Uterine Myometrial Cells (UTMECs). This assay incorporates a fluorometric growth indicator based on detection of metabolic activity. A standard Alamar Blue Proliferation Assay is prepared in EGM-2MV with 10 ng /ml of bFGF added as a source of endothelial cell stimulation. This assay may be used with a variety of endothelial cells with slight changes in growth medium and cell concentration. Dilutions of the protein batches to be tested are diluted as appropriate. Serum-free medium (GIBCO SFM) without bFGF is used as a non-stimulated control and Angiostatin or TSP-1 are included as a known inhibitory controls.

Briefly, LEC, BAECs or UTMECs are seeded in growth media at a density of 5000 to 2000 cells/well in a 96 well plate and placed at 37-C overnight. After the overnight incubation of the cells, the growth media is removed and replaced with GIBCO EC-SFM. The cells are treated with the appropriate dilutions of the protein of interest or control protein sample(s) (prepared in SFM ) in triplicate wells with additional bFGF to a concentration of 10 ng/ ml. Once the cells have been treated with the samples, the plate(s) is/are placed back in the 37° C incubator for three days. After three days 10 ml of stock alamar blue (Biosource Cat# DAL1100) is added to each well and the plate(s) is/are placed back in the 37°C incubator for four hours. The



plate(s) are then read at 530nm excitation and 590nm emission using the CytoFluor fluorescence reader. Direct output is recorded in relative fluorescence units.

Alamar blue is an oxidation-reduction indicator that both fluoresces and changes color in response to chemical reduction of growth medium resulting from cell growth. As cells grow in culture, innate metabolic activity results in a chemical reduction of the immediate surrounding environment. Reduction related to growth causes the indicator to change from oxidized (non-fluorescent blue) form to reduced (fluorescent red) form. i.e. stimulated proliferation will produce a stronger signal and inhibited proliferation will produce a weaker signal and the total signal is proportional to the total number of cells as well as their metabolic activity. The background level of activity is observed with the starvation medium alone. This is compared to the output observed from the positive control samples (bFGF in growth medium) and protein dilutions.

*Example 47: Detection of Inhibition of a Mixed Lymphocyte Reaction*

This assay can be used to detect and evaluate inhibition of a Mixed Lymphocyte Reaction (MLR) by gene products (e.g., isolated polypeptides). Inhibition of a MLR may be due to a direct effect on cell proliferation and viability, modulation of costimulatory molecules on interacting cells, modulation of adhesiveness between lymphocytes and accessory cells, or modulation of cytokine production by accessory cells. Multiple cells may be targeted by these polypeptides since the peripheral blood mononuclear fraction used in this assay includes T, B and natural killer lymphocytes, as well as monocytes and dendritic cells.

Polypeptides of interest found to inhibit the MLR may find application in diseases associated with lymphocyte and monocyte activation or proliferation. These include, but are not limited to, diseases such as asthma, arthritis, diabetes, inflammatory skin conditions, psoriasis, eczema, systemic lupus erythematosus, multiple sclerosis, glomerulonephritis, inflammatory bowel disease, crohn's disease, ulcerative colitis, arteriosclerosis, cirrhosis, graft vs. host disease, host vs. graft

disease, hepatitis, leukemia and lymphoma.

Briefly, PBMCs from human donors are purified by density gradient centrifugation using Lymphocyte Separation Medium (LSM<sup>®</sup>, density 1.0770 g/ml, Organon Teknika Corporation, West Chester, PA). PBMCs from two donors are  
5 adjusted to  $2 \times 10^6$  cells/ml in RPMI-1640 (Life Technologies, Grand Island, NY) supplemented with 10% FCS and 2 mM glutamine. PBMCs from a third donor is adjusted to  $2 \times 10^5$  cells/ml. Fifty microliters of PBMCs from each donor is added to wells of a 96-well round bottom microtiter plate. Dilutions of test materials (50  $\mu$ l) is added in triplicate to microtiter wells. Test samples (of the protein of interest) are  
10 added for final dilution of 1:4; rhuIL-2 (R&D Systems, Minneapolis, MN, catalog number 202-IL) is added to a final concentration of 1  $\mu$ g/ml; anti-CD4 mAb (R&D Systems, clone 34930.11, catalog number MAB379) is added to a final concentration of 10  $\mu$ g/ml. Cells are cultured for 7-8 days at 37°C in 5% CO<sub>2</sub>, and 1  $\mu$ C of [<sup>3</sup>H] thymidine is added to wells for the last 16 hrs of culture. Cells are harvested and  
15 thymidine incorporation determined using a Packard TopCount. Data is expressed as the mean and standard deviation of triplicate determinations.

Samples of the protein of interest are screened in separate experiments and compared to the negative control treatment, anti-CD4 mAb, which inhibits proliferation of lymphocytes and the positive control treatment, IL-2 (either as  
20 recombinant material or supernatant), which enhances proliferation of lymphocytes.

One skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides (e.g., gene therapy), antibodies, agonists, and/or antagonists and fragments and variants thereof.

It will be clear that the invention may be practiced otherwise than as  
25 particularly described in the foregoing description and examples. Numerous modifications and variations of the present invention are possible in light of the above teachings and, therefore, are within the scope of the appended claims.

The entire disclosure of each document cited (including patents, patent applications, journal articles, abstracts, laboratory manuals, books, or other  
30 disclosures) in the Background of the Invention, Detailed Description, and Examples

is hereby incorporated herein by reference. Further, the hard copy of the sequence listing submitted herewith and the corresponding computer readable form are both incorporated herein by reference in their entireties. Moreover, the hard copy of and the corresponding computer readable form of the Sequence Listing of Serial No.

5 60/124,270 are also incorporated herein by reference in their entireties.

Applicant's or agent's file reference number	PA102PCT	International application No.	UNASSIGNED
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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

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A. The indications made below relate to the microorganism referred to in the description on page <u>91</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit 20 May 1997	Accession Number 209059
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
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#### **CANADA**

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

#### **NORWAY**

The applicant hereby requests that the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on the list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

#### **AUSTRALIA**

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

#### **FINLAND**

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

#### **UNITED KINGDOM**

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

**ATCC Deposit No.: 209059**

#### **DENMARK**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

#### **SWEDEN**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PCT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent Office or any person approved by a applicant in the individual case.

#### **NETHERLANDS**

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

Applicant's or agent's file reference number	PA102PCT	International application No.	UNASSIGNED
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B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit 20 May 1997	Accession Number 209060
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
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#### **NORWAY**

The applicant hereby requests that the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on the list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

#### **AUSTRALIA**

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

#### **FINLAND**

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

#### **UNITED KINGDOM**

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.



**ATCC Deposit No.: 209060**

**DENMARK**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

**SWEDEN**

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**NETHERLANDS**

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Applicant's or agent's file reference number	PA102PCT	International application No.	UNASSIGNED
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B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit 20 May 1997	Accession Number 209061
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
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#### **NORWAY**

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#### **FINLAND**

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#### **UNITED KINGDOM**

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**ATCC Deposit No.: 209061**

**DENMARK**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

**SWEDEN**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PCT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent Office or any person approved by a applicant in the individual case.

**NETHERLANDS**

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

Applicant's or agent's file reference number	PA102PCT	International application No.	UNASSIGNED
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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>91</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit 20 May 1997	Accession Number 209062
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States) Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable) The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	
For receiving Office use only <input type="checkbox"/> This sheet was received with the international application Authorized officer	For International Bureau use only <input type="checkbox"/> This sheet was received by the International Bureau on: Authorized officer

**ATCC Deposit No.: 209062**

#### **CANADA**

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

#### **NORWAY**

The applicant hereby requests that the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on the list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

#### **AUSTRALIA**

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

#### **FINLAND**

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

#### **UNITED KINGDOM**

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

**ATCC Deposit No.: 209062**

**DENMARK**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

**SWEDEN**

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**NETHERLANDS**

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Applicant's or agent's file reference number	PA102PCT	International application No.	UNASSIGNED
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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>91</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit 20 May 1997	Accession Number 209063
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

For receiving Office use only	For International Bureau use only
<input type="checkbox"/> This sheet was received with the international application	<input type="checkbox"/> This sheet was received by the International Bureau on:
Authorized officer	Authorized officer



**ATCC Deposit No.: 209063**

### **CANADA**

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

### **NORWAY**

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### **AUSTRALIA**

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### **FINLAND**

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

### **UNITED KINGDOM**

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

ATCC Deposit No.: 209063

#### DENMARK

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

#### SWEDEN

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PCT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent Office or any person approved by a applicant in the individual case.

#### NETHERLANDS

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

Applicant's or agent's file reference number	PA102PCT	International application No.	UNASSIGNED
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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>91</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT <span style="float: right;">Further deposits are identified on an additional sheet <input type="checkbox"/></span>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit 20 May 1997	Accession Number 209064
C. ADDITIONAL INDICATIONS (leave blank if not applicable) <span style="float: right;">This information is continued on an additional sheet <input type="checkbox"/></span>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g. "Accession Number of Deposit")	

For receiving Office use only	For International Bureau use only
<input type="checkbox"/> This sheet was received with the international application	<input type="checkbox"/> This sheet was received by the International Bureau on:
Authorized officer	Authorized officer

**ATCC Deposit No.: 209064**

## **CANADA**

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

## **NORWAY**

The applicant hereby requests that the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on the list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

## **AUSTRALIA**

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

## **FINLAND**

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

## **UNITED KINGDOM**

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

**ATCC Deposit No.: 209064**

**DENMARK**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

**SWEDEN**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PCT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent Office or any person approved by a applicant in the individual case.

**NETHERLANDS**

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

Applicant's or agent's file reference number	PA102PCT	International application No.	UNASSIGNED
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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>91</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <u>American Type Culture Collection</u>	
Address of depositary institution (including postal code and country) <u>10801 University Boulevard</u> <u>Manassas, Virginia 20110-2209</u> <u>United States of America</u>	
Date of deposit <u>20 May 1997</u>	Accession Number <u>209065</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g. "Accession Number of Deposit")	

For receiving Office use only	For International Bureau use only
<input type="checkbox"/> This sheet was received with the international application	<input type="checkbox"/> This sheet was received by the International Bureau on:
Authorized officer	Authorized officer

**ATCC Deposit No.: 209065**

## **CANADA**

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

## **NORWAY**

The applicant hereby requests that the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on the list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

## **AUSTRALIA**

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

## **FINLAND**

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

## **UNITED KINGDOM**

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

**ATCC Deposit No.: 209065****DENMARK**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

**SWEDEN**

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**NETHERLANDS**

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Applicant's or agent's file reference number	PA102PCT	International application No.	UNASSIGNED
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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>91</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit 20 May 1997	Accession Number 209066
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

For receiving Office use only	For International Bureau use only
<input type="checkbox"/> This sheet was received with the international application	<input type="checkbox"/> This sheet was received by the International Bureau on:
Authorized officer	Authorized officer

**ATCC Deposit No.: 209066**

#### **CANADA**

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

#### **NORWAY**

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#### **AUSTRALIA**

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#### **FINLAND**

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#### **UNITED KINGDOM**

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**ATCC Deposit No.: 209066**

**DENMARK**

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**SWEDEN**

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**NETHERLANDS**

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Applicant's or agent's file reference number	PA102PCT	International application No.	UNASSIGNED
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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

<b>A.</b> The indications made below relate to the microorganism referred to in the description on page <u>91</u> , line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <u>American Type Culture Collection</u>	
Address of depositary institution (including postal code and country) <u>10801 University Boulevard</u> <u>Manassas, Virginia 20110-2209</u> <u>United States of America</u>	
Date of deposit <u>20 May 1997</u>	Accession Number <u>209067</u>
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (if the indications are not for all designated States) <u>Europe</u> In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable) The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

<b>For receiving Office use only</b> <input type="checkbox"/> This sheet was received with the international application  Authorized officer	<b>For International Bureau use only</b> <input type="checkbox"/> This sheet was received by the International Bureau on:  Authorized officer
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**ATCC Deposit No.: 209067**

#### **CANADA**

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

#### **NORWAY**

The applicant hereby requests that the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on the list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

#### **AUSTRALIA**

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

#### **FINLAND**

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

#### **UNITED KINGDOM**

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

**ATCC Deposit No.: 209067**

**DENMARK**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

**SWEDEN**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PCT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent Office or any person approved by a applicant in the individual case.

**NETHERLANDS**

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

Applicant's or agent's file reference number	PA102PCT	International application No.	UNASSIGNED
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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>91</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit 20 May 1997	Accession Number 209068
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

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Authorized officer	Authorized officer

**ATCC Deposit No.: 209068**

## **CANADA**

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

## **NORWAY**

The applicant hereby requests that the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on the list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

## **AUSTRALIA**

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

## **FINLAND**

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

## **UNITED KINGDOM**

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.



**ATCC Deposit No.: 209068**

**DENMARK**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

**SWEDEN**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PCT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent Office or any person approved by a applicant in the individual case.

**NETHERLANDS**

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

Applicant's or agent's file reference number	PA102PCT	International application No.	UNASSIGNED
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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

<b>A.</b> The indications made below relate to the microorganism referred to in the description on page <u>91</u> , line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <u>American Type Culture Collection</u>	
Address of depositary institution (including postal code and country) <u>10801 University Boulevard</u> <u>Manassas, Virginia 20110-2209</u> <u>United States of America</u>	
Date of deposit <u>20 May 1997</u>	Accession Number <u>209069</u>
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (if the indications are not for all designated States)	
<u>Europe</u> In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

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**ATCC Deposit No.: 209069**

#### **CANADA**

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

#### **NORWAY**

The applicant hereby requests that the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on the list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

#### **AUSTRALIA**

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

#### **FINLAND**

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

#### **UNITED KINGDOM**

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

ATCC Deposit No.: 209069

#### DENMARK

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

#### SWEDEN

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PCT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent Office or any person approved by a applicant in the individual case.

#### NETHERLANDS

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

Applicant's or agent's file reference number	PA102PCT	International application No.	UNASSIGNED
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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>91</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit 12 January 1998	Accession Number 209579
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States) Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable) The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	
For receiving Office use only <input type="checkbox"/> This sheet was received with the international application Authorized officer	For International Bureau use only <input type="checkbox"/> This sheet was received by the International Bureau on: Authorized officer

**ATCC Deposit No.: 209579**

## **CANADA**

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

## **NORWAY**

The applicant hereby requests that the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on the list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

## **AUSTRALIA**

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

## **FINLAND**

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

## **UNITED KINGDOM**

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

**ATCC Deposit No.: 209579****DENMARK**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

**SWEDEN**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PCT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent Office or any person approved by a applicant in the individual case.

**NETHERLANDS**

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

Applicant's or agent's file reference number	PA102PCT	International application No.	UNASSIGNED
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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>91</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT <span style="float: right;">Further deposits are identified on an additional sheet <input type="checkbox"/></span>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit 12 January 1998	Accession Number 209578
C. ADDITIONAL INDICATIONS (leave blank if not applicable) <span style="float: right;">This information is continued on an additional sheet <input type="checkbox"/></span>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

<p>For receiving Office use only</p> <p><input type="checkbox"/> This sheet was received with the international application</p> <p>Authorized officer</p>	<p>For International Bureau use only</p> <p><input type="checkbox"/> This sheet was received by the International Bureau on:</p> <p>Authorized officer</p>
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**ATCC Deposit No.: 209578**

#### **CANADA**

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

#### **NORWAY**

The applicant hereby requests that the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on the list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

#### **AUSTRALIA**

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

#### **FINLAND**

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

#### **UNITED KINGDOM**

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

**ATCC Deposit No.: 209578**

**DENMARK**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

**SWEDEN**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PCT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent Office or any person approved by a applicant in the individual case.

**NETHERLANDS**

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

Applicant's or agent's file reference number	PA102PCT	International application No.	UNASSIGNED
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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>91</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit 16 July 1998	Accession Number 203067
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

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Authorized officer	Authorized officer

**ATCC Deposit No.: 203067**

## **CANADA**

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

## **NORWAY**

The applicant hereby requests that the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on the list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

## **AUSTRALIA**

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

## **FINLAND**

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

## **UNITED KINGDOM**

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

**ATCC Deposit No.: 203067**

**DENMARK**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

**SWEDEN**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PCT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent Office or any person approved by a applicant in the individual case.

**NETHERLANDS**

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

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Applicant's or agent's file reference number	PA102PCT	International application No.	UNASSIGNED
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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>91</u> . line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT <span style="float: right;">Further deposits are identified on an additional sheet <input type="checkbox"/></span>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit  16 July 1998	Accession Number  203068
C. ADDITIONAL INDICATIONS (leave blank if not applicable) <span style="float: right;">This information is continued on an additional sheet <input type="checkbox"/></span>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

<p style="text-align: center;">For receiving Office use only</p> <p><input type="checkbox"/> This sheet was received with the international application</p> <p>Authorized officer</p>	<p style="text-align: center;">For International Bureau use only</p> <p><input type="checkbox"/> This sheet was received by the International Bureau on:</p> <p>Authorized officer</p>
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**ATCC Deposit No.: 203068**

#### **CANADA**

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

#### **NORWAY**

The applicant hereby requests that the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on the list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

#### **AUSTRALIA**

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

#### **FINLAND**

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

#### **UNITED KINGDOM**

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

ATCC Deposit No.: 203068

**DENMARK**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

**SWEDEN**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PCT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent Office or any person approved by a applicant in the individual case.

**NETHERLANDS**

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.



Applicant's or agent's file reference number	PA102PCT	International application No.	UNASSIGNED
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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>91</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit 01 February 1999	Accession Number 203609
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

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Authorized officer	Authorized officer

**ATCC Deposit No.: 203609**

#### **CANADA**

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

#### **NORWAY**

The applicant hereby requests that the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on the list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

#### **AUSTRALIA**

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

#### **FINLAND**

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

#### **UNITED KINGDOM**

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

**ATCC Deposit No.: 203609**

**DENMARK**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

**SWEDEN**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PCT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent Office or any person approved by a applicant in the individual case.

**NETHERLANDS**

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

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Applicant's or agent's file reference number	PA102PCT	International application No.	UNASSIGNED
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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>91</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit 01 February 1999	Accession Number 203610
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g. "Accession Number of Deposit")	

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Authorized officer	Authorized officer

**ATCC Deposit No.: 203610**

#### **CANADA**

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

#### **NORWAY**

The applicant hereby requests that the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on the list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

#### **AUSTRALIA**

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

#### **FINLAND**

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

#### **UNITED KINGDOM**

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

**ATCC Deposit No.: 203610****DENMARK**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

**SWEDEN**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PCT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent Office or any person approved by a applicant in the individual case.

**NETHERLANDS**

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

Applicant's or agent's file reference number	PA102PCT	International application No.	UNASSIGNED
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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

<b>A.</b> The indications made below relate to the microorganism referred to in the description on page <u>91</u> , line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <u>American Type Culture Collection</u>	
Address of depositary institution (including postal code and country) <u>10801 University Boulevard</u> <u>Manassas, Virginia 20110-2209</u> <u>United States of America</u>	
Date of deposit <u>17 November 1998</u>	Accession Number <u>203485</u>
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (if the indications are not for all designated States)	
<u>Europe</u> In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")     	

<b>For receiving Office use only</b>	<b>For International Bureau use only</b>
<input type="checkbox"/> This sheet was received with the international application	<input type="checkbox"/> This sheet was received by the International Bureau on:
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**ATCC Deposit No.: 203485**

#### **CANADA**

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

#### **NORWAY**

The applicant hereby requests that the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on the list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

#### **AUSTRALIA**

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#### **FINLAND**

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

#### **UNITED KINGDOM**

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.



**ATCC Deposit No.: 203485**

**DENMARK**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

**SWEDEN**

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**NETHERLANDS**

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

Applicant's or agent's file reference number	PA102PCT	International application No.	UNASSIGNED
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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>91</u> . line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit 18 June 1999	Accession Number PTA-252
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE. (if the indications are not for all designated States)	
Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

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**ATCC Deposit No.: PTA-252**

#### **CANADA**

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

#### **NORWAY**

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#### **AUSTRALIA**

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#### **FINLAND**

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

#### **UNITED KINGDOM**

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

**ATCC Deposit No.: PTA-252**

**DENMARK**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

**SWEDEN**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PCT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent Office or any person approved by a applicant in the individual case.

**NETHERLANDS**

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

Applicant's or agent's file reference number	PA102PCT	International application No.	UNASSIGNED
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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>91</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit 18 June 1999	Accession Number PTA-253
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

For receiving Office use only	For International Bureau use only
<input type="checkbox"/> This sheet was received with the international application	<input type="checkbox"/> This sheet was received by the International Bureau on:
Authorized officer	Authorized officer

**ATCC Deposit No.: PTA-253**

#### **CANADA**

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

#### **NORWAY**

The applicant hereby requests that the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on the list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

#### **AUSTRALIA**

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

#### **FINLAND**

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

#### **UNITED KINGDOM**

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

**ATCC Deposit No.: PTA-253**

**DENMARK**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

**SWEDEN**

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**NETHERLANDS**

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

Applicant's or agent's file reference number	PA102PCT	International application No.	UNASSIGNED
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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>91</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <u>American Type Culture Collection</u>	
Address of depositary institution (including postal code and country) <u>10801 University Boulevard</u> <u>Manassas, Virginia 20110-2209</u> <u>United States of America</u>	
Date of deposit <u>22 December 1999</u>	Accession Number <u>PTA-1081</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
<u>Europe</u> In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

<input type="checkbox"/> For receiving Office use only This sheet was received with the international application	<input type="checkbox"/> For International Bureau use only This sheet was received by the International Bureau on:
Authorized officer	Authorized officer



**ATCC Deposit No.: PTA-1081**

#### **CANADA**

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

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**ATCC Deposit No.: PTA-1081**

**DENMARK**

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*What Is Claimed Is:*

1. An isolated nucleic acid molecule comprising a polynucleotide having a nucleotide sequence at least 95% identical to a sequence selected from the group consisting of:
- 5 (a) a polynucleotide fragment of SEQ ID NO:X or a polynucleotide fragment of the cDNA sequence included in the related cDNA clone, which is hybridizable to SEQ ID NO:X;
- (b) a polynucleotide encoding a polypeptide fragment of SEQ ID NO:Y or a polypeptide fragment encoded by the cDNA sequence included in the related cDNA clone, which is hybridizable to SEQ ID NO:X;
- 10 (c) a polynucleotide encoding a polypeptide fragment of a polypeptide encoded by SEQ ID NO:X or a polypeptide fragment encoded by the cDNA sequence included in the related cDNA clone, which is hybridizable to SEQ ID NO:X;
- 15 (d) a polynucleotide encoding a polypeptide domain of SEQ ID NO:Y or a polypeptide domain encoded by the cDNA sequence included in the related cDNA clone, which is hybridizable to SEQ ID NO:X;
- (e) a polynucleotide encoding a polypeptide epitope of SEQ ID NO:Y or a polypeptide epitope encoded by the cDNA sequence included in the related cDNA clone, which is hybridizable to SEQ ID NO:X;
- 20 (f) a polynucleotide encoding a polypeptide of SEQ ID NO:Y or the cDNA sequence included in the related cDNA clone, which is hybridizable to SEQ ID NO:X, having biological activity;
- (g) a polynucleotide which is a variant of SEQ ID NO:X;
- 25 (h) a polynucleotide which is an allelic variant of SEQ ID NO:X;
- (i) a polynucleotide which encodes a species homologue of the SEQ ID NO:Y;
- (j) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(i), wherein said polynucleotide does not hybridize under stringent conditions to a nucleic acid molecule having a nucleotide
- 30

sequence of only A residues or of only T residues.

2. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises a nucleotide sequence encoding a protein.

5

3. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises a nucleotide sequence encoding the sequence identified as SEQ ID NO:Y or the polypeptide encoded by the cDNA sequence included in the related cDNA clone, which is hybridizable to SEQ ID NO:X.

10

4. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises the entire nucleotide sequence of SEQ ID NO:X or the cDNA sequence included in the related cDNA clone, which is hybridizable to SEQ ID NO:X.

15

5. The isolated nucleic acid molecule of claim 2, wherein the nucleotide sequence comprises sequential nucleotide deletions from either the C-terminus or the N-terminus.

20

6. The isolated nucleic acid molecule of claim 3, wherein the nucleotide sequence comprises sequential nucleotide deletions from either the C-terminus or the N-terminus.

25

7. A recombinant vector comprising the isolated nucleic acid molecule of claim 1.

8. A method of making a recombinant host cell comprising the isolated nucleic acid molecule of claim 1.

30

9. A recombinant host cell produced by the method of claim 8.

10. The recombinant host cell of claim 9 comprising vector sequences.
11. An isolated polypeptide comprising an amino acid sequence at least  
5 95% identical to a sequence selected from the group consisting of:
- (a) a polypeptide fragment of SEQ ID NO:Y or of the sequence encoded by the cDNA included in the related cDNA clone;
  - (b) a polypeptide fragment of SEQ ID NO:Y or of the sequence encoded by the cDNA included in the related cDNA clone, having biological activity;
  - 10 (c) a polypeptide domain of SEQ ID NO:Y or of the sequence encoded by the cDNA included in the related cDNA clone;
  - (d) a polypeptide epitope of SEQ ID NO:Y or of the sequence encoded by the cDNA included in the related cDNA clone;
  - (e) a full length protein of SEQ ID NO:Y or of the sequence encoded by the  
15 cDNA included in the related cDNA clone;
  - (f) a variant of SEQ ID NO:Y;
  - (g) an allelic variant of SEQ ID NO:Y; or
  - (h) a species homologue of the SEQ ID NO:Y.
- 20 12. The isolated polypeptide of claim 11, wherein the full length protein comprises sequential amino acid deletions from either the C-terminus or the N-terminus.
- 25 13. An isolated antibody that binds specifically to the isolated polypeptide of claim 11.
14. A recombinant host cell that expresses the isolated polypeptide of claim 11.
- 30 15. A method of making an isolated polypeptide comprising:

(a) culturing the recombinant host cell of claim 14 under conditions such that said polypeptide is expressed; and

(b) recovering said polypeptide.

5           16.    The polypeptide produced by claim 15.

          17.    A method for preventing, treating, or ameliorating a medical condition, comprising administering to a mammalian subject a therapeutically effective amount of the polypeptide of claim 11 or the polynucleotide of claim 1.

10

          18.    A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:

          (a) determining the presence or absence of a mutation in the polynucleotide of claim 1; and

15           (b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or absence of said mutation.

          19.    A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:

20           (a) determining the presence or amount of expression of the polypeptide of claim 11 in a biological sample; and

          (b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or amount of expression of the polypeptide.

25           20.    A method for identifying a binding partner to the polypeptide of claim 11 comprising:

          (a) contacting the polypeptide of claim 11 with a binding partner; and

          (b) determining whether the binding partner effects an activity of the polypeptide.

30

21. The gene corresponding to the cDNA sequence of SEQ ID NO:Y.
22. A method of identifying an activity in a biological assay, wherein the method comprises:
- 5 (a) expressing SEQ ID NO:X in a cell;
- (b) isolating the supernatant;
- (c) detecting an activity in a biological assay; and
- (d) identifying the protein in the supernatant having the activity.
- 10 23. The product produced by the method of claim 20.

## SEQUENCE LISTING

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Steve Ruben

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tttttttctt ttttcttttt ttttaaagat catgaatttg tgacttagtt ctgcccyytg 600
gagaacaaaa gaaagcagtc ttccatcaaa tcaccttaaa atgcacggct aaactattca 660
gagttaacac tccagaattg ttaaattaca agtactatgc tttaatgctt ctttcatctt 720
actagtaagg cctattaaaa aaaataatac cacttgannng gtgaaggctt ngcaatagga 780
agaagataga atccaggttt angg 804

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&lt;210&gt; 8

&lt;211&gt; 720

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (714)

&lt;223&gt; n equals a,t,g, or c

&lt;400&gt; 8

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gtgaggacag cctgccagag tctggtctct ggacactatg ggcacacgac tcctcccagc 60
tctgtttctt gtcctcctgg tattgggatt tgccccacgg gctctcctga cacactctcc 120
ccctgcagag gtccagggga cccaacagcc ccagcaagat gagatgccta gcccgaacctt 180
cctcaccag gtgaaggaat ctctctccag ttactgggag tcagcaaaga cagccgcccc 240
gaacctgtac gagaagacat acctgccgc tgtagatgag aaactcaggg acttgtagag 300
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ctcccctgat cccccagggt cagactgagc tcccccttcc cagtagctct tgcatectcc 480
tcccaactct agcctgaatt cttttcaata aaaaatacaa ttcaagttgc ttctcatgga 540
tggcactgct tttctgagga ctcaagggtc caagatggag gggctgactc agtccagcca 600
acatttaatg agcacctact ttatgtatgg agctctaacc catgggtcca tgggaataaa 660
gcagtgaata gtaacaataa ataattgtaa cagcaaaaaa aaaaaaaaaa aaanaaaaaa 720

```

&lt;210&gt; 9

&lt;211&gt; 540

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (463)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (524)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

<221> misc feature

<222> (535)

<223> n equals a,t,g, or c

<400> 9

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ctgtgttctc acatggcaga aggggcaaac aagccccctt gggcctcttt tataaaggca 180
ctaactctat gcctaaaggc agggccctca tgactctatc acctaccaa aggctccact 240
tctttatact attggagggg tagaaggaaac ttcctttcta gaccttgaag gtttaagaat 300
ttgaatctat aaaacaagct gacaatagac agattaacag gagaaaaagc atatacattt 360
tttaatgtgg gccagatggc agaagcttaa ataacacccc aagctacagg gaagtgaggc 420
ctctgatggg ggaggtagtt gacacaggct gtggggaggg gtnaggggga ggaatctgtg 480
gtggagcaaa tttgccttat tacactgata aatggtaatt tacnctaatt aagcntgggt 540
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<210> 10

<211> 561

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (406)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (450)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (546)

<223> n equals a,t,g, or c

<400> 10

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gagacccagc gtgtgctctc atccgtactc tgtgacaccc cttagtggac tgttccaacc 120
agttggggccc gggagaagga ctagggaagc ttccttccca tctgcacctc ccagcctgga 180
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acagaaaggc cttttgctaa gtagcagcct gatgcactcc gagtcagagc tggacagcga 360
tgatgccatc ttacatggc cagaccgaga gaagggcaaa ctccctngcat ggtcagaatg 420
gctctgtacc caacgggcag acccctctgn aaggccagga gcccgcgga rgagatcctg 480
tagccacctg gtctgtctyc tcagggcarg gccaggcaca attgccgggc cagttcttct 540
aacttnccga gttttgcggg g
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<210> 11

<211> 393

<212> DNA

<213> Homo sapiens

<220>  
<221> misc feature  
<222> (346)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (381)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (383)  
<223> n equals a,t,g, or c

<400> 11  
tcgacccacg cgtccgggtg agtgccatct taaaacttac tggagattgg ttttatattt 60  
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tagaaccaag caagattcac ctgtgttttg tgttcattgt catttgcttc tttaaaggcaa 180  
gggttgaaga taaataaggt agcaatgtct atagttttgg ccttaactat gccaatctaa 240  
ttataattcc ctgtatttaa aatggtttct tttacttatt gaaaggcatt ttagtggtgt 300  
ktatgtgtaa tattaaagat tattcaacac ctctcaraaa aaaaanraaa aagggggggc 360  
ccccctgggg gtcccaagct nancgtacgc ggg 393

<210> 12  
<211> 322  
<212> DNA  
<213> Homo sapiens

<400> 12  
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gctgaggtac gagaatcgct tgaacctggg aggcagagga tgcagtgagc cgggatcacg 120  
ccattgcact ccagcctggg ggacaagagt gaatctgtgt ctcacaaaaa aaaaaagaa 180  
aaagaaagat gcttaacaaa ggttaccata agccacaaat tcatraccac ttatccttcc 240  
agtttcaagt agaatatatt cataacctca ataaagttct ccctgctccc aaaaaaaaaa 300  
aaaaaaaaaa aaaaaaaaaa ag 322

<210> 13  
<211> 1907  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc feature  
<222> (1834)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (1843)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1888)

<223> n equals a,t,g, or c

<400> 13

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gagaaataat aatatagctt tatagaatth tccatcttgt attaaaaataa tcacatgtac 60
atcattgtaa ctcatgccat aacataagat tttgtacaac aatttctttt tgtgtgctgg 120
catcattaag gtttagtctg cccagatcac ctattagtac ctaatttata tattctgaat 180
taaaattatc tgttaattta aaaacatttt atctattgtc tttcaaaata gtattaactg 240
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gttttagaag gaaaaacctt tcagctctac tctcacatc ttatagcttt gtttgaacat 360
gccaaaaaac caggattagc tgcccatatt caaactcaca ggtttccaga ccgaatacta 420
ccaagaaaat tcgctttaac aacaaagatt cctgatacaa aaggctgcc acaatgtgtc 480
atagtcagaa acccttacac gggacataaa tacctctgtg gagctttaca gtctggaatt 540
gttttacttc agtggatga gccaatgcag aaattcatgt tgataaagca ctttgatttt 600
cctttgccaa gtcctttgaa tgtttttgaa atgctgtgta tacctgaaca ggaataacct 660
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tttgagtgtt tgggggtcaa cacacacatg caatttgctt aacaaaagta ttttataata 1800
cagttcatat agaataccyt aaaaggagc ytangtttcc acnacagata agtggttaagg 1860
gtcataccgg agataatgat gatagtgnaa tatcctagaa gggggtg 1907

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<210> 14

<211> 1140

<212> DNA

<213> Homo sapiens

<400> 14

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agaataaatt ccagggtctc agtctgcctt tggttcgcaa gtttggccac tcgattctgc 60
agtgtctgga tgctttgcac aaaaacagaa taattcactg tgaccttaag cccgagaaca 120
ttttgttaaa gcagcagggt agaagcggta ttaaagtaat tgattttggc tccagttgtt 180
acgagcatca gcgtgtctac acgtacatcc agtcgcgttt ttaccgggct ccagaagtga 240

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tccttggggc caggtatggc atgcccattg atatgtggag cctgggctgc attttagcag 300  
agctcctgac gggttacccc ctcttgccctg gggaagatga aggggaccag ctggcctgta 360  
tgattgaaact gttgggcatg cctcacagaa actgctggat gcatccaaac gagccaaaaa 420  
ttttgtgagc tccaagggtt atccccgtta ctgcaactgtc acgactctct cagatggctc 480  
tgtggtccta aacggaggcc gttcccggag gggaaactga gggggccacc ggagagcaga 540  
gagtggggka acgcgctgaa ggggtgtgat gatccccctt tccttgactt cttaaaacag 600  
tgttttagagt gggatcctgc agtgcgcatg accccaggcc aggcctttgcg gcacccttg 660  
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agagcaccgg tgctatcaca tctatatcca agttacctcc accttctagc tcagcttcca 780  
aactgaggac taatttggcg cagatgacag atgccaatgg gaattattcag cagaggacag 840  
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aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaagg gcggccgctc gcgatctaga 1140

<210> 15

<211> 2008

<212> DNA

<213> Homo sapiens

<400> 15

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gacacttagg gacagggtcac taagcagaat aggtattagt tggtttttta ttatttttaa 180  
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gggcttgaaa actgcccag attaaagagc taagatgaaa tagtttgaat aaactggtaa 360  
aataacaatt catactatct ctacatattt ttaggatatg aatttttttt tcctgctggg 420  
tagattgtcc agtgacttat ggcataaatt tcttttcatg ctacctcaa tcttcaacta 480  
aagatttcta aaaggggtaa gaaatgaggc agtagtttat taaatacata gaagtacaca 540  
gctattatat gtgtggtc ttgagaagta acctttgtgg aatatgaaac caaaggaaga 600  
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gaattttctg tcatttaatt tcagatccta gctcatcatc agtgaagtcc agcctactta 1740



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aatgctagtg actgcacaat attgtgactg tacttaatgc cactgaactg tacacttta 1860  
aatggaaaaat ttatatgtat ttttaccaca ataaacaaaa aaccctaaaa aaactttaat 1920  
gaaagggtgga aaataattta acttayaatg tgaaaatata atgtgaaatg tacaataaat 1980  
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<210> 16

<211> 371

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (350)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (360)

<223> n equals a,t,g, or c

<400> 16

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tgaagagttg tgtcttttgt ggccagtgc aaatccagga aatgaatgtt gctgatagg 120  
ataaatcttg aggctgaggg cgggtggtac agatgtgtat gggaaacccc aaccctata 180  
tattgtaaat agatgggctg ggctaaacat tgttgccgtt tcatacttct accaactcag 240  
cttttacaca ataaagctct actgtctctg aaaaaaaaa aaaaaaaaa aaaaaaaaa 300  
aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaatn gggggggggn 360  
ccccccccc c 371

<210> 17

<211> 763

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (6)

<223> n equals a,t,g, or c

<400> 17

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ggaagcactt ctgtggtcaa gcaggcagcc catgggggtg catcttctctg ttgggggatc 180  
atccattttc ttcaatgaat agttttaagt cttgtcaaat gctcacacag aggcccgcta 240  
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cattcgggca tgtgtcatta gggatgacat tctctgaagg ctgcccggct tgaatggcca 360  
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aaagcatctc ttgcttgga ggtggaatat aggcaatttt ggatttttaa tgcattggcat 540  
ggggcgggag tgaaatatct tgccagggtt tgtttgccct ataattgggag agaaccaggc 600

ctctggatga tacggtatca aacactgctg ctcctttctg ttttcttttg tgggaaaggg 660  
aggaggatag aatggagagg aattagtggg agcctggggg aagttcaaaa taaagaaact 720  
gtgaaatcct ccacctcaaa gttgggtctg caccaggatt ctg 763

<210> 18

<211> 1926

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (898)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1024)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1083)

<223> n equals a,t,g, or c

<400> 18

aataacttga ctggaattct agaaaccgct gtcagagcca ccaacgcaca gtttgacagt 60  
cctgagatcc tgcgaaggct ggacgtgcgg ctgctggagg tctctccagg tgacactgga 120  
tgggatgtct tcagcctcga ttatcatgtt gacggaccaa ttgcaactgt gtttactcga 180  
gaatgtatga gccactacct aagagtattt aacttcctct ggagggcgac ggatggaata 240  
catcctcact gacatacgga agggacacat gtgcaatgca aagctcctga gaaacatgcc 300  
agagtcttcc ggggtgctgc accagtgtca cattttggcc tctgagatgg tccatttcat 360  
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agacaccatc atctcccgtc gcctgctgga cagtgactcc agggcacttt taaatcaact 540  
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tcagattttt aaaatagtat agaaaaaagt aggagtgata gagaacaaaa atactcttat 1620  
acagtgcac ccaaataccg cgaatgcac agctaaagca gcgtgtaaat aggagtgcac 1680  
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atggataatg aagatttcct ttttccttgc ctattttttc attgtaaata tttatatact 1800  
actgmccaag atgttgggtt gggggggatt gttttttgta aaaatgtcat tatcaggtca 1860  
cataaatctg cctttatggt gcataagtga aaatttagaa aattaaaagc aattatcttt 1920  
maaaaa 1926

<210> 19

<211> 2301

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (190)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2052)

<223> n equals a,t,g, or c

<400> 19

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caggactagg acccacggct cccaaagccc gttccttctg tgttgtgctg cctccatata 180  
cgtcagaagn agcctttcca gaatgattct gggcatatac taagaagagc aggtatggaa 240  
agatctattt tcagggaatc ttagaattcc ctacacgagt gggagaaaaga tgtccaaatt 300  
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gggacagggg gaccggaatt gtcttagcac cccaatgtta tgacaaaact atgtacttt 600  
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<210> 20

<211> 538

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (507)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (514)

<223> n equals a,t,g, or c

<400> 20

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catctccgcc ctgagtctca tcaactctgtc caccgtgttc aacctgcca gccccctcaa 180  
cgccatgcag atcctatgga tcaacatcat catggatggg ccaccgggca gaggtgaggc 240  
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tgggccggca gagctgggtg aggatggaac tttctgcttc ctctggctgg atgctctctc 480  
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<210> 21

<211> 1403

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1370)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1386)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1393)

<223> n equals a,t,g, or c

<400> 21

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gcccgnatcc canttggccc aat 1403
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<210> 22

<211> 478

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (474)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (475)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (476)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (478)

<223> n equals a,t,g, or c

<400> 22

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gggcaaggcgc aggcttaaac ttcaggccag gggccacttt aagaattgct atatggccag 180
ggccgggcgc ggtggctcac gcctgtaatc ccagcacttt gggaggccga ggtgggcgga 240
tcacaaggctc aggagatcga gaccatcctg gctaacacgg tgaaccctg tctgtagtaa 300
aaatacaaaa aaattagcca ggcatgggtg tgggtgcctg tagtcccagc tacttgggag 360
gctgaggcag gagaatgggtg tgaaccaggg aggtggagct tgcagtgagc cgagatcgtg 420
ccactgcact ccagcctggg caacagagcg agacttccgt ctcaaaaaaa aaannncn 478
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<210> 23

<211> 1252

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1227)

<223> n equals a,t,g, or c

<400> 23

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tgcttgggct ccttggtgca gcagatcatc ttcttccctg gaaccacggc cctggccttc 180
ctggtgctca tgctgtgct ccatggcagg aacctcctgc tcttccgttc cctggagtcc 240
tcgtggccct tctggctgac tttggccctg gctgtgatcc tgcagaacat ggcagcccat 300
tgggtcttcc tggagactca tgatggacac ccacagctga ccaaccggcg agtgctctat 360
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cgagtgtctc tctctgccct ctacaacgcc atccaccttg gccagatgga cctcagcctg 480
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<210> 24  
<211> 1074  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc feature  
<222> (928)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (934)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (1028)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (1031)  
<223> n equals a,t,g, or c

<400> 24  
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cccactcget cagccctgag gtttccctct gcttcccag ggagcttgaa ggccaagcag 180  
tccatggcgg gaatccstgg tagggagagt aatgccccat ctgtgcccac tgtctccctg 240  
ctgccggggg cgccctggagg caatgccagc tccaggacag aggctcaggt gcccacggg 300  
caaggcagcc cagggggctg tgtctgttca agtcaggctt ccccggtccc tcgcgagca 360  
gcgcctccac gggcagcccg gggccccacc ccacgcaactg aagaggccgc ctgggctgcc 420  
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agaaacttcc gacgcgggga gagcatytac tgggggcca cagcggacag ccaggacaca 540  
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cggcctggga cctgccactg tggcgtgcgg ctccctcccg cgccgcgagg ccgcgacctc 720  
tgccacgtgg accgcgcgcg gggcgctccc tgggtggcgat ggcgcggcac tggccgagca 780  
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aaaaaaaaaa aaaaaggcgg ccgtttanag gatncctcga aggggcccga gttaacgcgt 960  
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<210> 25  
<211> 1186  
<212> DNA  
<213> Homo sapiens

<400> 25

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gacccagca ccagccttct ggaacagggc cacattgtcc attacctgtc acaggctcctc 180
atctccagcc ccaaggacca aacagtattc caacacctac tgcttcaggg ttctgtcctc 240
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ggttgggcat tttaattcat gttaataaat cacaattatg tcagttccca cgcgtccgcg 1140
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&lt;210&gt; 26

&lt;211&gt; 888

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (670)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (675)

&lt;223&gt; n equals a,t,g, or c

&lt;400&gt; 26

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gccccaccc gctgtgactg cattctggga tccccagcct gggaaatcaa gagctgtcgg 60
ccatttttat tcctccctcc cagacctgac cccttcacg gggctcaaga gacctctctc 120
tccaaatctc catttgctc ctctggctaa gctggaaaat gcacactctg ccctgggtgt 180
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caaggggctg accacagtgt tttaaggcat cgggcagccg gccttcagg taggcggggc 780
cagcaggagc ctgcgacctg gcttccctgg ccctaggcca ccgggcgctc agccccaccg 840

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cttctccctg cagcccgatt cgccgctgcc ttctgtgtca cctgcact 888

<210> 27

<211> 789

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (420)

<223> n equals a,t,g, or c

<400> 27

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tacgatgagc tacacaaggc tcattactta ttgggtggga atccaggaaa atcttgctct 180  
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gatcccccta gtgctctgaa atatttaca aatgatcttt atataactgt ggatcattca 360  
gaccagaag agacaaaaga gtttcagctc ctggcatcag ctctattcaa atctgggtcn 420  
agattttaca gctctgggct tttctgatgt ggatcacacc tatgctcaa gaactcagct 480  
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tgcaccagag ttctgaaggg atcttaacca tcacaagttt ttaccctctt ccttcatgcc 720  
tgacctcaac ccgcgtctcc tcatctatt cctaaattag gctaataaag tgaaattgg 780  
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<210> 28

<211> 847

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (799)

<223> n equals a,t,g, or c

<400> 28

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acctctgctg tattctatta gaggtcaagc catcactgaa gccatattca aggagaggga 180  
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gatgtcacc atttcatctg ccaggctgct gtgccaaga gtctccagct gcagctgcag 660  
gccccagtg ggaacacagt tccagctcgg ggtggccttc ctatcaccca gctcttcaga 720

atcctcaatc ctaacaaggc cccctcgcg ctaaagctgc gctcactacg accactttca 780  
 ccagtcggtg caggagatnt ttgaggtgaa caactgcctg tggaatcgtg gcagtaatgt 840  
 ctccaat 847

<210> 29

<211> 666

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (4)

<223> n equals a,t,g, or c

<400> 29

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 acatttttat ggccctacag ctacttctta tccctgcaag tatataaatt aaaaccaagt 300  
 cacttttagaa cagctttgaa actagagttt caaaggtaaa aggatctcat gtttctgaat 360  
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 agaaatgaat agtttgagct ctttaaaatg ttttaaaaaa tgtttgctta ctatctatat 480  
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 tacacatatg tatatatata tagtctatat attctatata agaatatatt ccaataagaa 600  
 tatattccat acgggaatat attagtcatt gatgtatttt gccggtaaaa ttaaaagata 660  
 ttttaa 666

<210> 30

<211> 517

<212> DNA

<213> Homo sapiens

<400> 30

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 gcaccaagga gccgttgag ggtccggcg gaggccgct cgtgtggaag tcgtcgacgc 120  
 cgccgctcgt ccgtctccc gtccgttctc gtcgccgcc gccatcatgc tggcgctcat 180  
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 cagtgaagat atgataccca cagtgggctt caacatgagg aaggtaacta aaggtaacgt 360  
 cacaataaag atctgggaca taggaggaca accccgattt cgaagcatgt gggagcggta 420  
 ttgcagagga gtcaatgcta ttgtttacat gatagatgct gcagatcgtg aaaagataga 480  
 agcttcccga aatgagctaa cataatcttc tagataa 517

<210> 31

<211> 2675

<212> DNA

<213> Homo sapiens

<400> 31

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gcagaaatga aaactgaaga tggcaaatga gaaaaaact atctcttcta tgacggagaa 240  
tccgtttcag gaaaggtaaa cctagccttt aagcaacctg gaaagaggct agaaccacaa 300  
ggaattagaa ttgaatttgt aggtcaaatt gaacttttca atgacaagag taatactcat 360  
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&lt;210&gt; 32

&lt;211&gt; 277

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

<221> misc feature

<222> (109)

<223> n equals a,t,g, or c

<400> 32

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gggagtcagg gctgaggggc tgcgccacgc cacggccccg ctggagctgg ggaccacaga 180
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aaggagggcag gtggataaga aggttgaaaa ggggggtt 277
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<210> 33

<211> 921

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (2)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (839)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (846)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (886)

<223> n equals a,t,g, or c

<400> 33

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cctgtgtgat gtggatgcct atggacartc cagttgagac cctttcaacg gctttccant 840
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<210> 34

<211> 1467

<212> DNA

<213> Homo sapiens

<400> 34

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<210> 35

<211> 2077

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (12)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (15)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (423)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (730)

<223> n equals a,t,g, or c

<400> 35

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<210> 36

<211> 384

<212> DNA

<213> Homo sapiens

<220>  
<221> misc feature  
<222> (366)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (370)  
<223> n equals a,t,g, or c

<400> 36  
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<210> 37  
<211> 468  
<212> DNA  
<213> Homo sapiens

<400> 37  
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<210> 38  
<211> 1095  
<212> DNA  
<213> Homo sapiens

<400> 38  
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<210> 39

<211> 1757

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (596)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (647)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (648)

<223> n equals a,t,g, or c

<400> 39

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&lt;210&gt; 40

&lt;211&gt; 1945

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 40

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ccgacgaagg ccacggggat tgacatcgcc cactccgac acccagtggt cgccttggt 1740
ggtgcggtct ctggtccaga tggaggaaac cagtgacttt atggggctga gctagtaggg 1800
aagcccctgg aaagatgctg cgttccgaac ctgtgcctaa tacacgcaag ggcgctgtcc 1860
cgcccaaccc cgcttttaaa cgccacaaa aaagagcatt gttaccgcca agtacgagc 1920
ggccgcgaat taccggaccg gtaac 1945

```

&lt;210&gt; 41

<211> 588

<212> DNA

<213> Homo sapiens

<400> 41

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aggcgtatac caccatgact gaaaacaaaa gacttttttt tgagactccc tctcaaaaac 60
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ttgaatctga agtttgacaga tatgcctata gatttttggg gtttaccact ttcttattct 180
gtatcattaa tgaatatatt taaattacta tatatgttac catttttctg gatttagtaa 240
gaaatttgca gttttgggtt gatgtaacaa gggttttaat gtaatttatg ttagattttg 300
catttttttc attactgtta tattttaacc tgactgactg atctaattgt attagtattg 360
tgaataatca tgtgaaatgt ttgagacag agtactatat ttgtgaatat aattttatgg 420
tttttttcac ttagaacctt tctgtgtgga aaactaagaa aattgctttc tgctgtataa 480
tctggcattc attgtagatt aaagcttatt tttctgtgaa taaaacgtat tcaataaaat 540
actattcttt aaaattawaw mawaaaaaaa aaaaaaaaaa aaaaaaaa 588
```

<210> 42

<211> 1568

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (104)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (112)

<223> n equals a,t,g, or c

<400> 42

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cattagattt cactttttta aaaaacccag tggacattgc tataaataag atttatttgg 60
ctacaaataa cctgggatgt tgcttattat gattgatgcc tgcnggtttg tncccaagct 120
gagtgaatga gaacctcgtc ctccctactc attttgatga ctgaggettg tttataagaa 180
aagggaagtt ggagaagaaa accgagatta gaaaatatca tgttttggtt ggagataaga 240
accagggatg gcaagtacca gtgtgtacaa atgtatttca cgaggtttga aggaacgcat 300
aatcaagagg gaaaacaatt tgccttcat tggacgtatt atttggattt gggtagcaaa 360
caaaatggaa tgtggtctgt taggagcatt ctgtttgttc tttgtccct gatgtgatga 420
atcattgccca catgctagat ggactcttca tatccaggtt ttgtccctca gggctgagca 480
ctgtattaaa gagtttttgt tgagtcattt aaccttagtg tccacatcca gatcagctgt 540
aaaatgggga agacgtgtgc tgatttggaa tgaatgcaaa atatcactat cattttccta 600
attacagagg agcaaagggt atcttcagcc ctttcagttc tatgctcaca tattcaaata 660
tcaaatgtaa tttagctgaa gttatttaaa aatcaagctt ttcaatatct gttcaaagaa 720
aaagaacaca ctttgaaaat tctgcaaagc tgtctcccag tctttaaaat gtctggaagc 780
actctccttc tttaacaata caacatcact ggcccagaat ctccctgtg ctaggttgta 840
aatataaata aattacttgt ttgttaaact ttgttaaaga atattttggg agaaataact 900
caaacatatt ctttgggtta tatttataca tatgtgaaat aaatatacta tcaaaagggt 960
atattttata caaaaagtaa attgctacct ttgtatgct aatatgcaaa gttttgtata 1020
atatgatggt ttatttttag ctctacactt aaaccatagg tgggtgagtg ggaacttttg 1080
aaaactatca agaggcttgt tagacaaatt tatattctga aacctcaata agaaagcatt 1140
```

```
ccaggtttca atccttggtt tttgtcctgc tcccaaattc ttttttaaac ccatagttct 1200
tgtgtcttat ttgattcttc tgcgtgacac attgtattgg tccttggtgc atgtagtcta 1260
ctgtgtgttt tccgatttta taaggcagca tttctccata caaaaaraaa aaaaatgatg 1320
tacatataaa cgcttttrtt gtatggctcc tccatgttac tgtatatatc tgccagcact 1380
tcccagttac actcctgtga gtcagcttat tttacccta acataaatag tatgttttgt 1440
agtagttatc aaatttaaga gataaagcaa tcagaatgtt tggattttct tctatcttaa 1500
tgtgaatttc ataattaatg tctatttatt cagctattca ttaaaatata ggattctttg 1560
gggaaaaa 1568
```

<210> 43

<211> 1060

<212> DNA

<213> Homo sapiens

<400> 43

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gcttgtcatg agaaggtggt aaatatccaa aaagaccccg gtgaatctct cggcatgacc 60
gtcgcagggg gagcatcaca tagaraatgg gatttgccta tctatgtcat cagtgttgag 120
cccggaggag tcataagcag agatggaaga ataaaaacag gtgacatttt gttgaatgtg 180
gatggggctg aactgacaga ggtcagcccg agtgaggcag tggcattatt gaaaagaaca 240
tcacctcga tagtactcaa agctttggaa gtcaaagagt atgagcccca ggaagmctgc 300
agcagcccag cagccctgga ctccaaccac aacatggccc caccagtgga ctggtcccca 360
tcctgggtca tgtggctgga attaccacgg tgcttgata actgtaaaaga tattgtatta 420
cgaagaaaca cagctggaag tctgggcttc tgcattgtag gaggttatga agaatacaat 480
ggaacaaac cttttttcat caaatccatt gttgaaggaa caccagcata caatgatgga 540
agaattagat gtggtgatat tcttcttgct gtcaatggta gaagtacatc aggaatgata 600
catgcttgct tggcaagact gctgaaagaa cttaaaggaa gaattactct aactattgtt 660
tcttggcctg gcactttttt atagaatcaa tgatgggtca gaggaaaaca gaaaaatcac 720
aaataggcta agaagttgaa acactatatt tatctgtcga gtttttatat ttaaagaaag 780
aatacattgt aaaaatgtca ggaaaagtat gatcatctaa tgaaagccag ttacacctca 840
gaaaatatga ttccaaaaaa attaaaacta ctagtttttt ttcagtgtgg aggatttctc 900
attactctac aacattgttt atattttttc tattcaataa aaagccctaa aacaacaaaa 960
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa gggcggccgc tctagaggat 1020
ccaagcttac gtacgcgtgc atgcgacgtc atagctcttc 1060
```

<210> 44

<211> 1344

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (144)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (163)

<223> n equals a,t,g, or c

<400> 44

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cccacgcgtc cggggccacc agggcctcct ggccccctg ggccccagc ccctgttggg 60
```

```

ccaccccatg cccggatctc ccagcatgga gaccatttgc tgtccaacac ctactgag 120
accaacaacc actggcccca gggnaaccac tgggcctcca ggncytccag ggcccatggg 180
tccccctggg cctcctggcc ccacaggtgt ccctgggagt cctggtcaca taggaccccc 240
aggcccccact ggacccaaaag gaatctcttg ccaccagga gagaaggcg agagaggact 300
gcgtggggag cctggccccc aaggtcttgc tggggcagcg gggggaactg gccctaaggg 360
agaccctggg gagaagagcc actgggtccc tagcttacag agcttcctgc agcagcaggc 420
tcagctggag ctcttgcca gamgggtcam cctcctgaa gccatcatct ggccagaacc 480
agagctgggg tctggggcgg gccctgccgg cacaggcacc cccagcctcc ttcggggcaa 540
gaggggcgga catgcaacca actaccggat cgtggccccc aggagccggg acgagagagg 600
ctgaggggtg tggcgccccc tgaggcagac caggccaggc tccccctcct acctggactc 660
ggccagctgc ctccaggac cgcccgcca tatttattaa tgcctcagg gtcccttctg 720
ccatctaggc cttaggggta agcaggtctc agtctggca ccatgcacat gtctgaggct 780
gagcaagggc tgagaggaga ggcttggcc tcagtttccc tctgtgaagt ggggggaggc 840
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gcccagaagg actgaggag tcaggagctg gggctcggca catgcagaga tgacagggca 960
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tccttgttgt ccagtgttg gytccccacc ccgaggtcag gctgccaat cctctgactg 1080
gatcacggg ggcttcttg ctcagttctt ccctctgag cccaggccc tcccgcattc 1140
caggttggg atggggacat ggagaggaag gggccgcta ctctgcaaa tgctgtgac 1200
agatgccagg aggtagatgt gtgctggcca ataaaggccc ctacctgatt ccccgcaaaa 1260
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa ggcggcgctc tagaggatcc aagcttacgt 1320
acgcgtgcaa cgcggtcat agct 1344

```

&lt;210&gt; 45

&lt;211&gt; 892

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (890)

&lt;223&gt; n equals a,t,g, or c

&lt;400&gt; 45

```

ttgagaagtt ggatgaatat atatatagac acttcttttg tcacactttt tccccccat 60
atggaccag tcgacctgat aaaaagcaac gtatggtaaa tattgaaaac tccaggcatc 120
gaaaacaaga gcagaagcac cttcagccac agccttataa aagggaagg aaatggcata 180
aatatggctg cactaatgga agacaaatgg caaatcttga aatagaattg gggcaattac 240
cttttgatcc tcaatactga ttcacaattg agttaaatta gacaactgta agagaaaaat 300
ttatgctttg tataatgttt ggtattgaaa ctaatgaaat taccaagatg acaatgtctt 360
ttcttttgtt tctaagtatc agtttgataa ctttatatta ttcctcagaa gcattagtta 420
aaagtctact aacctgcatt ttcctgtagt ttagcttcgt tgaatttttt ttgacactgg 480
aatgttcaa ctgtagtttt attaggaag ccaggcatgc aacagatttt gtgcatgaaa 540
tgagacttcc tttcagtgtg agagcttaaa gcaagctcag tcatacatga caaagtgtaa 600
ttaacactga tgtttgtgtt aaatttgag cagagcttga gaaaagtaca ttgttctgga 660
atttcatcat taacatttta taatcttaca ctacttctt gtctttttgt gggttcaaga 720
gccctctgac ttgtgaagaa ttgctgccc tcttaagagc ttgctgactt gttttcttgt 780
gaaatttttt gcacatctga atatcgtgga agaaacaata aaactacacc atgaggaaaa 840
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaccccg gggggggccn ga 892

```

&lt;210&gt; 46

<211> 496  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc feature  
<222> (496)  
<223> n equals a,t,g, or c

<400> 46  
aattcggcag agtcggagtg tgggtacttct cctagttgca gtcaggcttc atacgtatt 60  
gtcctgcccg taagttcccg ttttgtgtgt ggtagagca gccagcgggt acagaatgga 120  
ttttggaaga gggagtcacc actggacctc caaggaagcc acgtgcagac atctacaacc 180  
ttcgatctcc tgacgagttt attgttgcc aaaaccaggc tttgattgaa ccaggatgaa 240  
tgcgggtgtt ggaagtagaa tatatatata catataaaat tgaaactggc gatggaatat 300  
gagaggagcc ctctggaaag aaaaggacag accctgtgct ttcattgaaag tgaagatctg 360  
gctgaaccag ttccacaagg ttactgtata catagcctga gtttaaaagg ctgtgcccac 420  
ttcaagaatg tcattgktag actttgaaat ttctaactgc ctacctgcat aaagaaaata 480  
aaatctttta aatcan 496

<210> 47  
<211> 1229  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc feature  
<222> (764)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (1165)  
<223> n equals a,t,g, or c

<400> 47  
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ttgcataaag agttggtcca ttaacttgcc aatttgaagc ttctaactag atattcccta 180  
ctgaaagttt tggatttggt tttagtttgt ggagcagctc tagctgggga caggtaattg 240  
acaacggcag agatactttc ttttcctagg attctaagtc tgtaatccac atcctcaatg 300  
tattcacagg actttaaaaa tctctccaaa tgaggragg aaatatcctg gtgctttcta 360  
atgggttact aaaagttgtg tttagaacaa cagattttta taggcatctt cctttgttat 420  
gtgtcattag ccttttgccc gtttacctta gggctctttg aaggagaaat ggatgggaga 480  
aaacctgtca cttggcgaaa gtaaaaggga taattaactg gctcagagct tatgtgcaga 540  
gttccaagcc ccaaagttaa tctagaacca ctcgataaca ccaataaaaa tatttatttc 600  
acatctgtta tatatctgga aaatgktcta agcatcttac acatatttct cattaaatcc 660  
acaggtgacc attgtgaggt agawattttg ktctaawttt ccagatgagg aagctgagac 720  
cctaaaaggt taggtgacag gttatacaac ttggagtgtg ggaggaggag agaggaacct 780  
gaacagggca agttggggat ctgacttttg tttgggtaga tgtaagcaca ttgtattttt 840  
ggcttagatg ctttattcat catggctgaa ggaataacca ttactcact caccgaaaat 900

```

tgtttacaat aatctagatg aatttgctgt ctttggacat ctgtcttttg actggacccc 960
agtatatagt ctgtggaagc tcacttaagg agaragctcc tttttgtttg gttagagaaa 1020
ttttctgtcc taaaagtaga aatagccccct tctaggtaag gatggagcat ttgatcatac 1080
tggtttcatt atattcctct aacagggttg aaccgattgt ttttgagtac ttgtttcaaa 1140
cttctgagta ttttccttct ggaanatagc tcagtgtttt aaaatttaca tgaacttaaa 1200
aggttaattt ttttttaaaa gaatggtta 1229

```

<210> 48

<211> 1411

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1410)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1411)

<223> n equals a,t,g, or c

<400> 48

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catcctggct ccttgagtgg gagtratata acctctatcc taactgtcct tgtccctcct 60
ctccccacag ctggattatc accgaggcct cttgggtggac cgccctcttg aaactaagac 120
agaggagcag ggaataccac ggcccttgca cccccacccc ccacccccgg tccagccacc 180
acagcacccc cgggcagagc agcgggagca ggaacgggca gtgcgggaac agtgggcaga 240
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caaagtctga gaagggcccc gttcccgatc aaggtcccggt gaccgccgcc gcaaggaacg 360
tgcgaagtct aaagaaaaga agagtgagaa gaaagagaaa gccaggagg aaccacctgc 420
caagctgctg gatgaccttt tccgaaagac caaggcagct ccctgcatct attggctccc 480
actgactgac agccagatcg ttcagaaaga ggcagagcgg gccgaacggg ccaaggagcg 540
ggagaagcgg cgaaaggagc aagaagaaga agagcaaaag gagcgggaga aggaagccga 600
gcgggaacgg aaccgacagc tggagcgaga gaaacgtcgg gagcacagtc gggagaggga 660
caggagagaga gagagagaaa gggagcggga caggggggac cgagatcggg atagggaag 720
ggaccgagaa cgaggcaggg aaagggatcg cagggacacc aagcgcaca gcagaagccg 780
gagtcggagc acacctgtgc gggaccgggg tgggcgccgc tagctgggaa aacactagag 840
ctgcaggtag cagccactcg gccccagggg gttatggcca cagagggata ggcacagtct 900
ccaccacctt ggagccaagg gtctttcaca tcacctatcc ctacatacat accaaatgga 960
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cgaccctccc tctcatttcc cattaagtct gagaggcaag agctagggtta ggcaaggagg 1080
tggttggcca gagatgggga acagccaggt gccccagtc tctgattttt cctccatcct 1140
gcttaccacc tccttggtga cttacagcct tctcttggga acagccgggg ccaggactgg 1200
gtcacctatg agctgaatca gcctctcctc ctgagtccca gggccctgc agttcccagt 1260
ctcttctgtc ctgcagccct tgcctctttc ccacaggttc cactttatat ccaccttttc 1320
cttttgttca atttttattt ttattttttt tattattaaa tgatgtgggc tatggaaaaa 1380
aaaataaaaa tctgacttag ttttaaaaan n 1411

```

<210> 49

<211> 1685

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (5)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (344)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1606)

<223> n equals a,t,g, or c

<400> 49

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cgctnttccc cccacacccc gtgtggccag ggatccccgc atggcccac ttagaaactc 60
aactatttgg tggatgctaa acacttcact tcaggcaatc ccaaggcatt tgctccaggg 120
tatccgatga gattacagct gttaagcttg ctttccattt cataacttgc tgtgcagcta 180
gttaccaccc ccatgctgaa gagtaaagca aagtgccgtg gttcggcagt ggaatccacc 240
cccagcactc tgctcgcaact ggagcgttca agtccggtta tgtgagaaca gactaggact 300
ctcttgctgc ctctaattgc atttcactgt caccctcccc agtnttctga tgggtgtgcat 360
gtgaggagaa gatgagggtta ggactgagaa gtgcagaagt tggaacagtg gtaaggctgt 420
tttaaaataa gatgttttgt tttaataata tgctcctggc acaaagctag gagtaaagt 480
gactccaaag ggagttcagt taatctctga aatgcacaaa acctagctat tttctccctc 540
tcacacagct ctgagctctg tccattgcta cccaattct ctggggacat aaaaccaggc 600
tggaagaggga ccaggaaagt tgaatatgtg acatatcatc cactagtccc aagggctaag 660
gaatagttag tttattctgg aaggaaactg gaagcttagt ctaattagt cctggggatg 720
acctatgcaa tcacaccgct tatgaccatc cttagagagg ccctgagcac cagcttgatc 780
ttagggattt ccaaagtaac ctgctttttg cctggatagg gttaaaatag acctttcttg 840
cctatccttg ccttaacctt tctgcctgag gttggcctga gattgtgagt caacgacttt 900
gctatctttt cctcagtgtt gaactttcat taagaaataa agtcctagct tcttacagag 960
aggggtccaa atggtgaatg ctcacctcgc ctgggattca aggaattagc tcagagrttg 1020
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gcaacttatt caggcagtct ggaaaggggg ttctcagaaa actcagtttc tttattcctt 1260
cttttctccc aactactgtt actggttata gaggtctttg gactctaaag accaatgttt 1320
ggccactaac tggactaata tgtatctttc tgtgatttca tcatagaggt ctgttttgtg 1380
aggggttggg gtgcagaaaa ctttgattaa atcttaattg gaggtcgggt gacctggatt 1440
atctacagtg agcagactta aatggaacag aagtttatgt gtccaaatga tggaatcatt 1500
aaacctgagt gacttgacct gtgtggttcc ttaatagtat ctatatatct agacaaaaat 1560
agattgtgaa tgtaaagtgt gaatgaaaag gatggaaata atgttntcat atgttaatcc 1620
atgagcttga atccaggag gaatacctcg gtgctttaac caccttagtt ataacacatt 1680
tctta
```

1685

<210> 50

<211> 660

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (515)

<223> n equals a,t,g, or c

<400> 50

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cggcacgcgt gggcctactt tcacgcttcc tccctccccc ctctccctt atcccttcgc 60
tttcgctctt ttccgtcgag gccgaccctt gagttgtgag tctggggtct ggttggtgaa 120
aaagagccct tgaagctgga agacgggaga ggacaaaagc atgtcttccc ttcctgggtg 180
cattggtttg gatgcagcaa cagctacagt ggagtctgaa gagattgcag agctgcaaca 240
ggcagtgggt gaggaactgg gtatctctat ggaggaactt cggcatttca tcgatgagga 300
actggagaag atggattgtg tacagcaacg caagaagcag cttagcagagt tagagacatg 360
ggtaatacag aaagaatctg aggtggctca cgttgaccaa ctctttgatg atgcatccag 420
ggcagtgact aattgtgagt ctttggtgaa ggacttctac tcgaagctgg gactacaata 480
ccgggacagt agctctgagg acgaatcttc ccggnctaca gaaataattg rgattcctga 540
tgaagatgat gatgtcctca gtattgattc aggtgatgct gggagcagaa ctccaaaaga 600
ccagaagctc cgtgaagcta tggctgcctt aagaaagtca gctcaagatg ttcagaagtt 660
```

<210> 51

<211> 1572

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (2)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1555)

<223> n equals a,t,g, or c

<400> 51

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tnagtgaaag aatgtgccat attacatatt gcaacctaatt ttgttaaaac taactccagc 60
actaaagctg aaatgccaca aacactaaaa gtataaatat gtctgatttt tgaaacacat 120
aagctttgct ctttaggcag gaatgatctt ttcaaatcat tagcacaata tttaaatata 180
taaaaattta agagatccat actttctgta gctttacaat taatttaagt actaaaaaga 240
caaggatttc ttttaagaaa tttatagcat ttactgtgtt atttaaatgc taagccaaag 300
tatctgcact taggtatacc tctttatgcc aataatgatt ttaatgaagg ctcttttcag 360
atgtaacctt atgaaggaaa tatctgcttt gtgtatatgc cagttagaat actggtttct 420
aaagtctgtc aaattgtatt tcagtggcac aaaaaccagt tttgaggctc tagacttata 480
attctttgaa taaaactgat aacttatatt tataattgga gtggagacct acctccataa 540
ttagataaac tctttttgga ttataatcag aattttgcct tttttcttct caaattatta 600
catatgtatg tattatatat ccacatatat agttttccct gattaaatgg atattaaaa 660
aattgcgggt gcttcaggac tttttgcttc tataatttaag tatattgttt ttatagcaag 720
aacatatctt gaatgtttta taaatcttta ataatttata ttaggtaat atttttgtat 780
cacaatgcat ttttttttct ctcttttcc tccaaactat accactgtat ttaccacttc 840
taagagtgcac tgacgcaggg ccagatgacc cttgaagtag tcattatgta gcaataaatg 900
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```

aagcctgaaa caggtttttt tacttccact ttaatcctta gaaatttctt ggcaacttcg 960
catattttca ttgacaccgg tgtataagta taaattttaa tgaactaatt acttttgcg 1020
attttaaaatt ctttatatgg tagttatatt ttataacagg atattaacat aagttaaadc 1080
ctatgtatatt gaaatttgta cagagctttc ctctttactt caaacagcaa aaaagtgggg 1140
ggcatattgt agtcctgtca tttaagttat gtwaaaaatt taatcattat tttgatgctt 1200
taaacattct catgtgtaat atatgttttt gtatcaaaaa cactcatata tttcaagaaa 1260
aagaaattat gttaaatagc cctgttttaa gaaaaatatt tatgaagcat ctcaacttga 1320
agatcaagtc aaagttataa ctcaggatct gargtctcaa gctaggagag actgagaatt 1380
ttaatcagtt tgggcatata rtttgactg aatcacatct gtagtactta gccaaagaca 1440
atttgarga raatatcagc cttctggaar tagctacttc ctgaacaatg taaagtgtcg 1500
caratattca ataaaatggc aacctgttaa aaaaaaaaaa aaaaaaaaaa acccnaaggg 1560
ggggggggccc cg 1572

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<210> 52

<211> 635

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (632)

<223> n equals a,t,g, or c

<400> 52

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gctgctccag ctgttcgaag gtgatccaga cgcaagatgg ctgtcctctc taaggaatat 60
ggttttgtgc ttctaactgg tgctgccagc ttataaatgg tggcccacct agccatcaat 120
gtttccaagg cccgcaagaa gtacaaagtg gagtatccta tcatgtacag cacggaccct 180
gaaaatgggc acatcttcaa ctgcattcag cgagcccacc agaacacgtt ggaagtgtat 240
cctcccttct tattttttct agctgttgga ggtgtttacc acccgctat agcttctggc 300
ctgggcttgg cctggattgt tggacgagtt ctttatgctt atggctatta cacgggagaa 360
cccagcaagc gtagtcgagg agccctgggg tccatcgccc tcctgggctt ggtgggcaca 420
actgtgtgct ctgctttcca gcatcttggt tgggttaaaa gtggcttggg cagtggaccc 480
aaatgctgcc attaaagaat tataggggtt taaaaactct cattcatttt aaatgactta 540
cctttatttc cakttacatt ttttttctaa atataataaa aacttacctg gcatcagcct 600
catacctaaa aaaaaaaaaa aaaaaaaaaa tnggg 635

```

<210> 53

<211> 1367

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (106)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (958)

<223> n equals a,t,g, or c

&lt;400&gt; 53

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taccataacc aaacattttg tgcgtgtgct attggtgctg cgatantctc ctttgggtgg 120
aacacagtga agatcgacat gaggcgagcc cggagagatc ctcttccaat tgttccattt 180
ggattagctg catttgctac cactttgttt gccttgggat tagctttagg aacaaccata 240
gctgttgga tggtgttttt tatccagatg aaaataattc tcagaaacaa aacttctatt 300
gagtcattga ttgaagagaa ggctaaagat cgaattcagt attatcaact agatgaagtc 360
tttgtttttc catatgatat gggagtaga tggaggaaact ttaaacaggt atttacgtgg 420
tcagggggtcc ctgaaggaga tggacttgag tggccagtaa gagaaggctg tcaccaatac 480
agcttaacaa tagaacagtt gaaacaaaaa gcagataaga gagtcagaag tgttcgctat 540
aaagtaatag aagattatag tgggtgcctgc tgccctctga ataaaggaat caaaccttc 600
ttcacaagtc cctgcaccga agagcctcga atacagctgc aaaaagggga attcatttta 660
gccacaagag gtttacgata ctggttatat ggagacaaaa ttcttgatga ttccctttata 720
gaagggtgtt caagaataag ggggtggttc cctagaaaaat gtgtggaaaa gtgtccctgt 780
gatgctgaaa cagatcaagc cccagagggg gagaagaaaa atagatagct gctgttaaaa 840
caaaattatc ctttaagtct gcttaattac ttgaaaattg tacatattac taaagaatta 900
tgcaatgagc ctactctggt taagatgttc ttttcctcaa aggtgcccta gtgccatnga 960
tttaaatatt tttattacca ttttgaaatg gagaagccat tctgcatatg cctttgaatt 1020
cctgcccttc tttaccacct cttcctcccc ctcaaaggaa aaacatttca tccaagtaag 1080
ttaacggcat tttctgtagg attttcctta tgcaactgcac actctggacc tcacctgcag 1140
atacagttcc ccccttgcca ggagcatctg catgtggtac ttctcttttc cctcagttga 1200
tatttcttat atgatattct agatactata gaactcaatt tgtcagattc agtataacct 1260
cagattttgt tacctgtctt ttaaaaatgc agattttgtc aaatcaaata aagatcaatg 1320
gatgttgggt ataawmaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1367
```

&lt;210&gt; 54

&lt;211&gt; 378

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (14)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (29)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (363)

&lt;223&gt; n equals a,t,g, or c

&lt;400&gt; 54

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ggcagtggtg gggngtgaga accctgggnc ctgctgaaaa gcctcctctg taggaggtca 60
cccagcagga caragaagca ggaggaggac agggccacar aggaagccaa gaacggtgaa 120
aaggccaggc ggwggtcara ggagggtgac ggccagcacc cggcccaaga ggaggccccg 180
gaatcgcccc agacctctgg cccagagcag aaaataggtg tgggagcccc agggaggaaa 240
agccarytgg agaggaagca gagwtggaag aggtacaga ggtgaagggg gagaggggtgc 300
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aaaatgaaga ggtgggacct gaacatgaca gccaaagaaac aaagaagctt gaggagggag 360  
ctncagtga ggcgaccc 378

<210> 55

<211> 1058

<212> DNA

<213> Homo sapiens

<400> 55

tcgggtatga ggctgggact aagccaaggg attcaggtgt ggtgccggtg ggaactgagg 60  
aagcgcccaa gcttttttgt tctgaactcc cactgcgttg tggattcctg aggatgggat 120  
gactgtatct tgattaccg gagttttcaa gatggcagca tctatgcatg gtcmgcccag 180  
tccttctcta gaagatgcaa aactcagaag accaatggtc atagaaatca tagaaaaaa 240  
ttttgactat cttagaaaag aaatgacaca aaatatatat caaatggcga catttggaac 300  
aacagctggt ttctctggaa tattctcaaa ctctctgttc agacgtgct tcaagggtta 360  
acatgatgct ttgaagacat atgcatcatt ggctacactt ccatttttgt ctactgttgt 420  
tactgacaag ctttttgtaa ttgatgcttt gtattcagat aatataagca aggaaaactg 480  
tgttttcaga agctcactga ttggcatagt ttgtggtgtt ttctatccca gttctttggc 540  
ttttactaaa aatggacgcc tggcaaccaa gtatcatacc gttccactgc caccaaaagg 600  
aagggtttta atccattgga tgacgctttg tcaaacacaa atgaaattaa tggcgattcc 660  
tctagtcttt cagattatgt ttggaatatt aaatggtcta taccattatg cagtatttga 720  
agagacactt gagaaaaacta tacatgaaga gtaacaaaaa aaatgaatgg ttgctaactt 780  
agcaaaatga agtttctata aagaggactc aggcattgct gaaagagtta aaagtaactg 840  
tgaacaaata atttgttctg tgccctttgc ctgggtatata gcaaatactc aaaaagtatt 900  
caataattca atcaataaat ataagtttca tcttacacgt aagatacagg tcttatctcc 960  
tgatggtgtg tccattttgc ctgggtatata acagataata aatatccagt gtcaataaat 1020  
gtaacaataa aagtttcatc ttctctcttt gtatgtgg 1058

<210> 56

<211> 682

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (4)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (667)

<223> n equals a,t,g, or c

<400> 56

gggnccggaa catattccct tactcaaaag attgcatgac tgaatttgct taaggaaaaa 60  
aaaaattgta tcaagtccat taatacaatt atacattaat tatattacat taatacaata 120  
tatggtttgt gaattcagag acattaccag tttgcctcct tctctcaata gaacttgtat 180  
tttcattttc ttggttaagc agttgtctcc taatattatc ccatatgcta cctagtttgc 240  
tggtcccaag cagtttactg tacttcaacta gatttggtac ctgctctccc ctggacttct 300  
ttttcaatat tctagccttt cctagatgta aatctttacc tccttggttag tgaaattaga 360  
tataagccat gatttgagga ggaagaaat ctggaatact taatttcatt taattatcta 420

tgctgatgaa tgccctgtatc attgttaata aaggagaatt gaaaatactc atttctactt 480  
tctgccctca aatttctgtt tctatctcaa ctaggcaaga atcagcaggg tgcattgaygc 540  
cattttaagc tgcttcacat cagactgaaa tcctaattac agttcataag tgaaacagac 600  
taattcmatg ggcaatacct ttkgtawagg tccygtgctt aaaggaggca agtataaatt 660  
ttcccantaa ggaatccccg gt 682

<210> 57

<211> 644

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (5)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (27)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (458)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (619)

<223> n equals a,t,g, or c

<400> 57

ggagncctggg cctgtgcggc ggccgcngta gcgctttgga aggcgcacgg ggcgaagatg 60  
gcggcgagcg acaggaggcg ctgaggaggt tcgtggcggg gacgggcgcc gaggaggacc 120  
gggcccgcct ctttctcgag tcggccggct gggacttgca gatcgcgcta gagcttttta 180  
tgaggacgga ggggatgaag acattgtgac ctttctgcag gcaacccccca gttcagtgtc 240  
cagaggcaca gccccagtg ataataagat gacatccttc agagacctca ttcattgacca 300  
agatgaagat gaggaggaa aggaaggcca gaggtgagtc ttctagaggg ggtcaggggg 360  
acagttcaca gggaaagtcca gggtaattgtg taaatcacct agaacaggac ctggtaaaac 420  
atgtttgggt tattgttagc cattactact gtgggctngt ctgtgtgggt tatatcttag 480  
gaagtctctt ctactccttg tagcttagaa gtgacccttg ttccgttact taatgtatgt 540  
attgaggaat attaggggag ggaaaccaag gaaaagatct agcattccca ctttttggtg 600  
ttgactaaaa aggatttgna aatcagtttg taaaagaagg tgct 644

<210> 58

<211> 766

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (760)

<223> n equals a,t,g, or c

<400> 58

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gggtcgaccc acgcgtccgg aatgttttgg tgaataaatc tgttcttcag caaccctacc 60
tgcttctcca aactgcctaa agagatccag tactgatgac gctgttcttc catctttact 120
ccctggaaac taaccacgtt gtcttctttc cttcaccacc acccaggagc tcagagatct 180
aagctgcttt ccatcttttc tcccagcccc aggacactga ctctgtacag gatggggccg 240
tcctcttgcc tccttctcat cctaatacccc cttctccagc tgatcaaccy ggggagtact 300
cagtgttcct tagactccgt tatggataag aagatcaagg atgttctcaa cagtctagag 360
tacagtccct ctctataag caagaagctc tcgtgtgcta gtgtcaaaag ccaaggcaga 420
ccgtcctcct gccctgctgg gatggctgtc actggctgtg cttgtggcta tggctgtggt 480
tcgtgggatg ttcagctgga aaccacctgc cactgccagt gcagtgtggt ggactggacc 540
actgcccgct gctgccacct gacctgacag ggaggaggct gagaactcag tttgtgacc 600
atgacagtaa tgaaaccagg gtcccaacca agaaatctaa ctcaaacgtc ccacttcatt 660
tgttccattc ctgattctwg ggtaataaag acaaactttg tacctcaaaa aaaaaaaaaa 720
aaaactcgag gggggggccc gaamcaattc gggctatagn agagcg 766
```

<210> 59

<211> 2361

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1174)

<223> n equals a,t,g, or c

<400> 59

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gttctagatc gcgagcggcc gccctttttt tttttttttt tttggaaagc aaggatcaca 60
cttccccctc cctgttccct aatccccctt ctaaaaaggg gggaaaatcc ggatggattt 120
tagggattgg tctggtgtca gctgtgtttt attgcacacc taaatcctga ttataggctt 180
ttcattttct cgcaaagcct ttattttggc agttaagcca aatgtgtttt ccagaaagtt 240
agttattttc tcctctttct ttcttttctt tcctcccttt tcccgtctg accccaaacg 300
ttattgtcca aacatgactg gacagcagct tttgtttctt gaccctgtaa tatgacagtc 360
tgctaataat gacagaaggt gcagtttttg gggtatagtc gtgattttcg ctaatcaatc 420
atattagcag gaaaaaaaaa gacttgtttc tgttgtaact gagtcttaag aaaaagtgcc 480
catagtttag tgacaatttc caaaggcttt agtaccacct gtatttcaaa atgggggacc 540
caaactcccc gaagaaacaa gctctgaaca gactacgtgc tcagcttaga aagaaaaaag 600
aatctctagc tgaccagttt gacttcaaga tgtatatgac ctttgtattc aaggagaaga 660
agaaaaagtc agcacttttt gaagtgtctg aggttatacc agtcatgaca aataattatg 720
aagaaaaatat cctgaaaggt gtgcgagatt ccagctattc cttggaaagt tccctagagc 780
ttttacagaa ggatgtggtg cagctccatg ctctcgcata tcagtctatg agaagggatg 840
taattggctg tactcaggag atggatttca ttctttggcc tcggaatgat attgaaaaaa 900
tcgtctgtct cctgttttct aggtggaag aatctgatga gccttttagg cctgttcagg 960
ccaaatttga gtttcatcat ggtgactatg aaaaacagtt tctgcatgta ctgagccgca 1020
aggacaagac tggaatcggt gtcaacaatc ctaaccagtc agtgtttctc ttcattgaca 1080
gacagcactt gcagactcca aaaaacaaag ctacaatctt caagttagtc agcatctgcc 1140
tctacctgcc acaggaacag ctcacccact gggncagttg gcaccataga ggatcacctc 1200
cgctcttata tgccagagta gagtactgac cagcaaatg gagaagatca gagaatgcag 1260
cagcagtttt ttttcttgtt ttcttaccac tttattcttt cagagtttaa agaaaaatgga 1320
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ctcatgcaca gaacactatg cattttgaaa cttgttcac cttggattttt ttaaactcatt 1380  
tttatctcag aacttaaaca aaaattagat gtcgtgcacg gactgtgtga aagaagatgc 1440  
tttgcataatt tgctgcactg catcagatc ttactaaaaa tgtgaaatga aaggactatt 1500  
gtacactgaa atgcttaaat gtatctgaaa gcacaagggtg atactcattt ttatgggtctt 1560  
cccatttgtg ctgggtttttg cctctttgac atctgtcac agtattttaga gggtgagaag 1620  
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accatgggaa rgaaatctta aatgaaaaac gcatctcatt gtaggcattt ttgcctcata 1800  
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agaaacccatg ataggtagag gacttttctt ttgggtttgt tttgtttgt tttgtttgt 2040  
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aaagcagaac tcattttgtg caatgracat aagggaagac tactgtatag gtttttkttt 2280  
tctcctttta aatgaaraaa arcttgctta aggggtgcat acttttattg gagtaaatct 2340  
gaatgatcct actcccttg a 2361

<210> 60

<211> 1472

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (129)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (130)

<223> n equals a,t,g, or c

<400> 60

aattcggcac gagcccagat ggcgctggag gaccaggccg ccacactgga gtataagacc 60  
atcaaggaac atctcagcag caagagtccc aaccatgggg tgaaccttgt ggagaacctg 120  
gacagcctnn ccccaaagt tccacagcgg gaggcctccc tgggtccccc gggagcctcc 180  
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gactataaga ggagctaccc cacgaactcg ctcacgagaa gccaccaggc accactctca 300  
aaagaaacaa cactaactcc tccaattcct ctcacctctc cagaaaccag agctttggca 360  
ggggagacaa cccgccgccc gccccgcaga ggggtggactc catccagggtg cacagctccc 420  
agccatctgg ccaggccgtg actgtctcga ggcagcccag cctcaacgcc tacaactcac 480  
tgacaaggctc ggggtggaag cgtacgccct cgctaaagcc ggacgtaccc cccaaacat 540  
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tcaactgcct cgagtaccca ccagaccaag aargcctgcg gcagagccga ggacgctggg 720  
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caaaaaaaaa agaattcatt gataattcta actcagactt taacaatggc agaagtttac 1140  
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<210> 61

<211> 1672

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (884)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1583)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1645)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1663)

<223> n equals a,t,g, or c

<400> 61

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cgagaagatg ctccagtacc ggcgggacac agcaggctgg aagatttgcc gggaaggcaa 180  
tggagtttca gtttcctgga ggccatctgt ggagtttcca gggaacctgt accgaggaga 240  
aggcattgta tatgggacac tagaggaggt gtgggactgt gtgaagccag ctgttgagg 300  
cctacgagtg aagtgggatg agaatgtgac cggttttgaa attatccaaa gcatcactga 360  
caccctgtgt gtaagcagaa cctccactcc ctccgctgcc atgaagctca tttctcccag 420  
agattttgtg gacttggtgc tagtcaagag atatgaggat gggaccatca gttccaacgc 480  
caccatgtg gagcatccgt tatgtcccc gaagccaggt tttgtgagag gatttaacca 540  
tccttgtggt tgcttctgtg aacctcttcc aggggaaccc accaagacca acctggtcac 600  
attcttccat accgacctca gcggttacct cccacagaac gtggtggact cttcttccc 660  
ccgcagcatg acccggtttt atgccaacct tcagaaagca gtgaagcaat tccatgagta 720  
atgctatcgt tacttcttgg caaagaactc ccgtgactca tcgaggagct ccagctgttg 780  
ggacaccaag gagcctggga gcacgcagag gcctgtgttc actctttgga acaagctgat 840  
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ccccactcag gggtggcgtg tgatgagcca ttcattgtgt ccaaactcca tctgcctgtt 960  
acccaaacac gcctctcctg gcagggtaga cccaggcctc taaccatctg acagagactc 1020  
ggcctggaca ccatgcgatg cactctggca ccaaggcttt atgtgcccac cactctcaga 1080  
gaccacgttt cctgactgt catagagaat catcatcgcc actgaaaacc aggcctgtt 1140  
gccttttaag catgtaccgc tccctcagtc ctgtgtgca gcccccaaa tatatttttc 1200  
tgatatagac cttgtatatg gctttaatgc cgcaaatat ttatttttcc ttaaaaaagg 1260  
tgtcaacttg gaaataatgg tttaaaaaca ggataagcat taaggaaaaa cactttcaat 1320  
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gaagagcctt ccttttcttt cccttgggac atttgctttt ccttgctgtc ttactgaggg 1560  
cggaggcagg gaggggtctc gtncctttcca gggcctggg cagggccatc ctggccattc 1620  
agggaaagat gggaagagtt agggncctcc ttttaggcag cntgggtgg ga 1672

<210> 62

<211> 1540

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1265)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1468)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1507)

<223> n equals a,t,g, or c

<400> 62

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&lt;210&gt; 63

&lt;211&gt; 1044

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 63

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gacacaggaa gttccagggc acccaactgc agatatcggg ccatagcgag cactagacgt 180  
gttgctcattg cctgtgaggg taaccacag gtgcctgtgc actttgacgg ttagatgcca 240  
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gattgaaaga ttttttatgt tttccttgta ataaaggacc taaaccgaag gtacctgaaa 1020  
aaaaaaaaa aaaaaaaact cgag 1044

&lt;210&gt; 64

&lt;211&gt; 851

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 64

cacgagagaa ggtggttatt tatacaaaaca tggacatact cactcccaag ggctgatgag 60  
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ctggaagctg cctgtgctaa gaccacccag ctgtccctgg gttctcatcc tagggccttc 180  
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gaggcacagt tctctctact ggaaagaaaa cgatgtagcc gattgcacaa gggtgccaa 420  
ggaagaccca ggtggccca tcaaaggaa ctgggggagg atgcaggagg ctgaaggga 480  
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<210> 65

<211> 2793

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (2793)

<223> n equals a,t,g, or c

<400> 65

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gcatagacaa gcttaacatt gtagatgttt ctcttcaaaa atcatcttaa acatttgcatt 180  
ttggaattgt gttaaataga atgtgtgaaa cactgtatta gtaaaacttca tcacctttct 240  
acttccttat agtttgaact tttcagtttt tgtagtctcc aaacagttgc tcaattttaga 300  
gcaaattaat ttaacacctg ccaaaaaaag gctgctgttg gcttatcagt tgtctttaaa 360  
ttcaaatgct catgtgactt ttatcacatc aaaaaatatt tcattaatga ttcaccttta 420  
gctctgaaaa ttaccgcgtt tagtaattat agtgggctta taaaaacatg caactctttt 480  
tgatagttat ttgagaattt tgggtgaaaa tatttagctg agggcagtat agaacttata 540  
aaccaatata ttgatatttt taaaacattt ttacatataa gtaaaactgcc atctttgagc 600  
ataactacat ttaaaaaata agctgcatat ttttaaatca agtgtttaac aagaatttat 660  
atTTTTtatt ttttaaaatt aaaaataatt tatatttcct ctgttgcatg aggattctca 720  
tctgtgctta taatggtag agattttatt tgtgtggaat gaagtgaggc ttgtagtcat 780  
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<210> 66

<211> 303

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (108)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (278)

<223> n equals a,t,g, or c

<400> 66

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attaatactg atgtgaatgg atgcatttgt tttgcagtgg tgactggcct aggcagggtt 180
gggatctgtg aaagaattga ttcattttca aaattattcc ataaagttaa aaagttacac 240
tttaagggca acaggtcata cagttcttta aaatctgnat ccaactgtag ctttatttaa 300
aag 303

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<210> 67

<211> 1410

<212> DNA

<213> Homo sapiens

<400> 67

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gtgtgagcct gaatttgcca atgacaaggc cagggagccg agcgtgggtg gcagggtggc 180
agtgtccttg tacgaacggg ttgtgcagcc atgtctggtc gaactgctgg gctctgctct 240
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<210> 68

<211> 1024

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (2)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (7)

<223> n equals a,t,g, or c

<400> 68

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cgccatttta caacagctcc actcgcgccg gacacaggga gcagcgagca cgcgtttccc 180
gcaacccgat accatcggac aggttttctc cgcctcagcc caacggggag atctctggaa 240
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cagttatcca ttcagaaaat tttcagacat tgcttgatgc tggtttacca cagaaagttg 360
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tctt

1024

&lt;210&gt; 69

&lt;211&gt; 1848

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (1761)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (1844)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (1847)

&lt;223&gt; n equals a,t,g, or c

&lt;400&gt; 69

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<210> 70

<211> 2682

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (647)

<223> n equals a,t,g, or c

<400> 70

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tagacagact atgtctcttt ctgccacca aactcgaaaa gttgaagacc tggcaaggat 180  
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ggatggtctt gaacagaaga accgaaagaa gaagcttatg gtcttctttt catcttgtat 300  
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<210> 71

<211> 412

<212> DNA

<213> Homo sapiens

<400> 71

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ggaccgcccc aacctcggga gccccccact cagtaggtct gaaggcctcc atttgtaccg 180  
aaacaccccg ctacgctga cagcctccta ggytccctga ggtaccttc caccagacc 240  
ctccttcccc accccataag ccctgagact cccgcctttr acctgacgat ctccccctt 300  
ccgccttca ggttctctct aggcgctcag aggcgctctt ggggggttgc ctcgagtccc 360  
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<210> 72

<211> 1361

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (46)

<223> n equals a,t,g, or c

<400> 72

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tcagcagttg tttcaagagc agctgagata atwaattcaa ccaaagggcg ccttggttct 120  
ttawggatc tgawactcct ctaggacttg cgagggccgt gtcctgagta gtgtgtgmcc 180  
cttggtctac gttgcctctg ttttctctca gttgccagac ttagaagmct tgatgaaaag 240  
ggagaaccag aagattctga ctccctggt gagectggac accccagggg aagcaacagt 300  
acaggtggtc attctggccg accctgacgg acatgaaatt tgctttgtcg gggatgaagc 360  
atttcagaaa ctttctaaga tggatccaga gggaagcaaa ttgttggatg atgcaatggc 420  
agcagataaa agtgacgagt ggtttgccaa acacaataaa cccaaagctt cagggttaacg 480  
gaagacatga tgcagagcaa gcctctgtga ttcctgcccc gcacctgtga ggctgacgt 540  
gtcagttccc aataaatgct cttctgattt gtttcccgta caggcaagga ggcttgggta 600  
gtgcagattt gtgtatttca atctttgaaa gctctgatgt aatttagaaa tgaaatccaa 660  
tcagagtcc aggtagagaa cgcctgctgt aatctacact gttgctggga ctgcgcattc 720  
tgtatataac tgtgttgat gagtgacaga tgattgtcca gactaggaca gcggcatgaa 780  
catgactttg gttgggattg cggatagtta gggttacctc tgaatcgtgt agcttttatg 840  
agagcagctg tgcaagtga tccacattaa tgccttgctg tggtgccatt cccagcgcct 900  
gacgatacgc tcttctattg tcttattctg gcagggtttg acgtttttaa ttttttaaa 960

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aaattttatt ccttggaacca aaagggtttgg ttaaccaccc cctcttact tgctttcaca 1020
ttttgagtgt ccagaggaaa cagaaaggaa tgagtgtgtg acgttgctgc acgcctgact 1080
ctgtgcgagc ttctttctgt gtatatattt tgttttattt ttttccgtgt atatttttaa 1140
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agcttctgaa atcaaaaaaa aaaaaaaaaa aaaaaaaaaa a
1361

```

&lt;210&gt; 73

&lt;211&gt; 928

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 73

```

cagcaatggc agcatctgcc ttgatatcct gcgggtctcag tgggtctccag cgttgactgt 60
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ggtgccagag atagcacaca cctacaaggc cgacagagag aagtacaaca gactagcaag 180
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cagtgccacg tgggtgaattt tctcgcttcc acaccaagaa agcagcaaag tggaaaattt 840
tcaaggatac aaaggcacat aacamcccca taagragatg attaaaggtt tttagaagca 900
agagcaaaat tttgaaaacc tctaggag
928

```

&lt;210&gt; 74

&lt;211&gt; 1186

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 74

```

gcggacgcgt gggcagcccg ggcggctgcc cttgggtgct cccttccctg cccgacaccc 60
agaccgacct tgaccgcca cctggcagga gcaggacagg acggccggac gggccatgg 120
ccgagctccc ggggcccttt ctctgcgggg ccctgctagg ctctctgtgc ctgagtgggc 180
tggccgtgga ggtgaaggta cccacagagc cgctgagcac gcccctgggg aagacagccg 240
agctgacctg cacctacagc acgtcggtgg gagacagctt cgccctggag tggagctttg 300
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```



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```

<210> 75

<211> 933

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (791)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (794)

<223> n equals a,t,g, or c

<400> 75

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gtgtaactgt gcataatccc gaaaatcaaa gctacttgat agcatataaa gattcccaac 180
ttattgtttc atcagctaaa gcattacagc attgtgaaga actgattcag cagtacaacc 240
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accatgtagg caaagcagtg gaggactgca tgagggccat catcggggtg ttgcttaatt 360
taactaatga taatgagtgg ggcagcacca aaacaggaga gcaggacggt ctcataggca 420
cagcgctgaa ctgtgtgctt cagggtccaa agtacctacc tcaggagcag agatttgata 480
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gtgggtgtca ntgnaaaaga ctgatggtac agaagagaaa cataagaagg agggaggagga 840
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tagtggtttg attttgtttt tttcctccaa acc 933

```

<210> 76

<211> 1964

<212> DNA

<213> Homo sapiens

<400> 76

```

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caccgggtcc ctgacccgcg gcccccgcg cccggttccc ggcattgcctc gcgcccgtaa 180
gggcaacacg ctccggaagg gtggtcagcg ccgtggagga ggtgcccgga gcagtgccca 240
agctgactcg ggttccagtg acgatgaggc agccagttag gccgcagca ccgccagtga 300

```

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caagagtgcc aagaccggc aggtgctctt gagagcctgc gcctggccct agcgtcccgc 480
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ggatgaccca ctcttagggg ggtggtggca tctggacaaa tgccaccaca gcagggtggg 1860
tggaagct acctggaatg gatttgtgtg ctgattttta aggattatta cagataatta 1920
aacagaacgg tcagccttca aaaaaaaaaa aaaaaaaaaa aaaa 1964
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<210> 77

<211> 1802

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1680)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1747)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1757)

<223> n equals a,t,g, or c

<220>

<221> misc feature

&lt;222&gt; (1800)

&lt;223&gt; n equals a,t,g, or c

&lt;400&gt; 77

```
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gttcttgtat tgatgaagtg aaacaaagtg gggccattgt tcattttatt gctttgggaa 180
gagctgctga tgaagcagta atagagatga gcaagataac aggaggaagt catttttatg 240
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saaagtgagg cacttgggca tacaatctty aagccaaagc gamcccagaa acmttaacta 600
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gctcatggag gagcaaacac tgccaggcta aaattacggc ctccactgaa tagagccgcg 960
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gtggtatcac aagtcccaag ccttccttgc ctgaccaata cccaccaagt caaatcacag 1140
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tgctctgat tgggtctgtt gkaattgkta actttatttt aagtaccacc atttgaaact 1620
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ataattntaa gatgtcngga aaaggatact ttgattaaaa taaaaacact catggatatn 1800
ta
```

1802

&lt;210&gt; 78

&lt;211&gt; 995

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 78

```
cggggtgcct ggggcagacg aggccggctt ctccgcggac agctaggag agtgtcctgg 60
gtgtcagcca gaacatgtct ttcaacctgc aatcatcaaa gaaactgttc attttcttag 120
gaaaatcact gtttagtctt ctggaggcta tgatttttgc ctactccca aagccacgga 180
agaacgttgc tggtgaaata gtcctcatca caggtgctgg aagtggactc ggaaggctct 240
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cctgcgattg cagccaaaag gaaggagtgt atagagtasc cgaccagggt aaaaaagaa 420
tcggcgatgt ttccatccta atcaacaatg ccggaatcgt aacaggcaaa aagttccttg 480
actgtccaga tgagcttatg gaaaagtcac ttgatgtgaa tttcaaagca catttatgga 540
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cttataaagc ctttctacct gctatgattg ctaatgacca tggacatttg gtttgcattt 600
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ctccaaatcc cmccaggaaa aaccactttt aaaaa 995

```

&lt;210&gt; 79

&lt;211&gt; 1215

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 79

```

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ttattgatga aggtgaaaca gattggaaat taattgctat caatgcgaat gatcctgaag 660
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agggcgcccg ctcta 1215

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&lt;210&gt; 80

&lt;211&gt; 2660

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 80

```

gcagacttga ttagcctgcc taccactgta gagggacttc agaagagtgt agcttccatt 60
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gtcagtaatc ttaccagag agtcaacctg atagaaagcg atgtggttgc tatgagcaag 420
gtagaaaaga aagcaaacct gtccttcagc atgatgggtg atagatctgc cactctgaaa 480

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gctcttacia acaaacctga gagcaacmgg cctccagaga ccgccgatga agagcaagta 660  
gagagtctca catcaaagcc atcagcattg ccaaaatttt cacagtctct tggagacca 720  
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<210> 81

<211> 1790

<212> DNA

<213> Homo sapiens

<400> 81

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<210> 82

<211> 1350

<212> DNA

<213> Homo sapiens

<400> 82

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<210> 83

<211> 1746

<212> DNA

<213> Homo sapiens

<400> 83

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<210> 84

<211> 1491

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (176)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (711)

<223> n equals a,t,g, or c

<400> 84

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<210> 85

<211> 968

<212> DNA

<213> Homo sapiens

<400> 85

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<210> 86

<211> 3068

<212> DNA

<213> Homo sapiens

<400> 86

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<210> 87

<211> 2230

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (2227)

<223> n equals a,t,g, or c

<400> 87

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<210> 88

<211> 1163

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (159)

<223> n equals a,t,g, or c

<400> 88

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<210> 89

<211> 1939

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (20)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (31)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (33)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1609)

<223> n equals a,t,g, or c

<400> 89

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<210> 90  
<211> 2032  
<212> DNA  
<213> Homo sapiens

<400> 90  
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<210> 91  
<211> 1788  
<212> DNA  
<213> Homo sapiens

<400> 91  
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&lt;210&gt; 92

&lt;211&gt; 495

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (402)

&lt;223&gt; n equals a,t,g, or c

&lt;400&gt; 92

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&lt;210&gt; 93

&lt;211&gt; 1377

<212> DNA  
<213> Homo sapiens

<220>  
<221> misc feature  
<222> (1367)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (1371)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (1376)  
<223> n equals a,t,g, or c

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<210> 94  
<211> 2819  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc feature  
<222> (82)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (83)

<223> n equals a,t,g, or c

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<221> misc feature

<222> (84)

<223> n equals a,t,g, or c

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<221> misc feature

<222> (2816)

<223> n equals a,t,g, or c

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<221> misc feature

<222> (2817)

<223> n equals a,t,g, or c

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<221> misc feature

<222> (2818)

<223> n equals a,t,g, or c

<400> 94

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<211> 705

<212> DNA

<213> Homo sapiens

<220>

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<222> (488)

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<220>

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<220>

<221> misc feature

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<220>

<221> misc feature

<222> (687)

<223> n equals a,t,g, or c

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<211> 3472

<212> DNA

<213> Homo sapiens

<220>

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<220>

<221> misc feature

<222> (69)

<223> n equals a,t,g, or c

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<221> misc feature

<222> (3457)

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<221> misc feature

<222> (3466)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (3470)

<223> n equals a,t,g, or c

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&lt;210&gt; 97

&lt;211&gt; 1216

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 97

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&lt;210&gt; 98

&lt;211&gt; 1186

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 98

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<211> 1120

<212> DNA

<213> Homo sapiens

<400> 99

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<210> 100

<211> 1225

<212> DNA

<213> Homo sapiens

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<221> misc feature

<222> (286)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (287)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (288)

<223> n equals a,t,g, or c

<220>  
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 <223> n equals a,t,g, or c

<220>  
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 aaaaaaaaaat ttnggggggg cccgn 1225

<210> 101  
 <211> 1213  
 <212> DNA  
 <213> Homo sapiens

<400> 101  
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<210> 102

<211> 1564

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1509)

<223> n equals a,t,g, or c

<400> 102

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tcta 1564

<210> 103

<211> 1457

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 103

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aaaaaaaaaa ctcgtag 1457
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&lt;210&gt; 104

&lt;211&gt; 785

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (748)

&lt;223&gt; n equals a,t,g, or c

&lt;400&gt; 104

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tggctgatcc cagcactttt caaatgatgc cgctcaaagc cgtgacttgg cctactttga 240
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<210> 105

<211> 921

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (40)

<223> n equals a,t,g, or c

<400> 105

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<210> 106

<211> 592

<212> DNA

<213> Homo sapiens

<400> 106

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aacgtcgggg gtgagttcca caccaccacc ctgggtaccc tgaggaagtt tccgggctca 180  
aagctggcag agatgttctc tagcttagcc aaggcctcca cggacgcgga gggccgcttc 240  
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gcagaagcca taacagcacg gaaktccagg tgyttgtgtg cctgggtgaaa cttgagggag 540  
caggatgcat tattattcag aggtcctgtg tttttcttgc aggataagaa gg 592

<210> 107

&lt;211&gt; 2248

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 107

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2248

&lt;210&gt; 108

&lt;211&gt; 785

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc feature

<222> (769)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (771)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (785)  
<223> n equals a,t,g, or c

<400> 108  
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ccaan 785

<210> 109  
<211> 611  
<212> DNA  
<213> Homo sapiens

<400> 109  
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tgacctgaaa cttcaagagt accaaagtgc awtcaaagtg gagcctgcat ctccacctta 540  
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<210> 110  
<211> 664  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc feature  
<222> (24)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (72)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (614)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (616)  
<223> n equals a,t,g, or c

<220>  
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<222> (633)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (649)  
<223> n equals a,t,g, or c

<400> 110  
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tcgttccata tttggtgaag atgcacttgc aaatgtcagc attgagaagc caattcacca 180  
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tttc 664

<210> 111  
<211> 4065  
<212> DNA  
<213> Homo sapiens

<400> 111

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&lt;210&gt; 112

&lt;211&gt; 1492

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (8)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (1487)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (1491)

&lt;223&gt; n equals a,t,g, or c

&lt;400&gt; 112

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&lt;210&gt; 113

&lt;211&gt; 1482

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 113

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&lt;210&gt; 114

&lt;211&gt; 3731

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

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<211> 1315

<212> DNA

<213> Homo sapiens

<400> 115

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<210> 116

<211> 1320

<212> DNA

<213> Homo sapiens

<400> 116

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<211> 2025

<212> DNA

<213> Homo sapiens

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<220>

<221> misc feature

<222> (1916)

<223> n equals a,t,g, or c

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<221> misc feature

<222> (1944)

<223> n equals a,t,g, or c

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<210> 118

<211> 1295

<212> DNA

<213> Homo sapiens

<220>

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<222> (1286)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1292)

<223> n equals a,t,g, or c

&lt;400&gt; 118

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&lt;210&gt; 119

&lt;211&gt; 1257

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 119

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atttagaaat atgaaactgc ttaacaggta tgagcaggta tagcaagtgt ttgctaaagt 360
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gcactttggg aattactttt ctaggatttc ctaccagtta taaatgacat tgacatttgt 720
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<210> 120  
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<212> DNA  
<213> Homo sapiens

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<223> n equals a,t,g, or c

<220>  
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<222> (378)  
<223> n equals a,t,g, or c

<220>  
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<222> (395)  
<223> n equals a,t,g, or c

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cttgcatga ccacatgacc tgcagagccc ctgttataga actcattttt atattttcct 180  
tagtataaca gttaataataa tatgtcattt ttgttaatag tgtctttttg tcattttact 240  
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ataactaaca accagaantc tccgtgtact ccctncc 397

<210> 121  
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<212> DNA  
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cccgggacgt gagccgctgc gccaccggg ctagaccggg cgccatcatg ctgcttctgc 180  
caagcgcgcg ggacggccgg ggcaccgcca tcaccacgcg tctgacctct gcctctacac 240  
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gacagatcaa agcagctcat aaagcaatgg ttttaaaaca tcaccagac aaacggaaag 540  
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<210> 122  
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<212> DNA  
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<223> n equals a,t,g, or c

<220>  
<221> misc feature  
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<223> n equals a,t,g, or c

<220>  
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<222> (149)  
<223> n equals a,t,g, or c

<220>  
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<222> (1228)  
<223> n equals a,t,g, or c

<220>  
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<222> (1231)  
<223> n equals a,t,g, or c

<220>  
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<223> n equals a,t,g, or c

<220>  
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<222> (1269)  
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taagtggaaa atcaaaatcc ggccgatccc ttgaatgaag agctggggga tgaggacagc 720  
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<210> 123

<211> 3115

<212> DNA

<213> Homo sapiens

<400> 123

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ggatcgagga tactcaccag aaaccgaaaa tgccgaaacc aatcaatgtc cgagttacca 180  
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ataataaagg atttcttacc tggtgaagc tggataagaa ggtgtctgcc caggaggtca 360  
ggaaggagaa tccccccag ttcaagttcc gggccaagtt ctaccctgaa gatgtggctg 420  
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ttagcgatga gatctactgc cccctgaga ctgcccgtgct cttgggggtcc tacgctgtgc 540  
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<210> 124

<211> 379

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (340)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (344)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (366)

<223> n equals a,t,g, or c

<400> 124

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tcacacaaaa aataattcgt ctttctaggt tatgaagaga taattatttg kctggtaagc 300  
atttttataa acccacycat tttatattta graaaatccn aaanggggtg gggacgccct 360  
tgtagngacc ttccaatac 379



<210> 125  
<211> 1267  
<212> DNA  
<213> Homo sapiens

<400> 125  
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caacctg 1267

<210> 126  
<211> 841  
<212> DNA  
<213> Homo sapiens

<400> 126  
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gcgatcaata ctttgatatt ttaatttcta gatttggcaa ttcttcgctg aagtcacatc 180  
gagctttttc caactcctga tgaaaaggaa ggaactcatt cccttgggtg tttcatgac 240  
tgtggcgggc ggtggagcct catctttcgc tgtgtattct ctttggaaaa ccgatgtgat 300  
ccttgatcga aaaaaaaatc cagaaccttg ggaactgtg gaccctactg tacctcaaaa 360  
gcttataaca atcaaccaac aatggaaacc cattgaagag ttgcaaaatg tccaaagggt 420  
gaccaaataa cgagccctcg cctctttctt ctgaagagta ctctataaat ctagtggaaa 480  
catttctgca caaactagat tctggacacc agtgtgcgga aatgcttctg ctacattttt 540  
agggtttgtc tacatttttt gggctctgga taaggaatta aaggagtgc gcaataactg 600  
cactgtctaa aagtttgtgc ttattttctt gtaatttga atattgcata ttgaaatttt 660  
tgtttatgat ctatgaatgt ttttcttaaa atttaciaaag ctttgtaaat tagattttct 720  
ttaataaaaat gccatttgtg caagaaaaaa aaaaaaaa aaagggcggc cgctctagag 780  
gatccctcga ggggcccgaag cttacgcgtg catgcgacgt catagctctg tccctacgaa 840  
g 841

<210> 127  
<211> 1172  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc feature  
<222> (119)  
<223> n equals a,t,g, or c

<400> 127  
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ttctgaagct gcttctctt ataaaatagc ttttgccgaa acatagttt tttttagcag 180  
atcccaaaat ataatgaagg ggatgggtgg atatttgtgt ctgtgttctt ataatatatt 240  
attattcttc cttggttcta gaaaaataga taaatatatt tttttcagga aatagtgtgg 300  
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ctagaggcgt cactgtatgt agttcatggc tactgtactg acagcgagag catgtccatc 660  
tgttggacag cactattcta gagaactaaa ctggcttaac gagtacagc ctcagctgtg 720  
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cccagctggg gcctgtgtc tgggaccctc cctctcctga gaggggaggc ctggtggctt 840  
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ctgtaggcac ctctcacact gttgtctgtt actgattttt tttgataaaa agataataaa 1080  
acctggtact ttctaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1140  
aaaaaggcg gccgctcgcg atctagaact ag 1172

<210> 128  
<211> 891  
<212> DNA  
<213> Homo sapiens

<400> 128  
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tcgttgtgac ccaacctgga gtcgggtccc gtccggcccc ccagaactcc aactggcaga 180  
caggcatgtg tgactgttgc agcgactgag gactctgtct ctgtggcaca tttgtttcc 240  
cgtgccttgg gtgtcaagt gacagtgata tgaatgaatg ctgtctgtgt ggaacaagcg 300  
tcgcaatgag gactctctac aggaccgat atggcatccc tggatctatt tgtgatgact 360  
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gaaggagagc catgcgtact ttctaaaaac tgatggtgaa aagctcttac cgaagcaaca 480  
aaattcagca gacacctctt cagcttgagt tcttcacat cttttgcaac tgaatatga 540  
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attttactga taagattctt catgcttctt tgctctcctt aaaatgtctt tttcactagt 780

tagttccaag ggtcagtctc ataattttgt tcttatactt tgatttcctt tttctttttt 840  
ttttttttta atagagttgg gggatcyttc yttctttttt tttttttttt t 891

<210> 129

<211> 2461

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (14)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1164)

<223> n equals a,t,g, or c

<400> 129

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acagcctgga atgagtttgc ttattaccca gtcactttcg tagtgaatgt tcaaacccca 180  
aagcaaatgt ttgcatctcc ttgtccataa aggagaaagc caggttatag gagaaagaga 240  
gagaaaggcg catgtctgtt tgcacagaga gaggcaattt tgtctacctt tcgagaatca 300  
gttataaaca gaaggcctc ttaggatttt gagctctcct gacaatgaag gaaaagctct 360  
cttgagtata caagttccac actcattacc tttcagtggt gacccatcac ccactacaat 420  
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<210> 130

<211> 2197

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1381)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2194)

<223> n equals a,t,g, or c

<400> 130

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tcagttgttc ccaacaaaag caataatgaa atagtccttg tgctccaaca gtttgatttt 300
aatgtggata aagccgtgca agcctttgtg gatggcagtg caattcaagt tctaaaagaa 360
tggaatatga caggaaaaaa gaagaacaat aaaagaaaaa gaagcaagtc caagcagcat 420
caaggcaaca aagatgctaa agacaagggt gagaggcctg aggcagggcc cctgcagccg 480
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaanaaa 2197

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<210> 131

<211> 464

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (397)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (405)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (420)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (449)

<223> n equals a,t,g, or c

<400> 131

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gcgttggaac ggttggttac taccaattta tggaccgcct attaatgtgc atggttacag 180
ccaatacgat agtgagaaaa ccaaaacgca gcctagttag agtagaaagt gtaacaccat 240
tgcccacaac tggttgctgc ctactgtcgc taaggcggct taggcaaaat ttgctgcagc 300
gtacgcggag agttgtttac caaagatgcc ttacaaccct gcgctgaaaag ggggctgctg 360
cttatgccaa ttatgtttta aggttggtct ctgggtanttt tgcnaaatgg ttttgatttn 420
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<210> 132

<211> 1950

<212> DNA  
<213> Homo sapiens  
  
<220>  
<221> misc feature  
<222> (1941)  
<223> n equals a,t,g, or c

<400> 132  
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ccactgctgc acttctatgg ccgtaaatta acttgagaaa gtggaatcga attccgatgt 180  
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tgaggtcagg atttctcaaa ctgattcctt tctttgcata tgagtatttg aaaataaata 1860  
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aaaaaaaaa aaaaaaaaaa naaaaaaaaa 1950

<210> 133  
<211> 2093  
<212> DNA  
<213> Homo sapiens

<400> 133  
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gctgttcttg tgaatctcca aattttgtac cttgttctaa gctaataat agcaattaaa 2040
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<210> 134

<211> 729

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (646)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (665)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (725)

<223> n equals a,t,g, or c

<400> 134

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ggacaagggtg gacaacaaca ccctgctcaa cgtcatcgcc tgcacccacg tgccctgcaa 180
cacctcctgc agccctggct tcgaactcat ggaggccccc ggggagtgct gtaagaagtg 240
tgaacagacg cactgtatca tcaaacggcc cgacaaccag cacgtcatcc tgaagcccg 300
ggacttcaag agcgaccga agaacaactg cacattcttc agctgcgtga agatccacaa 360
ccagctcatc tcgtccgtct ccaacatcac ctgccccaac tttgatgcc a gatttgcac 420
cccgggctcc atcacattca tgcccaatgg atgctgcaag acctgcaccc ctcgcaatga 480
gaccagggtg ccctgctcca ccgtcccggt caccacggag gtttcgtacg ccggctgcac 540
caagaccgtc ctcatgaatc attgctccgg gtccctgcggg acatttgtca tgtamtcggc 600
caaggccagg ccctggacca cagcttgctc ctgctgcaaa gaaganaaaa ccagccagcg 660
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gccantgcc                                     729
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<210> 135

<211> 1189

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (5)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (8)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (17)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1160)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1175)

<223> n equals a,t,g, or c

<400> 135

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tgtaactggg cttggccccc gccttaggcc ccgccagcag gcgaagcagg gagatgtcag 180  
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tgtctaagta cagcctgggc aagaacaaga tcagcaagag cagcttccgc gagatgtcc 300  
agaaagagct gaaccacatg ctgtcggaca cagggaaccg gaaggtgag gataagctca 360  
tccagaacct ggatgccaat catgatgggc gcatcagctt cgatgagtag tggacctga 420  
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<210> 136

<211> 1466

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (2)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1291)

<223> n equals a,t,g, or c

<400> 136

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ggagggttac agccacatcc caccctctcg tccaatccca taatccatga tgaaagggtga 180  
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aagggaagag aaaggatctg gccttgttgt cactggcatc tgagccctgc tgatggctgg 300  
ggctctcggg catgcttggg agtgcagggg gctcgggctg cctggcctgg ctgcacagaa 360  
ggcaagtgtt ggggctcatg gtgctctgag ctggcctgga ccctgtcagg atgggcccc 420  
cctcagaacc aaactcactg tccccactgt ggcatagggg cagtggagca coatgtttga 480  
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aattatggac tgttgggaaa aggggtttgt ccagaaggac aagccggaca aatgagcgac 600  
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gacctgatga ggaaatcttc aatasgacgc aaagatcaat gcaaaaattg ttctatctga 1380  
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<210> 137

<211> 140

<212> DNA

<213> Homo sapiens

<400> 137

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<211> 4142

<212> DNA

<213> Homo sapiens

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&lt;211&gt; 1747

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

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<223> n equals a,t,g, or c

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&lt;210&gt; 141

&lt;211&gt; 671

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 141

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&lt;211&gt; 3265

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

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&lt;221&gt; misc feature

&lt;222&gt; (3234)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

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&lt;222&gt; (3256)

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<400> 142

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<211> 765

<212> DNA

<213> Homo sapiens

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<211> 1694

<212> DNA

<213> Homo sapiens

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tgatttttta attgctgaat tttgtgaaat tttacttttt ccaagtgtt ccaacttta 1020

aaagagaagt gaagacaaat aggttggaat ggtgaagaca aatggrttgg ratttcacag 1080  
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cttgaaaact gactcagcct catgttgctc ctaattagtg tttaaggctc ccatgagttg 1500  
cagataaaat gatttatttt aacaagtaga aggaggtgat tcaccttttg gattgtaaat 1560  
atatgaaaat gtctacaagg tctttatctg ctttctgtca gcatttatat taaatgataa 1620  
attaatgagg aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1680  
aaaaaagggc ggcc 1694

<210> 145

<211> 823

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (182)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (731)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (743)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (749)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (755)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (817)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (821)



<223> n equals a,t,g, or c

<400> 145

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tgtcacagac tacttcatca gtcgcttadc tggagctggg accaagggtt ctgccaggcc 60
ttgggatcag ctcttggggg tcagagcagc cttcccacat cctctggcac tgctgaactt 120
ttgcagcagc tctttcctcc tctyttggat gcccttcgag agcccagggt acgacggatt 180
tnctgccagc ctgcagatcc tgcgcctgtc gccctgcagg tctctgtacc cttcagacca 240
ccttgctctg gttcctgggc agagctcagc agtacttggc agcatgggac ccagcttcct 300
tcctgctcct gatccaaaag gacttacctc ctctgttgca tgaggcagaa gctttgtata 360
gcctggcctc agaggaaaag ttagctctgg aagtggagca gcagctgggc ctggagatcc 420
agaagctgac tgcacagatc cagctcctgc ctgaagagtc actaagtgtc ttttctcaag 480
aatgtcataa acaagccatg caagggttca agctctacat gccacggggc cggtagctggc 540
ggcttcgtct ctgtcctgaa cctcccagtg ctcctagtga gtatgctggg ttagtggtcc 600
gcaccgtact ggagcctgtg ttgcaaggat tgcaagggtt gcacctcaag cccaggcccc 660
tgcccttggt caggctctga cggscatcgt ggggtgcctgg cttgaccaca ttcttaccce 720
tgggattcgg nttcaacctg canggagcnc tkcancttaa acaagacttt ggaatggtca 780
ggagtttgtg gaaaagagca tggacctgtc cctgatntcg nca 823
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<210> 146

<211> 1134

<212> DNA

<213> Homo sapiens

<400> 146

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ggttataata aaggataata gtcttgtgct gacaccatca cacatcaaaag cctacatggt 120
gatgactctt caaggattag aatatttaca tcaacattgg atcctacata gggatctgaa 180
accaaacaac ttgttgctag atgaaaatgg agttctaaaa ctggcagatt ttggcctggc 240
caaattcttt gggagcccca atagagctta tacacatcag gttgtaacca ggtggtatcg 300
ggcccccgag ttactatttg gagctaggat gtatggtgta ggtgtggaca tgtgggctgt 360
tggctgtata ttagcagagt tacttctaag ggttcctttt ttgccaggag attcagacct 420
tgatcagcta acaagaatat ttgaaacttt gggcacacca actgaggaac agtggccgga 480
catgtgtagt cttccagatt atgtgacatt taagagtttc cctggaatac ctttgcacat 540
catcttcagt gcagcaggag acgacttact agatctcata caaggcttat tcttatttaa 600
tccatgtgct cgaattacgg ccacacaggc actgaaaatg aagtatttca gtaatgcgcc 660
agggccaaca cctggatgtc agctgccaaag accaaaactgt ccagtggaaa ccttaaagga 720
gcaatcaaat ccagcttttg caataaaaag gaaaagaaca gaggccttag aacaaggagg 780
attgcccaag aaactaattt tttaaaagaga acactggaca acattttact actgagggaa 840
atagccaaaa aggcaataaa tggaaaaata gtaaacatta agtaaatgct gtagaagtga 900
gtttgtaaat attctacaca tgtaaaatat gtaaaactat gggttatttt tattaatgt 960
attttaaaat aaaaatttaa ttctgggttt tctgattaga gtgcmaaagt gagaaaagt 1020
caatactctt gaatgtagaa ttgaaaatgc attagggaaa acttaataaa aattattacc 1080
agttatttgg aagatctgac ccatatagta tcacaaatct gtagtagcat gggt 1134
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<210> 147

<211> 1486

<212> DNA

<213> Homo sapiens

<400> 147

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gcggacgcgt ggggggcggg gtgtcgtttc ctttcgctga tgcaagagcc tagtgcggtg 60
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ttcccgtccg tgccgagccc actcgagccg cagccatgtc tggggacgag atgatttttg 180  
atcctactat gagcaagaag aaaaagaaga agaagaagcc ttttatgtta gatgaggaag 240  
gggatacca aacagaggaa acccagcctt cagaaacaaa agaagtggag ccagagccaa 300  
ctgaggacaa ggatttgga gctgatgaag aggacactag gaaaaaagat gcttctgatg 360  
atctagatga cttgaacttc tttaatcaaa agaaaaagaa gaaaaaaact aaaaagatat 420  
ttgatattga tgaagctgaa gaaggtgtaa aggatcctaa gattgaaagt gatgttcaag 480  
aaccaactga accagaggat gaccttgaca ttatgcttgg caataaaaag aagaaaaaga 540  
agaatgttaa gttcccagat gaggatgaaa tactagagaa agatgaagct ctagaagatg 600  
aagacaacaa aaaagatgat ggtatctcat tcagtaatca gacaggccct gcttgggcag 660  
gctcagaaag agactacaca tacgaggagc tgctgaatcg agtggttcaac atcatgaggg 720  
aaaagaatcc agatatggtt gctggggaga aaaggaaatt tgtcatgaaa cctccacaag 780  
tcgtccgagt aggaaccaag aaaacttctt ttgtcaactt tacagatatc tgtaactat 840  
tacatcgtca gcccacacat ctccttgcat tttgttggc tgaattgggt acaagtgggt 900  
ctatagatgg taataaccaa cttgtaatca aaggaagatt ccaacagaaa cagatagaaa 960  
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gccaagattt ttggcgagtg gttggtctga agtccttgca agacgctgat gctcaagctg 1320  
ttgacatact cattgcctac tttaacacct gtcagagaaa cgtgatattg ggtaaggagg 1380  
tgctttttta aaatcggtca tagacttctg taaaatgcaa gataaattaa agttattata 1440  
acagtgataa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 1486

<210> 148

<211> 153

<212> DNA

<213> Homo sapiens

<400> 148

cgctgtgca ggcgaagatc gaggtcgtc cggcagagga ctccttcaca ggcttcgtcc 60  
ggaccctgta ctttgctgac acctacctga aggagtgcc aggtgagcg gccaggcctc 120  
cagaacatgg agctggcgcc tgtgcagcgc aag 153

<210> 149

<211> 882

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (14)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (25)

<223> n equals a,t,g, or c

<220>

<221> misc feature  
<222> (870)  
<223> n equals a,t,g, or c

<400> 149  
acgaaggcca aagntgggtg cacnccgggtg cgccgtctag actagtggat cccggctcag 60  
gattcgcaag tgccctcctgg tctcagtatg gcgctgtcct gggttcttac agtcctgagc 120  
ctcctacctc tgctggaagc ccagatccca ttgtgtgcca acctagtacc ggtgcccatac 180  
accaacgcca ccctggaccr gatcactggc aagtggtttt atatcgcatc ggcctttcga 240  
aacgaggagt acaataagtc ggttcaggag atccaagcaa ctttctttta cttcaccccc 300  
aacaagacag aggacacgat ctttctcaga gagtaccaga cccgacagga ccagtgcatac 360  
tataacacca cctacctgaa tgtccagcgg gaaaatggga ccactctccag atacgtggga 420  
ggccaagagc atttcgctca cttgctgac ctcagggaca ccaagaccta catgcttgct 480  
tttgacgtga acgatgagaa gaactggggg ctgtctgtct atgctgacaa gccagagacg 540  
accaaggagc aactgggaga gttctacgaa gctctcgact gcttgcgcat tccaagtca 600  
gatgtcgtgt acaccgattg gaaaaaggat aagtgtgagc cactggagaa gcagcacgag 660  
aaggagagga aacaggagga gggggaatcc tagcaggaca cagccttga tcaggacaga 720  
gacttggggc catcctgccc ctccaacccg acatgtgtac ctcagctttt tccctcactt 780  
gcatcaataa agcttctgtg tttggaacag ctaaaaaaaa aaaaaaaaaa aaaaaaaaaa 840  
actcgagggg gggcccgkaa cccaatcgcn tgatattatt ag 882

<210> 150  
<211> 1508  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc feature  
<222> (126)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (155)  
<223> n equals a,t,g, or c

<400> 150  
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ccgcantcta gccttggaag cagtgaaga ctgtntcaaa aacagcaaca garagcagga 180  
cgtgagactt ctacctgctc actcagaatc atttctgcac caacctggc cacgtttgtg 240  
gagctcagta ccaaagccaa gatgcccatt gtgggcctgg gcacttgga gtctcctctc 300  
ggcaaaagtga aagaagcagt gaaggtggcc attgatgcag gatatcgga cattgactgt 360  
gcctatgtct atcagaatga acatgaagtg ggggaagcca tccaagagaa gatccaagag 420  
aaggctgtga agcgggagga cctgttcac ctcagcaagt tgtggcccac tttctttgag 480  
agacccttg tgaggaaaagc ctttgagaag accctcaagg acctgaagct gagctatctg 540  
gacgtctatc ttattcactg gccacagga ttcaagtctg gggatgacct tttcccaaa 600  
gatgataaag gtaatgccat cggtggaaaa gcaacgttct tggatgcctg ggaggccatg 660  
gaggagctgg tggatgaggg gctggtgaaa gcccttgggg tctccaattt cagccacttc 720  
cagatcgaga agctcttgaa caaacctgga ctgaaatata aaccagtgc taaccaggtt 780  
gagtgacc caccctcac gcaggagaaa ctgatccagt actgccactc caaggccatc 840

accgttacgg cctacagccc cctgggctct ccggatagac cttgggccaa gccagaagac 900  
ccttcctgc tggaggatcc caagattaag gagattgctg caaagcacia aaaaccgca 960  
gcccagggttc tgatccggtt ccatatccag aggaatgtga ttgtcatccc caagtctgtg 1020  
acaccagcac gcattgttga gaacattcag gtctttgact ttaaattgag tgatgaggag 1080  
atggcaacca tactcagctt caacagaaac tggagggcct gtaacgtgtt gcaatcstct 1140  
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acaggagatt ctctttcttc gctgaagtgt gactacctcc actcatgtcc cattttagcc 1260  
aagcttattt aagatcacag tgaacttagt cctgttatag acgagaatcg aggtgctgtt 1320  
ttagacattt atttctgtat gttcaactag gatcagaata tcacagaaaa gcatggcttg 1380  
aataaggaaa tgacaatttt ttccacttat ctgacagaa caaatgttta ttaagcatca 1440  
gaaactctgc caacactgag gatgtaaaga tcaataaaaa aaataataat cataaaaaaa 1500  
aaaaaaaaa 1508

<210> 151

<211> 1232

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (7)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1213)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1217)

<223> n equals a,t,g, or c

<400> 151

naactgngct agcatgccca gccacagag agcctccact agagtgatgc taagtggaaa 60  
tgtgaggtgc agctgccaca gagggccccc accagggaat tgtctagtgt ctagtggatc 120  
caggccacag gagagagtgc cttgtggagc gctgggagca ggacctgacc accaccagga 180  
ctccagcctg ggtgacaggg tgaacgccat ctcaaaaaat aaaaattaaa aaataaaaaa 240  
agaacctgga tctcaattta atttttcata ttcttgcaat gaaatggact tgaggaagct 300  
aagatcatag ctagaataac agataattcc acagcacatc tctagcaaat ttagcctatt 360  
cctattctct agcctattcc ttaccacctg taatcttgac catatacctt ggagttgaat 420  
attgttttca tactgctgtg gtttgaatgt tccctccaac actcatgttg agacttaatc 480  
cctaattgtg caaactgaa aggtggggcc tttagatgtg gattggatcg taaggctgtg 540  
ccttcattca tgggttaatg gattaatggg ttatcacagg aatgggactg gtggctttat 600  
aagaagagga aaagagaact gagctagcat gccagccca cagagagcct ccactagagt 660  
gatgctaagt ggaaatgtga ggtgcagctg ccacagaggg cccccaccag ggaaatgtct 720

agtgtctagt ggatccaggc cacaggagag agtgccttgt ggagcgctgg gagcaggacc 780  
tgaccaccac caggacccca gaactgtgga gtcagtggca gcatgcagcg ccccttggg 840  
aaagcttttag gcaccagcct gcaaccatt cgagcagcca cgtaggctgc acccagcaaa 900  
gccacaggca cggggctacc tgaggccttg gggggccaat ccctgctcca gtgtgtccgt 960  
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tgacccttta acagcatctg cttcattccc ctcaccttcc caggctgac tgaggtaaac 1080  
tttgaagtaa aataaaaagct gtgtttgagc atcaaaaaaa aaaaaaaaaa aaaaaaaaaa 1140  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1200  
aaaaaaaaaa aangggnggc cgttttaaaag ga 1232

<210> 152

<211> 999

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (917)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (951)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (995)

<223> n equals a,t,g, or c

<400> 152

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ggertcctcc gcggccggct gcgtggtgat cgttggcagt ggagtcattg ggygaagctg 120  
ggccatgctg tttgccagtg gaggcttcca ggtgaaactc tatgacattg agcaacagca 180  
gataaggaay gccctggaay acatcagaaa ggagatgaag ttgctggagc aggcagggtt 240  
tctgaaaggc tccctgagtg tggaagagca gctgtcactc atcagtgggt gtcccaatat 300  
ccaagaagca gtagagggg ccatgcwcat ycwgtgaatc cgccatacta catcccgtg 360  
gttgagctgg tccccacccc ggagacggcc cctacgacag tggacagaac ccacgccctg 420  
atgaagaaga ttggacagtg ccccatgcga gtccagaagg aggtggccgg ctctggttctg 480  
aaccgcctgc aatatgcaat catcagcgag gcctggcggc tagtggagga aggaatcgtg 540  
tctcctagtg acctggacct tgtcatgtca gaagggttgg gcatgcggta tgcattcatt 600  
ggaccccttg aaaccatgca tctcaatgca gaaggtatgt taagctactg cgacagatac 660  
agcgaaggca taaaacatgt cctacagact tttggacca ttccagagtt ttccagggcc 720  
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gctgccagga ggcagtggag ggacgagtg ctcagtgagc tcgccaagtt gaaragtcaa 840  
gtgcagmyaa sctggaratt tccacctttt cttttcagct tgattgcatt tgactatatt 900  
ttacagccag tgattgnagt ttcattgtaa tatgtggcaa aatatttttg naattatttt 960  
ctaataccctt tcttaagtac tctggggccc tgcanttat 999

<210> 153

<211> 1212

<212> DNA  
<213> Homo sapiens  
  
<220>  
<221> misc feature  
<222> (794)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (1047)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (1146)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (1176)  
<223> n equals a,t,g, or c

<400> 153  
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ggccgactta tgcaagcaga tgctggagaa gtccccttat gaccaggcgg ctgctgcaga 180  
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tgccccatca gtgcttcagg ctggctctgg tcaacaacaa caaccacgcc gaggcctaca 420  
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aaactgcac atcattagca ccccatatgt atgaaccgca ttttaatttt gcaacaatct 540  
ctgataagat tggagatctg cagagaagct atgttgctgc gcagaagtct gaagcagcat 600  
ttccagacca tgtggacaca caacatttaa ttaacaatt aaggcagcat tttgctatgc 660  
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gcactatgtc tgtgtatgta tgtatatagt gtaatacgtat tttttaaca aacctgtcct 780  
tgatattagt taanggtgac acataagggt gacacagaat gtgtaatgca aatttcata 840  
taatagtaac tttataaaat aatattataa aatacaggat ttaaaccttt ctaaatagat 900  
cctgaaactg tctctcacat tatatagtag atgtttgttt ataattgtta caaacatttt 960  
tggtgaattt cctcaatgtt ttataaatgt acatttttta agtccttaag ctgactctta 1020  
gccatcatgt agcttaagga gtctggnaat ctggccattg aaaactggca cctttgaagc 1080  
cagggtgtgt tagcatgtgc ctatagctcc agcttacttg gggagggtgg aggtggggag 1140  
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aaacctattt tt 1212

<210> 154  
<211> 2361  
<212> DNA  
<213> Homo sapiens

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (92)

&lt;223&gt; n equals a,t,g, or c

&lt;400&gt; 154

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cagaaggagg agggcagaat catcacgaag gntgaagttc atggatgtct atcagcgcac 120
actgccatcc aatcgagacc ctggtggaca tcttcaggga gtaccctgat gagatcgagt 180
acatcttcaa gccatcctgt gtgcccctga tgcgatgcgg gggctgctgc aatgacgagg 240
gcctggagtg tgtgcccact gaggagtcca acatcaccat gcagattatg cggatcaaac 300
ctcaccaagg ccagcacata ggagagatga gcttcctaca gcacaacaaa tgtgaatgca 360
gaccaaagaa agatagagca agacaagaaa aatgtgacaa gccgaggcgg tgagccgkgc 420
aggagggaagg agcctccctc aggggttcgg gaaccagatc tctcaccagg aaagactgat 480
acagaacgat cgatacagaa accacgctgc cgccaccaca ccatcaccat cgacagaaca 540
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ccggagggcg agactccggc ggaagcattc ccgggagggt gaccagcac ggtccctctt 660
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gagttttatt tctgggattc ctgtagacac acccaccac atacatacat ttatatatat 780
atatattata tatatataaa aataaatatc tctattttat atatataaaa tatatatatt 840
ctttttttaa attaacagtg ctaatgttat tgggtgtctc actggatgta tttgactgct 900
gtggacttga gttgggaggg gaatgttccc actcagatcc tgacagggaaggaggaggaga 960
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&lt;210&gt; 155

&lt;211&gt; 1831

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

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<210> 156

<211> 1186

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1045)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1078)

<223> n equals a,t,g, or c

<220>

<221> misc feature



<222> (1118)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1134)

<223> n equals a,t,g, or c

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<210> 157

<211> 1448

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (456)

<223> n equals a,t,g, or c

<400> 157

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gtcaaggagt actccaagac agagacagag gcgccctggg tggtggaagg cagccgccct 180
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aaaaaaaaa
1448

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&lt;210&gt; 158

&lt;211&gt; 1004

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 158

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1004

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&lt;210&gt; 159

&lt;211&gt; 1509

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (1420)

&lt;223&gt; n equals a,t,g, or c

&lt;400&gt; 159

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tctgggatg 1509

<210> 160

<211> 2160

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (470)

<223> n equals a,t,g, or c

<400> 160

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&lt;210&gt; 161

&lt;211&gt; 3609

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 161

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<210> 162

<211> 1603

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1600)

<223> n equals a,t,g, or c

&lt;400&gt; 162

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cgttgccttt tctccagct acctcccaa gcagcctgac ctgcgtggga gaggcgtagm 180
gagtcggagg ggaaaggag atcccacgtg caagtagggg gaatatctcc cccttttccc 240
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&lt;210&gt; 163

&lt;211&gt; 853

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 163

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attacaaata gtgctgcagt gaacattcac atacacatct tttggtgaac atgtgttaca 780
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<210> 164  
<211> 1917  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc feature  
<222> (1433)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (1856)  
<223> n equals a,t,g, or c

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<210> 165

<211> 2420

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 165

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&lt;210&gt; 166

&lt;211&gt; 2061

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens



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<210> 167

<211> 2567

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (16)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (55)

<223> n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (74)

&lt;223&gt; n equals a,t,g, or c

&lt;400&gt; 167

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<211> 2324  
<212> DNA  
<213> Homo sapiens

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<210> 169  
<211> 1784  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc feature  
<222> (200)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (215)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (1759)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (1778)  
<223> n equals a,t,g, or c

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tgaaatgggc cataacttag tggcaattga actggcttat atcaacacaa aacatccaga 180  
ctttgctgat gcttgtgggn taatgaacaa taatntagag gaacaaagga gaaacaggct 240  
agccagagaa ttaccttcag ctgtatcacg agacaagggt gcatctggag gtggtggggt 300  
tgagagatggt gttcaagaac caaccacagg caactggaga ggaatgctga aaacttcaa 360  
agctgaagag ttattagcag aagaaaaatc aaaaccatt ccaattatgc cagccagtcc 420  
acaaaaagggt catgccgtga acctgctaga tgtgccagtt cctgttgac gaaaactatc 480  
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tgtcagaaaag aatattcaag acagtgtgcc aaaggcagta atgcattttt tggttaatca 600  
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gagtagaatc ttatttatga actcctgtgt attgcaatgg tatgaatctg ctcatgtgga 900  
gactggctat aaactgaaaa gtgtattcca aattgcagaa cacatcacac atttaatacca 960  
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tcagaaaaatc aaatgatgac ctaaaattcc cttaatttgc aaatacagta gtaattaaag 1620  
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aaaccagtgt actgtatgta tgcattggta atagctactt tkgttcata gcttccatac 1740  
caacmaata tatttrttna gratagtatg aaagtcangg gagg 1784

<210> 170  
<211> 1296  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc feature  
<222> (1261)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (1276)  
<223> n equals a,t,g, or c

<400> 170  
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cctcggtcgc aagctgcgat gccgcagtgg ctcaagtgcct cctggccgag aacgactggg 180  
agatggaaaag ggctctgaac tcctacttcg agcctccggt ggaggagagc gccttggaac 240  
gccgacctga aaccatctct gagcccaaga cctatgttga cctaaccaat gaagaaacaa 300  
ctgattccac cacttctaaa atcagcccat ctgaagatac tcagcaagaa aatggcagca 360  
tggtctctct cattacctgg aatattgatg gattagatct aaacaatctg tcagagaggg 420  
ctcaggggggt gtgttcctac ttagctttgt acagcccaga tgtgatattt ctacagggaag 480  
ttattccccc atattatagc tacctaaaga agagatcaag taattatgag attattacag 540  
gtcatgaaga aggakatttc acagctataa tgttgaagaa atcaagagt aaattaaaaa 600  
gccaaagagat tattcctttt ccaagtacca aaatgatgag aaacctttta tgtgtgcatg 660  
tgaaygtgtc aggaaatgag ctttgccctta tgacatccca tttggagagc accagagggc 720  
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gccagtatac atgggatata caaatgaact ctaatcttgg aataactgct gcttgtaaac 960  
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gtttggacct tcttgatta gaaaaactgg actgtggtag atttcctagt gatcactggg 1080  
gtcttctgtg caacttagat ataattattgt aaaatgcttt tcaagtgtgg gttttgccct 1140  
gattgttgca aatacaattt ccaccttctg gaaaggtagg tttgctgtgg aggaaataat 1200  
gwactagatc attgtcacag aaaaaccaac tatgatttat ggkkggtgtt tcmccaryat 1260  
nagacggaaa gaccncccc ttcttcccc cccct 1296

<210> 171  
<211> 1897  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc feature  
<222> (952)  
<223> n equals a,t,g, or c

<400> 171

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cggagtggga agtacatgtg tcgtatcata gttcatttta tgtgggagga tgttcagcag 180  
cgcgagagt catgggggtt aatccctata tcctgaagaa gaacatgac ctcagacaa 240  
atcatttcta tgcagcgatc ttgggatatg atgaggggat ctttcagat gatcatgggc 300  
tggccgctgc cctctggaga accttcttca accggaaatg tgaagaccct cgacatcttg 360  
aattgctggt agagtatgtg aggaaacaga tacagtacct ggactccatg aacggggagg 420  
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tcctgaagcc ccattctccg acctacaacg acgagggact ttgatgggct gggcctccgc 540  
acggcccgc agctggcttc gaggaacctc caggagagaa gtgcctgttg gtccaggacc 600  
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agcacacact ccccaacccc ctccagcaac tacatgtgac tgatagcttt tcccaaaggc 840  
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caggaatttg ctgattaatt tatttttaat ggagtgaagt ataccatgca ccaaaataaa 1860  
ctttactgtg tgtacctaaa aaaaaaaaaa aaaaaaa 1897

&lt;210&gt; 172

&lt;211&gt; 1723

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 172

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cgaccgsgg acacacagt caggcgccca agccgcccgc gccagatcgg tgccgattcc 180  
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gatcaagcaa ctccctgag gatcctcaac aatggtcatg ctttcaacgt ggagtgtgat 420  
gactctcagg acaaagcagt gctcaaggga ggacccttg atggcactta cagattgatt 480  
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gctaaaccgg gccttcagaa agttgttgat gtgctggatt ccattaaaac aaagggcaag 720

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ataaatgaag tattatctgt aaaaattgtt ataattagag ttgtgatata gagtatat 1620
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aattcagaat tctaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1723

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&lt;210&gt; 173

&lt;211&gt; 1416

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 173

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ccagtagctt ggaaagtaga gatgactaat gttttagcct tttcttgag aaaaggaaga 60
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gaaaagttac ttgtaaatct ttagaccttt gttgtcactt aggctgggga gtcactacc 240
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cctttactct cactatgcaa tagagggttt catgtagtta atctgacatg tcaaaattgg 360
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&lt;210&gt; 174

&lt;211&gt; 1956

<212> DNA  
<213> Homo sapiens

<220>  
<221> misc feature  
<222> (1)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (4)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (6)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (24)  
<223> n equals a,t,g, or c

<400> 174  
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aacaagacca caggaagggt atctgatggt gcaacagttt cagtacctag gatgggcttc 180  
tcatcgagaa gtgcctggtt ccaaaaggtc attcttgaaa ctgatacttc aggtggaaaa 240  
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caaaactgtaa actgtcaggg tgataaaatg tttctcttga tgtttacatg cacaagcttt 1680  
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aacttcacat catcagcttg cagtttgtaa ttgactaaag cattccagtg tcctctttct 1860  
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gtttttataa ttataaaaaa aaaaaaaaaa aaactc 1956

<210> 175

<211> 1689

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1688)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1689)

<223> n equals a,t,g, or c

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aaaaaaaann

1689

&lt;210&gt; 176

&lt;211&gt; 1016

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (895)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (928)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (970)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (992)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (1001)

&lt;223&gt; n equals a,t,g, or c

&lt;400&gt; 176

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tgagctgctg gcgtgaatgc ttattttctt ttgtttatga taatttcact taactttaaa 180  
gacatatattg cacaaaacct ttgtttaaag atctgcaata ttatatatat aaatatatat 240  
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tggaaacttc tcttggtgtc gttgagactt taaggagaa atgtcggaa ttcagagtcg 540  
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ggctttcccg aggggccact gtccctgcag agtggatgct tctgcctagt gacaggttat 660  
caccacgtta tatattccct accgaaggag acaccttttc cccctgacc cagaacagcc 720  
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<210> 177  
<211> 1364  
<212> DNA  
<213> Homo sapiens

<400> 177  
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ctgcacacccc agaatctatt acagatcctg gcatgtagct gatgcataaa tatttggtga 180  
atgaaagtct gtacattgta tttatgctat tggatttgct atgacctgaa actaaaagga 240  
gttggtggaaa agatttctta tggaacagaa atatcccttt tgattaatat cacaatctcg 300  
taaattgaga aaacaaawaa tatatactac tggagcattc atgtatagtt ggagattatg 360  
actcatttat tgggtgtgtt ttggactcag aacaaagatg agggaaatatt ccttaaagct 420  
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atgtatggtg ggggacagaa ggtttcaaaa gttaagaat ctgtgttgct ttaacaaata 660  
gatgcttctc aaggasstta cgytagtggg tactctgtcc agtcagggtt tttcttctt 720  
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ctatggtcct tagctatggg gagcagcatc agcgacctgt gacatgtaaa ttaaaaaatac 840  
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gatgttccag gttagtctga ttaacaccct tgggttaagaa ccattgggag gatctgattg 960  
ccagtttaag gggaccttca agcctgtagg tctttatagt taaaaaaaaaaa aaaagatttt 1020  
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gaaatgtttt tcccaaataa attstcttgt tatagcttct atgtgtgatt tgggtccagct 1140  
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acccacttaa aaacccttct tattacaggt cttcacattt aggttaaatg tgcttaattc 1260  
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<210> 178  
<211> 740  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc feature  
<222> (38)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (171)  
<223> n equals a,t,g, or c

<400> 178  
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cctcagcctc ccaaggtgct gggattacaa gtgtgagcca ctgtgtacag nctttgtgtt 180  
aacttacttt gaattagccc cttattccaa agctgcctcc tgaaaggasg cttcctaaaa 240  
ggtgttgctt tggggtaaat aagaggtgct ggtgaagtga gactagcttg cgcactcttc 300

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ctgtgttggc accgctgccg gaaactcttg agaatgagca tcgtgtgccg cttatccact 480
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gccacacatt gttttatgag ctgagtcacg agactggctg gtcctttaa tgctgtgtgt 600
tgattctcta ggcagcagaa aacaaggaga gaagatatga agtgatatct atcgagcttt 660
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tgtgataaaa aattattgat                                     740
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&lt;210&gt; 179

&lt;211&gt; 1410

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 179

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cacgtgggtc ctgaggcctg cagcacgtcg gatgctaccc cactatgaca gaggattgtg 240
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caagttcgag tcaaagttga aaattcatag taagattgat atctataaaa tagatataaa 660
tttttaagag aaagaattta gtattatcaa agggataaaag aaaaaaatac tatttaagat 720
gtgaaaatta cagtccaaaa tactgttctt tccaggctat gtataaaata catagtgaag 780
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gttgtaacca gtgaaattat tttggagatt ataataata tatacattca aaaaaaaaaa 1380
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa                                     1410
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&lt;210&gt; 180

&lt;211&gt; 1493

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (1328)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

<221> misc feature  
<222> (1352)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (1376)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (1406)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (1436)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (1484)  
<223> n equals a,t,g, or c

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cctgcccctg gctgaacagc ggggaagcctg ccgacgtgcc tgctgcttcg cccgtgtgga 540  
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<210> 181  
<211> 2040  
<212> DNA  
<213> Homo sapiens

<400> 181  
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gtaccaccgg gtggtaggtg cccagcgtg ccccatcgtg gacaccttct ggcaaacaga 540  
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aggtgaagct gaaggttatc tgggtgtcaa gcagccctgg ccagggatca tgcgcacagt 720  
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<210> 182  
<211> 969  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc feature  
<222> (11)  
<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (128)

<223> n equals a,t,g, or c

<400> 182

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<210> 183

<211> 1452

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (17)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (18)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1430)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1441)

<223> n equals a,t,g, or c

<400> 183

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gtcgaccac gcgtccnncc acggtccggt ggggagaagc cgggaggact ggggtgcgct 60
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tcaaaactca ttcgaaaagc taaagaggca ccattcgtac ccgttggaat agcgggtttt 240  
gcagcaattg ttgcatatgg attatataaa ctgaagagca ggggaaatac taaaatgtcc 300  
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<210> 184

<211> 2119

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (2090)

<223> n equals a,t,g, or c

<400> 184

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<210> 185

<211> 1325

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

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<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1319)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1320)

<223> n equals a,t,g, or c

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aaaaa 1325

<210> 186

<211> 433

<212> DNA

<213> Homo sapiens

<400> 186

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gaaagatggc aaatgctgat cccacaggag cacctcaagc catgaagtgt cagctggaga 360  
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aaaaaaaaaa aaa 433

<210> 187

<211> 859

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (803)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (853)

<223> n equals a,t,g, or c

<400> 187

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<211> 833

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (65)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (798)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (803)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (809)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (812)

<223> n equals a,t,g, or c

<400> 188

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gctggcaaaa cttctagcta gcaacctatg tctagcacat gggtaactaa ccatagcgag 240  
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aatctcacat ggacggaacg tctgtatttc cctctcctgc acgaatcact catcattctt 360  
ggaggggcttc tctgcattcc tcttttctt ctctccctc ccctgccttt tgtcttttct 420  
aaagagtctg aactccgatt tccatgctct cctgctacat taataagcaa aacctgcttg 480

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&lt;210&gt; 189

&lt;211&gt; 2211

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 189

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<212> DNA  
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<211> 3894  
<212> DNA  
<213> Homo sapiens

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<210> 192

<211> 695

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (2)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (3)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (11)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (23)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (28)

<223> n equals a,t,g, or c

<400> 192

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<210> 193

<211> 3131

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (4)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (5)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (10)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (26)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (3128)

<223> n equals a,t,g, or c

<400> 193

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cagcgccgga gccgggagct agcggccgcc gccatgtccc accagaccgg catccaagca 180  
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gaaattataa ttttgcccaa cacaacaaat acagaactga aagatttgcc aaagaggatt 840  
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<210> 194

<211> 2058

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (2045)

<223> n equals a,t,g, or c

<400> 194

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<210> 195

<211> 831

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (2)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (28)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (44)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (791)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (793)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (806)

<223> n equals a,t,g, or c

<400> 195

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agtattggtg tcatgggaat gtacgttatt tccaaagtca tttcattaaa gatgaaaact 780
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<210> 196

<211> 961

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (31)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (32)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (923)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (947)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (953)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (954)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (960)

<223> n equals a,t,g, or c

<400> 196

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tatgtatata tgcttaacta cacccgagga agctgtagag ttagaaaaac atgaaccatt 180
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<210> 197

<211> 606

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (488)

<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (500)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (603)  
<223> n equals a,t,g, or c

<400> 197  
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ccacccacag gactcgggga gtatgccgca tgccagtcac acgccttcat gaagggcgtt 180  
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<210> 198  
<211> 393  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc feature  
<222> (253)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (354)  
<223> n equals a,t,g, or c

<400> 198  
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<210> 199  
<211> 1061  
<212> DNA  
<213> Homo sapiens

<220>

<221> misc feature

<222> (1035)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1056)

<223> n equals a,t,g, or c

<400> 199

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<210> 200

<211> 1359

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1005)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1128)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1342)

<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (1343)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (1344)  
<223> n equals a,t,g, or c

<400> 200  
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<220>

<221> misc feature

<222> (179)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (724)

<223> n equals a,t,g, or c

<400> 201

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<210> 202

<211> 2714

<212> DNA

<213> Homo sapiens

<400> 202

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<221> misc feature

<222> (2334)

<223> n equals a,t,g, or c

<400> 204

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<211> 1655

<212> DNA

<213> Homo sapiens

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<210> 206

<211> 5145

<212> DNA

<213> Homo sapiens

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<221> misc feature

<222> (17)

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<222> (5126)

<223> n equals a,t,g, or c

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<221> misc feature

<222> (5143)

<223> n equals a,t,g, or c

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<210> 207

<211> 487

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (470)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (483)

<223> n equals a,t,g, or c

<400> 207

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<210> 208

<211> 2296

<212> DNA

<213> Homo sapiens

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<223> n equals a,t,g, or c

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<221> misc feature  
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<223> n equals a,t,g, or c

<220>  
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<222> (2258)  
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<220>  
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<223> n equals a,t,g, or c

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<210> 209

<211> 625

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

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<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (10)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (25)

<223> n equals a,t,g, or c

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<221> misc feature

<222> (26)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (600)

<223> n equals a,t,g, or c

<400> 209

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<210> 210

<211> 1551

<212> DNA

<213> Homo sapiens

<220>  
<221> misc feature  
<222> (760)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (1543)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (1544)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (1545)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (1546)  
<223> n equals a,t,g, or c

<400> 210  
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<210> 211

<211> 1011

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (309)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (801)

<223> n equals a,t,g, or c

<400> 211

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<210> 212

<211> 1639

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1630)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1637)

<223> n equals a,t,g, or c

&lt;400&gt; 212

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&lt;210&gt; 213

&lt;211&gt; 2127

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 213

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&lt;210&gt; 214

&lt;211&gt; 1166

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (1163)

&lt;223&gt; n equals a,t,g, or c

&lt;400&gt; 214

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<211> 3323

<212> DNA

<213> Homo sapiens

<400> 215

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<211> 1408

<212> DNA

<213> Homo sapiens

<400> 216

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<211> 2111

<212> DNA

<213> Homo sapiens

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<222> (2102)  
<223> n equals a,t,g, or c

<220>  
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<222> (2104)  
<223> n equals a,t,g, or c

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<210> 218

<211> 2493



&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 218

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&lt;211&gt; 1259

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

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<210> 220  
<211> 1849  
<212> DNA  
<213> Homo sapiens

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<210> 221

<211> 1267

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (11)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (17)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (26)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1244)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1252)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1264)

<223> n equals a,t,g, or c

&lt;400&gt; 221

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tgagtaacga aagaggcttt gaaaatgtag aactgggagt cataggaaaa aagaagaaaag 180
tcccaaggag agtcatccac tttgttagtg gtgaaacaat ggaagaatat agcacagatg 240
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cttntct 1267
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&lt;210&gt; 222

&lt;211&gt; 754

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (702)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (710)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (754)

&lt;223&gt; n equals a,t,g, or c

&lt;400&gt; 222

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gcaggatata agaaatatga ggccccaatt ggaacagcag catggagggt ccaggttggg 180
tccccaacgt gctcccatg ggcaagacaa tggaaacttc cacaagcagg gaaggcaaac 240
cctctttatt gaacattagc cagcccgacc cagacccag ggctgctaag gacacagaga 300
ttctccatgg gaaggggact gccaaagcatg aggaaataga agattcaggg gcctgarctc 360
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tggaagctgc aagcaaaagg gatgggacta gggctgagtt gtgtctycat ttgataagg 420  
aaaggatatg ctacactct tgcttggtca gattccaaga cagaaggctt cacaaggcca 480  
acgcctggaa aatgggcatc tctccctccc atgttaagct ttaacctctg taatctgcct 540  
gtatctatag gtgggcatct cactccatca aaggagccca gcctcttttg tcctctacca 600  
tgcacagtct ttctgtgcat ttccccaagc tgggccctct tctactctca tttaggcctg 660  
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<210> 223

<211> 1258

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (41)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1205)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1241)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1247)

<223> n equals a,t,g, or c

<400> 223

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gggactgaca gagcaggaca tcattgacct gcccgctctg ttcaagatgg acgaggacca 180  
ccgtgccaga gccttcttcc caaacatggt gaacatgac gtgctggaca aggacctggg 240  
catccccaag ccattcgggc cacaggttga ggaggaatgc tgcctggaga tgcacgtgcg 300  
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ggatggcagg ctcccccgca ttgcatgggg gattttttcc ccagaccagg cataatttgt 1200  
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<210> 224

<211> 584

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (494)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (495)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (577)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (583)

<223> n equals a,t,g, or c

<400> 224

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aaactggggg taatgcgaga tgatacaata tacgaggatg aagatgtaaa agaagccata 180  
agaagacttc ctgagaacct ttataatgac aggatgtttc gcattaagag ggcactggac 240  
ctgaacttga agcatcagat cttgcctaaa gagcagtggc ccaaatatga agaggaaaat 300  
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ttgaaacaaa caattttaag aattatttgg tctgaagatg ttttacttta aataaatgtc 480  
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<210> 225

<211> 3449

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (2330)

<223> n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (3434)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (3443)

&lt;223&gt; n equals a,t,g, or c

&lt;400&gt; 225

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gaggaaccac gagcgaggga agaaggacag ggactcgtgt ggacaggaaga actcagagcc 180  
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<210> 226

<211> 1866

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1859)

<223> n equals a,t,g, or c

<400> 226

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catcagcaag gaagacctcg cccgggccac attggtcacc atcaccaaca acattggctc 180  
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aggacaactg aaagctctgt ttttgaaca tgagggttat tttggagccg ttggggcact 360  
gttggaactg ttcaaatga ctgatgayaa gtagagacga gcagtggagg aaacagcctc 420  
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cccatgatct tgtgtattga gcttattgtt gaaagggatt tttgaaggac agaacaatta 1680  
ctccatgatg aatcttcctt tctctgcctt ctgagcaccg tctttaattt ccatatcttc 1740  
aagtcttgaa gaagttagtg ttaattgaag aattcacttg tctggttgaa ataaagcctg 1800  
tttctgttgt gaaaaaaaaa aaaaaaaact sgtggggggc ccggacccaa ttgccctang 1860  
ggagcc 1866

<210> 227

<211> 1064

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (209)

<223> n equals a,t,g, or c

<400> 227

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ctgcggaaca gagatgagct tattgaggag aagcagcgca tgcagcagaa aatagacacc 180  
atgacaaaag aggtgtttga cctccaggng acacttcttt ggaaagataa aaaaattgrg 240  
aaacatggct tagttataat ccccgatggc actcccaatg gtgatgtcag tcatgaacca 300  
gtggctggag ccatcactgt tgtgtctcag gaagctgctc aggtcttgga gtcagcagga 360  
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cagattagaa aactgaagct tcagttagag gaggaacgac agaaatgctc caggaatgat 480  
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cagagagatg ccaatagaca aattagcgaa tacaaattta agctttcaaa agcagaacag 600  
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gaaaaccacc cttcaacctg ggtgatgctc cttggggccc tacctagagg gactgacttt 900  
tgtccattga cacaaccacc ttttagtact gttttgagtt ttgtcattaa aacagccacc 960  
tttgtatttt ataatttatg acagratgaa gtcattttga atctacatga atgaacactt 1020  
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<210> 228

<211> 373

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (329)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (332)

<223> n equals a,t,g, or c

<400> 228

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ggcccagggc cctgcggggc accccccccac catggcccag gccctgcgg gccaccccc 180
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ccccccacc atggtccagg gccctgcgg cctccccctg gccatggccc aggtcaccca 300
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gagaaattgc cca                                     373
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<210> 229

<211> 2844

<212> DNA

<213> Homo sapiens

<400> 229

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gtcctgggag cacagcagaa gtgtttttct ttttttaatg aacaagtaaa ccatacaaat 180
tgtcaacatg ggacggagat ctacatcatc caccaagagt ggaaaattta tgaacccac 240
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gatggttcga gctgcagttt taaagatgaa ggatccaaaa cagataatcc gagacatgga 360
gaaattggat gaaatggagt ttaacccagt gcaacagcca caattaaatg agaaagtact 420
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agagaatcca gatatttaca aagaattgag aaagctagaa gtagaatatg aacagaagag 540
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<210> 230

<211> 1798

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (15)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (24)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (31)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (501)

<223> n equals a,t,g, or c

<220>

<221> misc feature  
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<223> n equals a,t,g, or c

<400> 230  
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atcagcactg aacacagagg actcaccatg gagtttgggc tgagctgggt ttctctcgtt 180  
gctcttttaa gaggtgtcca gtgtcaggtg cagctggtgg agtctggggg aggcgtggtc 240  
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ggcatgcact gggtccgccca ggctccaggc aaggggctgg agtgggtggc agttatatsr 360  
tatgatggaa gtaataaata ctatgcagac tccgtgaagg gccgattcac catctccaga 420  
gacaattcca agaacacgct gtatctgcaa atgaacagcc tgagagctga ggacacggct 480  
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caaggactac ttccccgaac cgggtgacgg gtctgtggaac tcaggcgccc tgaccagcgg 720  
cgtgcacacc ttcccggctg tcctacagtc ctacggactc tactccctca gcagcgtggt 780  
gaccgtgccc tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc 840  
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<210> 231  
<211> 1823  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc feature  
<222> (82)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (1593)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (1714)  
<223> n equals a,t,g, or c

<400> 231  
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gcagatttcc aaagaaggcc agtagaactg ctagaatagc ctccgatgag gaaattcaag 180  
gcacaaagga tgctgttatt caagacctgg aacgaaaact tcgcttcaag gaggacctcc 240  
tgaacaatgg ccagccgagg ttaacatacg aagaaagaat ggctcgtcga ctgctagggtg 300  
ctgacagtgc aactgtcttt aatattcagg agccagaaga ggaaacagct aatcaggaat 360  
acaaagtctc cagctgtgaa cagagactca tcagtgaat agagtacagg ctagaagggt 420  
ctcctgtgga tgaatcaggt gatgaagttc agtatggaga tgtgcctgtg gaaaatggaa 480  
tggcaccatt ctttgagatg aagctgaaac attacaagat ctttgaggga atgccagtaa 540  
ctttcacatg tagagtggct ggaaatccaa agccaaagat ctattggttt aaagatggga 600  
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caaaagaaga tgctgggttg tatactgtgt cagccaagaa tgaagcaggg attgtgtcct 1440  
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scttgaccaa catattcctt tgtcacatta tgtnaaaggc agaamcatac ctttgctatt 1740  
agaaattaaa aaaacaccaa aatatatttt ctacttgaat accaacttag ttttaagtaga 1800  
taatgctaata acaaatatac aca 1823

<210> 232  
<211> 970  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc feature  
<222> (936)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (960)

<223> n equals a,t,g, or c

<400> 232

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cccatcgccc ctgctccag cagcaccctt ggctccagca cccctgggccc gggcaccccg 180
gtccctacag gaagcgtccc gtcgcgctcg ggctcagtgc caggagcccg cgctcctttc 240
agaccgctgt ttaacgactt tggaccgcct tccatgggct acgtgcaggc gatgaagcca 300
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ggaagcgccct cggcctcagc gtctggacct atccggccac tgcagagcac ccgcttctcc 480
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ggtccctccc aggaaccaag gagtggccct ccagggtggca gactaagga cccccccca 600
caacaagagt tagcagcgag gtcccatga gtccaccca tgacctgccg acagtgttgc 660
ccaccggaac ttttgtggcc cctaccgctc agcccttccc agcacttctc ccactttgtc 720
ccgagcctcc ttctccccc gcaggggcac aggcctggca cctccctgcc ttgtgtcctg 780
agccatagtg actcttttat ctgtgtgtct tttgctaaat atgccctttt tatattaata 840
aaagatgatt tggagttgtg ctctcaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 900
aaaaaaaggg cggccgctct agaggatcca tgcttnacgt acgcgtgcat gcgtacgctn 960
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<210> 233

<211> 967

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (923)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (926)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (955)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (957)

<223> n equals a,t,g, or c

<400> 233

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tggagatgca ggcacctgag ccaaggcgtc cagtggctct tgcttctggc tgtcctggtc 180
ttctttctct tcgcttgcc ctcttttatt aaggagcctc aaacaaagcc ttccaggcat 240
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caacgcacag agaacattaa agaaagggtct ctacagtccc tggcaaagcc taagtcccag 300  
gcacccacaa gggcraggag gacaaccatc tatgcagagc cagygccaga gaacaatgcc 360  
ctcaacacac aaaccagcc caaggccac accaccggag acagaggaaa ggaggccaac 420  
caggcaccgc cggaggagca ggacaagggtg cccacacag cacagagggc agcatggaag 480  
agcccagaaa aagagaaaac catggtgaac aactgtcac ccagagggca agatgcaggg 540  
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yccacaggag cagtgtcaac aaggacgaga cagaaaggar tkaccacagc agtcatccca 780  
cctaaggaga agaaacctca ggccacccca cccctgccc ctttcagag cccacgacg 840  
cagagaaacc aaagactgaa gggcggcaac ttcaaactctg agcctcgggtg ggattttgag 900  
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tcaaaag 967

<210> 234

<211> 2163

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1140)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1157)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1158)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1166)

<223> n equals a,t,g, or c

<400> 234

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ctgcacygcc gacctgctgg tggggcgcgc catgactttc catggccacg gcttccttcg 180  
cctggcgctc tcgaacgtgg caccgctcac tggcaacgtc tactccggct tcggcttcca 240  
cagcgcaccg gacagtgcgc tgctctacta ccgggcgtcc ccggatgggc tatgccaggt 300  
gtccctgcag caggggcgtg tgagcctaca gtccttgagg actgaagtga aaactcaagc 360  
gggcttcgcc gatgggtgcc cccattacgt cgcctctac agcaatgcc cgggagctctg 420  
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ccagccgcag cctgaggggc ccccgaggct cctcctggga ggcctgcctg agtctggcac 540  
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ttatatttgg cccttccacc catttttaat tgtgagagat ttgtcaccaa tcatcactg 2100  
ttcctcctta aaaattaaaa agtaacttct gtgtaaaaaa aaaaaaaaaa aaaaaaaaaa 2160  
aaa 2163

<210> 235

<211> 1321

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1313)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1320)

<223> n equals a,t,g, or c

<400> 235

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tcaacatccg gggcaaacctg gtgtcgtctg agaagtaccg cggatcgggtg tccctgggtg 180  
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agcgagacct gggcccccac cacttcaacg tgctcgctt cccctgcaac cagtttggcc 300  
aacaggagcc tgacagcaac aaggagattg agagctttgc ccgccgcacc tacagtgtct 360  
cattccccat gtttagcaag attgcagtca ccggtactg tgcccatcct gccttcaagt 420  
acctggccca gacttctggg aaggagccca cctggaactt ctggaagtac ctagtagccc 480



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ccatcattct tgtgggggaa aaattctagt attttgatta tttgaatctt acagcaacaa 780  
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&lt;210&gt; 236

&lt;211&gt; 683

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 236

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ggagtggagg tgctcagcag caccagaag aagtcagggg cctctggcak acctgcgggg 480  
agcttatgtt ctctctggag ccaaggcttc gacacctcgg actggggaag gagggaatca 540  
ccacctattt ctctgggaat tgtaccatgg aagatgccaa attggccmag atttctggac 600  
tcacagaacc tyartgccta caacaaccgg stcttyaaag aagtcsatgg garaaaggaa 660  
rccctamtac gaagggtgcgg gtt 683

&lt;210&gt; 237

&lt;211&gt; 2115

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (2112)

&lt;223&gt; n equals a,t,g, or c

&lt;400&gt; 237

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ccaggctgggt gtgcagtgggt gcgaccacgg ctacagcgag cctcagccac ccagatgtaa 180  
gcgatctgggt tcccacctca gcctcccag tagtgatctt aggatccggc ttccaacatg 240  
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gcaagcttcg atgcacggga acaatggcca cagtgtccca ccatcaaaga gatcagagac 540
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cccattggcc tntgg

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2115

&lt;210&gt; 238

&lt;211&gt; 1642

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (1633)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (1638)

&lt;223&gt; n equals a,t,g, or c

&lt;400&gt; 238

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taagcaggca ctagaggacc tggagcgcac atcaggccgt ggcaccctga tgcgccacc 60
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gatgtggcaa aacagctgaa caacctggcc ctcttggtcc aaaaccaggg caagtatgag 360  
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tatgctgagg ctgagacact atacaaagag atcctgaccc gtgcccattg acaggagttt 540  
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<210> 239

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (461)

<223> n equals a,t,g, or c

<400> 239

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cctacctctg ctggaagcca gatccattg tgtgccaacc tagtaccggt gccatcacc 120  
aacgccaccc tggaccggat cactggcaag tggttttata tcgcatcgcc ctttcgaaac 180  
gaggagtaca ataagtcggt tcaggagatc caagcaacct tcttttactt taccaccaac 240  
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aactccagtt acctgaatgt ccagcgggag aatgggaccg tctccagata cgagggaggc 360  
cgagaaacat gttgctcacc tgctgttcct tagggacacc aagaccttga tgtttggtty 420  
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<210> 240

<211> 1329

<212> DNA

<213> Homo sapiens

&lt;400&gt; 240

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gagaccagcc tggacaacac agtgagacct catctctatc aaaaaataaa aattagctag 180  
atgtgggtggc atgagcctgt gttcccagct gcttaggagg ctgaagcagg aggattgatt 240  
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ctgtaagttt cttattttctg tagtgcaagt aaaatttcac tttttgaaac tatagagaga 480  
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tcawaaaaaa aaaaagggaat tcgatatcaa gcttatcgat accgtcgacc tcgagggggg 1320  
gcccgtacc 1329

&lt;210&gt; 241

&lt;211&gt; 1652

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 241

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agtgtaaagt acaactaaga gtctcggcta cagggaataa taccatcagt taaatatcca 180  
tagtcctaga gcatthtatgt aaaactgcaa tttgaatcct gcaatacatt ttggcttttt 240  
cctcagtgat accatgtgtg ggaagttgtt ctgtcaagggt gggtcggata atttgccttg 300  
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<210> 242

<211> 1946

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (84)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (538)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1932)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1941)

<223> n equals a,t,g, or c

<400> 242

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aagagccgag tatcttcag ccgctgcctc ctgactgtaa taatattaaa cttttttaa 1860
aaaccataaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1920
aaaaaaaaa anaaaaaaaaa ngggggg 1946
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<210> 243

<211> 518

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (298)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (472)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (494)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (500)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (507)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (513)

<223> n equals a,t,g, or c

<400> 243

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aaggggggtg caanccttn gggagtnaca agngcttg 518
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<210> 244

<211> 621

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (460)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (569)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (593)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (609)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (612)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (621)

<223> n equals a,t,g, or c

<400> 244

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tctgtctggg caatgggtca cacctgtaat tccaacactt tggggggctc aggtgggagg 180  
atctctagtc cccaggagtt tgagaccagc ctgggcaata aactagaccc catgtctcta 240  
aaaaatgtaa aaaacatcaa gaggtgagt caggaggatc atttgagctt aggagttcaa 300  
ggctgcagta agttatgatt gtgccactgc attccagcct gggtgacaag agtgagaccc 360  
tgacccaaaa aaagtatctt ctgataaagt ggcatttgaa aattgcagaa aattttaata 420  
ttttttcttt taatattaag aactttattg atctctctan gacaccttg tgaggaaatt 480  
aatggcactt ttcttgacat tcaacctggg actttgggtg attctgggtt ctggtgaatt 540  
taaagtttca acatttcttt ggggcaccnt ttacaagggg tttggccctt ggnaccttat 600  
gaccggtcna anggtccaaa n 621

<210> 245

<211> 480

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (340)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (366)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (431)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (447)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (458)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (460)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (469)

<223> n equals a,t,g, or c

<400> 245



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gcgcctgtag tcccagctac tcgggaggtt gaggcgggag tatgacttga acctgggagg 120  
cggaggttgc agtgagctga gattgtgcca ctgcactcca gcctgggtga cagagcaaga 180  
ctccgtttca gaaaaaaaaa aaaactgtgt ctcatcattg cactgttctt ttaaaattgt 240  
atatatatat ttttcttgca gatacactct ggaaatgatt aaactagtac cacataatga 300  
aagtgcattg aactatttga aagggatttt gcaggatcgn ggtctttcca aatatcccaa 360  
tctgtnaaat caattacctt gatttacaac caagtcaaag ttccccctac ctaattgcct 420  
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<210> 246

<211> 451

<212> DNA

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<220>

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<220>

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<400> 246

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ccaaagtgct ggganttaca ggcgtgagcc accgtgcccg gcctgattct cttaaaattg 180
aagagggtgct gccaaagnct tcagatctaa cgcagatgca tagaccttgt tcatgggtact 240
tgttcagcct gtgctgggga gccgtgggtc cgagtttcct gggaggntga cagggtgaag 300
ccaccgtanc cacnaccnc cganttcncn tncgctttct tntcagcant aggattaaag 360
ggattttgaa tgaagcaant tttaaggggt aggagggtgt ggggaaaata aataattatt 420
caagtaaggc ctnngggnnt ttaggggggt n 451
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<210> 247

<211> 530

<212> DNA

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<220>

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<222> (404)

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<400> 247

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ggttgctctg atatagcagc cctggtgtag tttcttcatt tcaggaagac tgacagtgt 180  
tttgcttctt ccttaaagca ttgcaacag ctacagtcta aaattgcttc ttaccaagg 240  
atatttacag aaaagactct gaccagagat cgagaccatc ctagccaaca tcgtgaaacc 300  
ccatctctac taaaaataca aaaatgagct gggcttggtg gcgcacacct gtagtccag 360  
ttactcgggg aagctgaggc aggagaatcg cttgaaccg ggantggaga ttgcagtga 420  
cccagatcgc accactgcac tccagtctgg ccaacagagc aagactccat ctcaaaaaag 480  
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<210> 248

<211> 635

<212> DNA

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ctgggagatg gaggttgag tgagctgaga tcatgccact gcactccagc ctgggcaaca 120  
gagcaagact ctgcctcaaa aaaaaattaa aataaattta aatacaaaaa aaaatagcca 180  
ggtgtgggggt gcatgcctgg aatcccagct acttganaag gctnaaggca ccaanaattg 240  
cttgaaccca ggaggtggag gttgcagtga gccaaagatca caggagccac tgcactccag 300  
cctgggtgac agagtggagac tctgtctcaa aaaaaaatt aaataaatta ttataacctt 360  
tcaaaaatgc tgtgtgcatt ttcattgttct tttttttaac attactgnca ctctccctaa 420  
tgaaatggac ttcaanaag cagtattttg ttaaataaat acataacctc attctgaata 480  
atgnccctca ttttgactat aactgggctt ggnttnaaaa gcaaaattta acaaaaattt 540  
aatccccttc caaaggaacn ttgggtancc tgggtnaaaa aatgccaaat ggggtacttt 600  
tanttaaaat ttggaattta acatcttttt tggan 635

<210> 249

<211> 360

<212> DNA  
<213> Homo sapiens

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<220>  
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<220>  
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<223> n equals a,t,g, or c

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<222> (305)  
<223> n equals a,t,g, or c

<220>  
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<222> (360)  
<223> n equals a,t,g, or c

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cccaggttta aggggtggtt atggccatac gtggaggttt tttgttggtg tttttganac 120  
tgagtttcac tcttgttgcc caggctggag tgcaatggca ccactctggc tcaactgcaac 180  
ctccacctcc tggttcaagc gatctcaggc ctcagcttcc caagtagttg ggattacagg 240  
cgcttgccac cacacctggc taattttgta ttttttagtan anatgggggt ctccatgttg 300  
gtcangctgg tctcaaaact ccgaactcaa gtgatctgcc cgccttgggc tcccaaaatn 360

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<220>  
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<220>  
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<222> (446)  
<223> n equals a,t,g, or c

<220>  
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<222> (459)  
<223> n equals a,t,g, or c

<220>  
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<222> (460)  
<223> n equals a,t,g, or c

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cgccattgca ctccagcctg ggcaacaaga gcgaaaccct gtctcaaaaa aaaaacaaaa 120  
aaccaccaca aaactaggag cctggaaggc cggactgggt ctccgtggga ggggcctggg 180  
tctggagagc agggcagggt ctccctgggc taggggatgg ggatggggct gggcttcaga 240  
ggaggcaggg ttacgtgca gaagagcgga cttggtctcc ggggtcccga gtgggtgacg 300  
cggcccgccca cagggtgctt ctgaaggtga gccggctgga ggcacaactg ctccctggagc 360  
gctaccccga gtgcgggaac ctgctgctgc gggccancgg ggacggcgcc gacggcgtgt 420  
cggtcaccac tcggcngatg ccaacnggaa cgcacgtggn ccgg 464

<210> 251  
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<212> DNA  
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gtcgacccac gcgtttingct cctgttcag gctgggtctgg aactggcgac ttnggggtgat 120  
ccgcccgcct cggcctccca aagtgggtggg attacagggtg tgagccaccg tgcccagccc 180  
tgaaatagtc ttaattgctt gnttttcttn ttgtctgan gtgtgctttt taaaatctct 240  
atgggagatgg agaagactga cattntctgg cctgatgtga aaaacctctc attaaaaacc 300  
gngtntgtag ntttg 315

<210> 252  
<211> 333  
<212> DNA  
<213> Homo sapiens



<220>  
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<222> (302)  
<223> n equals a,t,g, or c

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<222> (325)

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<400> 252

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gaactcctga cctcaggtna tccaccacc ccagcctccc aaagtgctgg gattacaggc 120
gtgagccact gagccagcc nacttttcag tttttaacat aatttttggt ttatccacaa 180
cttttcaagt attganagtn caataaaaaa catgggttct tagtctgtaa ctntctgtta 240
aagcctatga atnncttctg aaaatcatgt ttttaaagtc ataaaatata tacgattacg 300
anngaattctt attattgtcg aaatncagtt att                                     333
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<210> 253

<211> 307

<212> DNA

<213> Homo sapiens

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<222> (7)

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<222> (42)

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<222> (48)

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<400> 253

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agtcagatc actccccttc catgagttgt tttcttaaga tgctagaact tggccaggca 120
tggtaggctca cccctgtaat ccagcactt tgggaggctg aggctggcag atcacttgag 180
gtcaggagtt ccagaccagc ctggccaaca tggtgaaacc ccatctctac taataatata 240
aaatttagcn ggggtgtgggn ggtgtgcacc tgtggcccta nctacttggg aaggctgana 300
cnaggag                                           307
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<210> 254

<211> 401

<212> DNA

<213> Homo sapiens

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<222> (340)

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<220>

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<222> (359)

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<220>

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<222> (378)

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<220>

<221> misc feature

<222> (379)

<223> n equals a,t,g, or c

<400> 254

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cccacacttt gggaggccga ggcgggcaga ttgcctgagg tcaggaattt gagatcagcc 120
tggccaacat gatgaaaccc cgtctctact aaaaatacaa aaattagccg ggcattggtgg 180
caggcacctg taatcccggc tactcgggag gctgaggcag gaaaatcgct tgaacccggg 240
agtcggaagt tgcagngagc caaggatcatg tcatcattgc actccagctt gggcaacaag 300
agtgaagact tcgtctcaaa aaaaaaactt acagactttn ttttcctttn gtaaattgnt 360
agtttaactt tgaattcnng atgaaggatt tattcttatt t 401
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<210> 255

<211> 406

<212> DNA

<213> Homo sapiens

<220>

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<222> (149)

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<220>

<221> misc feature

<222> (243)

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<220>

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<222> (369)

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<222> (370)

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<222> (376)

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<222> (390)

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<222> (392)

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<400> 255

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tcccctcccc tcccctcctc tcccctcctc tcttaccccc aattaaaaaa tagcacatcc 120
```

ctaattgtggg aaacagtaag aaagcatana ttacatttta ggcagggcac agtggctcac 180  
gcctgtaatc ccagcacttt cggaggctga ggtgggtgga tcacttgagg tcaggagttt 240  
ganaccagcc tggccaacat ggtgaaaccc tgtctctact aaaagtacaa aaattagcca 300  
ggcatggagg cgggtgcctg taatcccagc tacttgggag gctgaggcag gagaattgct 360  
tgagccann aggcanaagg tgcagtagn anagatcggg ccattg 406

<210> 256

<211> 415

<212> DNA

<213> Homo sapiens

<220>

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<222> (27)

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<220>

<221> misc feature

<222> (324)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (378)

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<220>

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<222> (379)

<223> n equals a,t,g, or c

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<222> (411)

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<220>

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<222> (412)

<223> n equals a,t,g, or c

<400> 256

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caggagcaga gcaaagaggt ggccatccgc atctttcagg gctgccagtt tcgctccgtg 120  
gaggctgtgc aggagatcac agagtatgcc aaaagcattc ctggttttgt aaatcttgac 180  
ttgaacgacc aagtaactct cctcaaatat ggagtccacg agatcattta cacaatgctg 240  
gcctccttga tgaataaaga tggggttctc atatccgagg ggccaagctt catgacaagg 300  
gagtttctaa agagcctgcg aaancctttg gtgactttat gggagcccag tttgagtttg 360  
ccgtgaaatt ccatggcnng ggattatatg gacagcggct tgggcaaatt nnagc 415

<210> 257

<211> 414  
<212> DNA  
<213> Homo sapiens

<220>  
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<220>  
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<220>  
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<220>  
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<222> (380)  
<223> n equals a,t,g, or c

<220>  
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<222> (384)  
<223> n equals a,t,g, or c

<220>  
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<222> (397)  
<223> n equals a,t,g, or c

<220>  
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<222> (411)  
<223> n equals a,t,g, or c

<400> 257  
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caccggcaag gaggtgatg acggatgtgc ccttgggggc angtgatggg agcacagctg 120  
gaacaatgtg ctcgccccc agtgctctgt gggagcccca ggacaagtga gctggtgtca 180  
cctcctgcct gggggaagag ccaggccctg aagaacagcc gcagcgtgtc acaggtgttg 240  
gtgaggacac acactaggcc caaggtgcct gtgctcccag caggttccaa gtgcaanttc 300  
aagccaactt tgcgtgttaa cttcaacggg gacttccaag cttccaagct aacttttgtg 360  
gtgttaacct tcaanaaaan caanaaaggg gggcttnggg gcattttggt ncct 414

<210> 258  
<211> 373  
<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (321)

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<220>

<221> misc feature

<222> (324)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (328)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (351)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (361)

<223> n equals a,t,g, or c

<400> 258

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ctcccagtcagggtgcagctctccgggtggacacagaatgcagccatgctgaggg60
cagccggagc caaggccctg agaaagccttcagcccggtcttccatgtgcctggaacgt120
gtgtgtcacc aggaaggccc cctgctggcctctgacagt agctcctctg ggggtccca180
cagcgaggatggcgaccagaaggcagcgagtccatggatgcggtgagcaggggtcccg240
ccgggaggcccccgtgcccacagtggcc aagacagaagaagcttttggcaagggttcgg300
ttttctgaca accggtttt naancctncc ttgccccgcgccaaaagga nttaatttct360
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<210> 259

<211> 529

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (287)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (377)

<223> n equals a,t,g, or c

<220>  
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<222> (438)  
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<220>  
<221> misc feature  
<222> (443)  
<223> n equals a,t,g, or c

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<222> (495)  
<223> n equals a,t,g, or c

<400> 259  
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caagtcaact atgaagaatt cgtacagaat gatgactgca aaatgaagac ctactttcaa 120  
ctcctttttc cccctcttta gaaagaatca aatttgaatc ttttacttac ctccttgcaa 180  
aaaaaagaaa aaagaaaaaa ttccatttat tcatccttgt ttcctatata gccaaactga 240  
atgttcaaaa gtaccttcct tgtcccacac acacaaatct gcatgtntgg ttgggggggt 300  
ccctgtcccc cttaaagatca agctacactt cccattttta caatataata cttgttctac 360  
cttatgatag atccctnaaa agtttcccct ttgctaataa ttataacctgt ttgggtggcc 420  
agttttccct gcttgcantt gannaatgac ccagccggcc tttgttttaa attgaaatga 480  
aaacaattcc aaccttccat ggttcccgtc cattgttaat taatggcca 529

<210> 260  
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<212> DNA  
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<220>  
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<220>  
<221> misc feature  
<222> (413)  
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<220>  
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<222> (437)  
<223> n equals a,t,g, or c



<220>  
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<223> n equals a,t,g, or c

<220>  
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<222> (473)  
<223> n equals a,t,g, or c

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<222> (562)  
<223> n equals a,t,g, or c

<400> 260  
actgtctgta tattacggaa gctcttttca cataatatga ctcgtctgcg aaagtttatg 60  
gtttactttg gaaagaacca aagtttgacg aagatacaga aaactcctct ctttggtggc 120  
gcgatctgtg ctcattggtt tcagtatcct ttgacccat ctttgatga tgtggctgtt 180  
ttcaagtcct atatggaacg cttttcctta aggaacaaag cgacactgaa aattctcaaa 240  
gcaactgtgt cctcctgtgg tgagctggcc ttgaaagggt ttttttcatg ttgctttgag 300  
tttaatggat ggatggatct cgcagaagca ggggggtggat ggaagatgaa gatctaacca 360  
ngtgccttga tgagcaaatt ttacagccca gagactaaga ccattctacc ggntttttaa 420  
gttccggcct tccaagnaatt tcttggcggg ggatgaggcn ggattgaact ccngggatcc 480  
agataggcag gaacatcaag attggggang gtaaccattg gaacaaacca ctcacccagg 540  
tgacggtaag cgctacaac antttt 566

<210> 261  
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<212> DNA  
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<223> n equals a,t,g, or c

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<222> (47)  
<223> n equals a,t,g, or c

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<223> n equals a,t,g, or c

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<223> n equals a,t,g, or c

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<222> (211)  
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<222> (376)  
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<220>  
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nataacctgt cnaanttatc tgatgacana ttaccaangt gctcccccat cccacagta 120  
tagaangatt atttgcattg gtgcanaana naatggnttg ccgctggant atcaanagan 180  
gttaanagcn ttanaaccaa atgactatac ntgaaaggtc tcanaagaaa ntgangacat 240  
catcannaag ggggaaacac anactcttta gancataaca gaatatatct aagggtattc 300  
tatgtgctaa tatanaatat tattaacact tganaacang gatctggggg atctccacgt 360  
tngatccatt ttcannagtg ctctgagagg agtatcttac ttgggggtgac tccttgtttt 420  
tagactatac tcagaaactg ggatanggag ttanaccatt taaaacgggt gtatganggc 480  
ctgnaatatg tgacaantga at 502

<210> 262  
<211> 489  
<212> DNA  
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<220>  
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<220>  
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<222> (3)  
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<222> (464)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (477)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (483)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (486)  
<223> n equals a,t,g, or c

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tgggaccagg agcccgccag ggagcaggca ggcgggggct ggcgggccag gcggccccgg 120  
gcccgtccg tggacgccct ggacgacctc accccgccga gcaccgccga gtcaggaggc 180  
aggtctccca cgagtaatgg tgggaggaga agccgggcct acatgcccc gcggagccgc 240  
agccgggacg acctctatga ccaagacgac tcgagggact tcccacgctc ccgggacccc 300  
cactacgacg acttcaggtc tcgggagcgc cctcctgccg accccaggtc ccaccaccac 360  
cgtaccggg accctcggga caacgntcc aggtccgggg acctccccta tgatgggcgg 420  
ctactggagg aggctgtgan gaagaagggg tcggacgaga ggangagacc ccacaangag 480  
gangangaa 489

<210> 263  
<211> 93  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (22)  
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<220>  
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<220>  
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<223> n equals a,t,g, or c

<220>  
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<222> (76)  
<223> n equals a,t,g, or c

<220>  
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<222> (93)  
<223> n equals a,t,g, or c

<400> 263  
gcggctgcc gccctgcgcg tntccctgc ccgggtctcc tcgctgtcgc ngccgatgcc 60  
acaccatggc cttcnnccacc aggcagttca tgn 93

<210> 264  
<211> 389  
<212> DNA  
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<222> (24)  
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<223> n equals a,t,g, or c

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<223> n equals a,t,g, or c

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<223> n equals a,t,g, or c

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<220>  
<221> misc feature  
<222> (344)  
<223> n equals a,t,g, or c

<220>  
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<222> (358)  
<223> n equals a,t,g, or c

<400> 264  
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ctttaatctg cnttactacg tggggcacaa gggcaagtcc ggccangagt tcctggagtt 120  
tgaaagtttcg accggacgga gcttgaaatc gtcattggag atgaacacat ttcttttnac 180  
aacatcaaaa attggttccc ttattgatgt caatcatgcc aaggatccag aaggcttacg 240



nagtatttna ttatcttgtc caggacctga agtggttggt ctccagtctt attgggttac 300  
acttcaagnt taaacctct agactgnata ttngtgtggg acangggggg ggggtggngt 360  
aggaaatttt gtgtattttc aggggcatt 389

<210> 265

<211> 400

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (296)

<223> n equals a,t,g, or c

<220>

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<222> (308)

<223> n equals a,t,g, or c

<220>

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<222> (342)

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<222> (343)

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<220>

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<222> (389)

<223> n equals a,t,g, or c

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<222> (390)

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<400> 265

tttgcccacg cgtccgcccc cgcgtccgcc cagcgcgtcg cccacgcgtc cgcacccccca 60  
tcccagtcac agcctacttc cgccacgcag aacctggatt ctccctcaag agggcccagg 120  
ggctcagccg gagcctcccc cctccgcccc ctgccaaagg cagcattccc atcagccgcc 180  
tcttccctcc tcggaccccc ggctggcacc agctgcagcc ccgcgggtgt cattccgggc 240  
gaaggcctag agactctgca gagccctggg tatgacccaa gccgcaaaag tctttnttca 300  
agcaaagntt caaaaggtta agccgcttgg gcaatggttt annngaaaag ttttaagggg 360  
gcctccaagg gaggcagggc gggttttttn ggaaaagggt 400

<210> 266

<211> 382

<212> DNA

<213> Homo sapiens

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<222> (10)

<223> n equals a,t,g, or c

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<221> misc feature

<222> (42)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (44)

<223> n equals a,t,g, or c

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<222> (88)

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<222> (103)

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<222> (109)

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<222> (162)

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<222> (166)

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<222> (185)

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<223> n equals a,t,g, or c

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<222> (341)  
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<223> n equals a,t,g, or c

<220>  
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<222> (362)  
<223> n equals a,t,g, or c

<400> 266  
ggacctggan cggaggcggg aagaaagtca taccagatc cnanatccnc acgcagaatg 60  
cacaggtgag ctgccgctgg gcccgganca tgctgggctg tcncacctng cagactgcac 120  
gctccaaccg cccgctccac ctactcttc caggcccggc ancttntgga gaaggaattc 180  
agcannctta tctccttagg cacagacagg ctgctggacn aggacatgcg ccaagtcttt 240

cagttcgnct cccatcctgg cggaagatgt tccggganga aggacctccg aggcgtaact 300  
ngccgactca ctgagatggt gcccncnaac tttcgttcgg ntgcagcggn attcctgggc 360  
tnttcggggg ctccccttttc cc 382

<210> 267  
<211> 449  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc feature  
<222> (374)  
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<220>  
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<222> (433)  
<223> n equals a,t,g, or c

<220>  
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<222> (446)  
<223> n equals a,t,g, or c

<220>  
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<222> (447)  
<223> n equals a,t,g, or c

<220>  
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<222> (448)  
<223> n equals a,t,g, or c

<400> 267  
gggcgatggc tgaaggacca ggagctgagc cctcgggagc cgggtgctgcc cccacagaag 60  
atggggccta.tggagaaatt ctggaataaa tttttggaga.ataaatcccc ttggaggaaa 120  
atggtccatg gggatataca aaagagtatc tttgttttca ctcatgtact tgtacctgtc 180  
tggattatct attattacat gaagtatcat gtttctgaaa aaccatatgg catagttgaa 240  
aagaagtcca gaatattccc tgggtatata attctggaga ctggagaagt aattccacca 300  
atgaaagaat ttcctgatca acatcattaa agattatgta aaaaggtaaa aggccttatga 360  
gcctaagttt ggtncatatat taccatattt actggaattt tcttgaaaa gtactttaat 420  
aaagtttaat ctnagaaaaa aaaaannna 449

<210> 268  
<211> 594  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (1)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (8)

<223> n equals a,t,g, or c

<400> 268

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ngcaagcnga caccaaccct cactaaaggg aacaaaagct ggagctccac cgcgggtgcgg 60
ccgctctaga actagtggat cccccgggct gcaggaattc ggcacgaggt cagtgtcggg 120
cgcagacggc ggcagtgcgg cttgctcttg gaagttcagg ctcggttgtc ttttgggagc 180
catggagagt gacttttata tgcgttacta cgtggggcac aagggaagt tcggccacga 240
gttcctggag tttgagtttc gaccggacgg gaagttaaga tatgccaaca acagcaatta 300
caagaatgat gtcatgatca gaaaagaggc ttatgtacat aaaagcgtga tggaggaact 360
gaagagaata attgacgaca gtgaaattac caaagaggat gatgcattgt ggcctcctcc 420
tgaccgagtg ggccggcagg agcttgaaat cgtcattgga gatgaacaca tttcttttac 480
aacatcaaaa attggttccc ttattgatgt caatcaatcc aaggatccag aaggcttacg 540
agtattttat tatcttgccc aggacctgaa gtgtttggtc ttcagtctta ttgg      594
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<210> 269

<211> 332

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (19)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (240)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (275)

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<222> (321)

<223> n equals a,t,g, or c

<220>

<221> misc feature  
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<400> 269  
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atcttcgtga agactctgac tggtaagacc atcaccctcg aggttgagcc cagtgcacacc 120  
atcgagaatg tcaaggcaaa gatccaagat aaggaaggca tccctcctga ccagcagagg 180  
ctgatctttg ctggaaaaca gctggaagat gggcgacccc tgtctgacta caacatccan 240  
aaagagtcca ccctgcacct ggtgctccgt ctcanagggtg ggatgcaaat cttcgngaag 300  
accctgactg gcaagaccat nacccttgag gn 332

<210> 270  
<211> 515  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (3)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (4)  
<223> n equals a,t,g, or c

<220>  
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<222> (7)  
<223> n equals a,t,g, or c

<220>  
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<222> (10)  
<223> n equals a,t,g, or c

<400> 270  
gcnnnganacn aaccctcact aaagggaaca aaagctggag ctccaccgcg gtgcggccgc 60  
tctagaacta gtggatcccc cgggctgcag gaattcggca cgagggatgt tgatgtcctg 120  
catctaacgc ggtgtaaccc ccgaagccga gcgagctccg gaggaatttc agtatctgct 180  
acggtaaactt catcagccc ccaagatggc gatgcaagcg gccaaagagg cgaacattcg 240  
acttccacct gaagtaaatc ggatattgta tataagaaat ttgccataca aaatcacagc 300  
tgaagaaatg tatgatatat ttgggaaata tggacctatt cgtcaaatca gagtggggaa 360  
cacacctgaa actagaggaa cagcttatgt ggtctatgag gacatctttg atgccaagaa 420  
tgcatgtgat cacctatcgg gattcaatgt ttgtaacaga taccttgtag ttttgtacta 480  
taatgccaac agggcatttc agaagatgga caca 515

<210> 271  
<211> 141  
<212> DNA

<213> Homo sapiens

<220>  
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<222> (12)  
<223> n equals a,t,g, or c

<220>  
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<222> (13)  
<223> n equals a,t,g, or c

<220>  
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<223> n equals a,t,g, or c

<220>  
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<223> n equals a,t,g, or c

<220>  
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<222> (39)  
<223> n equals a,t,g, or c

<220>  
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<222> (141)  
<223> n equals a,t,g, or c

<400> 271  
cactccatgg gnnnctctgt gtggnatttg gggccctnc atacttcatt tattatatta 60  
tcaaaactga gagggatagg aaagtaaaaa cttatccagg taggaaaatt ggategaaca 120  
tttcacctct catattaagg n 141

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ggcccaagat gaccggttct aacgaagttc aagntgaacc agccaccccg aggatagcat 120  
ctcctccgta aagttcagnc ccaacacctc ccagttcctg cttgtntcct cctgggncac 180  
gtccgtncca ctctacgnat gtgccggcca actccatgcg gctcaagtac cagcacaccg 240  
gagncgtntc ggactgcgnc ttctacggtc caangnatgc ctggagtnga ggactagatc 300  
atcagttgaa aatgcatgat ttgacactga tcaagaaaat ttcttggacc catgntgccc 360  
tatnagatgt gttgaatact gtcagaagtg aattanaatg gnactggaag ttgggggtag 420  
ccagtttacc tgt 433

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<220>  
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tgaaccgagt agaagacaag gtgacgcagc tggaccagag gctggcactc atcacgcaca 120  
tgcttcacca gctgctctcc ttgcacggtg gcagcaccoc tgagcccact gtgcgtgggg 180  
ctcccgnctn caaccctctg cccagtccca gcagccagcc aaacacacag aaggggactg 240  
ccacccttccc ttgccagctg ctgagccgca gagaagtgc ggttcctaca caggacaggg 300  
gttccttctg ggcattacat cgcataaaaa tnaataattt gtggtgattt ggatctgggt 360

tttaatgaat ntnacagtgn gacttttgatt attaattgag caagcttttc ctaataaacg 420  
tggagaattn cn 432

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<211> 276

<212> DNA

<213> Homo sapiens

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<222> (234)

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<222> (264)

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<220>

<221> misc feature

<222> (265)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (269)

<223> n equals a,t,g, or c

<400> 274

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gctgaggacg aggctgatta ttactgcagc tcatntacaa gtagtatctc ttatgtcttc 120  
ggaactggga ccaagggtcac cgtcctagtc cagcccaagg ccaacccac tgttcaactcc 180  
tgtttccccc cctcctcctt aagaacttcc aagcccaaca aaggcaacta tgtnttttgg 240  
aaccattact tctancggg aaanntttna aaatgc 276

<210> 275

<211> 351

<212> DNA

<213> Homo sapiens

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<220>  
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<223> n equals a,t,g, or c

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<220>  
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<222> (241)  
<223> n equals a,t,g, or c

<220>  
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<222> (329)  
<223> n equals a,t,g, or c

<220>  
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<223> n equals a,t,g, or c

<400> 275  
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gggccgtgga aaacgggnac cggacangaa gccgccggcc ctgccgcgcc ccatccncaa 120  
cctggaagtc gagttcacca agatatttan caanaatgga atgggacgaa tccnagantg 180  
ggaaaaagtg tgctacatgt taccntcaa ctccggganc aaatatgtga agtggaaaga 240  
ngagatangg ccgacgtggg acgaaggctg tggaagctgc acagggtngc tnccaaaaag 300  
ggntcccca tgggcgcccg gtgggatgnc ctgaattcct tggccggtng c 351

<210> 276  
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<212> DNA  
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<400> 276  
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catcttctcg ccggtgctgg gcctcccatg ggggtgcctg tcacaggtgc agctgcagca 120  
gtcagggtcca ggactggtga agccctcgca gaccctctca ctcacctgtg ccatctccgg 180  
ggacactgtc tctaggaaca gtgctggttg gaactggatc aggcagtccc catcgagagg 240

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ccttgagtgg ctgggaagga catactacag gtccaaatgg tataatgatt atgccgtatc 300
tgtgaaaagt cgaataacca tcaacgcaga ttcaaccaag aatcagttct ctctgcagct 360
gaactctgtg actcccagag acacggctct gtattactgt gcaagagatc ggggcagctg 420
gtccgatgaa gccgaggggc tcccgccgcg ttacttctac tac 463
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<210> 277

<211> 463

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (392)

<223> n equals a,t,g, or c

<400> 277

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cctcttcttg gtggcagcag ctacaagtgc ccactcccag gtgcagctgg tgcagtctgg 120
tgctgagggtg aagaagcctg gggcctcagt gaaggctctc tgcaaggctt ctggatacac 180
cttcaccagt tatgatatca actgggtgcg acaggccact ggacaggggc ttgagtgggt 240
gggatggatg aaccctaaca gtgctaacac aggctatgca cagaagttcc agggcagagt 300
caccatgacc aggaacacct ccataagcac agcctacatg gagctgagca gcctgagatc 360
tgaggacacg gccgtctatt actgtgagag anggaggcgg tgggagctgc tcgggatgat 420
gtgggacttt gactactggg gccagggaac cctggtcacc gtc 463
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<211> 343

<212> DNA

<213> Homo sapiens

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<222> (271)

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<220>

<221> misc feature

<222> (284)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (293)

<223> n equals a,t,g, or c

<220>

<221> misc feature  
<222> (294)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (315)  
<223> n equals a,t,g, or c

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ctcgccctcc tcctggctgt tctccaagga gtctgtggcg aggtgcagct ggtacatgct 120  
ggaggagaga tgaggaaagc ccggggagtc tctgaagatc tcctgtgaag gntgttggga 180  
tacacctttg aacatctact gggatcggtt ggggtgcgcca gatgcccggg gaaggcctgg 240  
gagtgggtgg ggcatacatat gtcctgggtga ntctgatggc cagngatagc canncttttc 300  
gagggccaga tgcancatgt gcagtcgaca agtgccacca aca 343

<210> 279  
<211> 436  
<212> DNA  
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<220>  
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<222> (151)  
<223> n equals a,t,g, or c

<220>  
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<223> n equals a,t,g, or c

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<223> n equals a,t,g, or c

<220>  
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<223> n equals a,t,g, or c

<220>  
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<222> (384)  
<223> n equals a,t,g, or c

<220>  
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<222> (392)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (403)  
<223> n equals a,t,g, or c

<400> 279  
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tctcccagct tgtgtgact caatcgccct ctgcctctgc ctcccctggga gcctcggtca 120  
ngctcacctg cactctgagc agtgggcaca ncgactacgc catcgcatgg catcagcagc 180  
agccagagaa gggccctcgg tacttgctga ngcttaacac tgatggcagc cacaggaagg 240  
gggacgggat ccctgatcgc ttctcaggct ccagctctgg ggctgagcgc tacctacca 300  
tctccagcct ccagtctgag gatgangctg actattactg tcagaactgg ggctttggga 360  
tngtattcgg cgaaggggac caanctgaac gncctaagtc agnccaaggc tgccccctcg 420  
gtcaatctgt tcccgg 436

<210> 280  
<211> 315  
<212> DNA  
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<222> (138)  
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<223> n equals a,t,g, or c

<220>  
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<222> (246)  
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<220>  
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<222> (280)  
<223> n equals a,t,g, or c

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<220>  
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<400> 280  
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tcccgggcta tacagnccat ctgcctgccc tcgatgtata acgatcccca gtttggcaca 120  
agctgtgaga tcaactggncct ttggaaaaag gaattctagt gaagtgaaca attgcgaact 180  
gaacttagga aggtcctgga ggagtgtttt gacctggaaa atgnagccca gtgtgggttca 240  
agggtnagac tgcagagttt agagggtggg agcactgagn cgggtggcaga ttgggtccca 300  
gggttggnntt gaagn 315

<210> 281  
<211> 411  
<212> DNA  
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<220>

<221> misc feature

<222> (411)

<223> n equals a,t,g, or c

<400> 281

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agaagaatat gaaaaagcag agcgactcgg ttaagggaaa gcgccgagat gacgggcttt 120
ctgctgccgc ccgcaagcag agggactcgg agatcatgca gcagaagcag aaaaaggcaa 180
acgagaagaa ggaggaaccc aagtagcttt gtggttcgt gtccaacct ctggcccttc 240
gcctgtgtgc ctggagccag tcccaccacg ctgcggttcc ctccctgtagt gctcacagg 300
cccancaccg atggcattcc ctttgccctg agtctgcanc gggtcccttt tgtgcttnc 360
tccctcaag tacctntttc cccctgggcc acttccgggg gtnagggggg n 411
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<210> 282

<211> 570

<212> DNA

<213> Homo sapiens

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<220>

<221> misc feature

<222> (7)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (12)

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<220>

<221> misc feature

<222> (217)

<223> n equals a,t,g, or c

<400> 282

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cgctctagaa ctagtggatc ccccgggctg caggaattcg gcacgagtag agacagcgcc 120
ggggcaagtg agagccggac gggcactggg cgactctgtg cctcgctgag gaaaaataac 180
taaacatggg caaaggagat cctaagaagc cgagagnaaa atgtcatcat atgcattttt 240
tgtgcaaact tgtcgggagg agcataagaa gaagcaccca gatgcttcag tcaacttctc 300
agagttttct aagaagtgtc cagagagggtg gaagaccatg tctgctaaag agaaaggaaa 360
atttgaagat atggcaaaaag cggacaaggc ccgttatgaa agagaaatga aaacctatat 420
ccctcccaaa ggggagacaa aaaagaagtt caaggatccc aatgcacca agaggcctcc 480
ttcggccttc ttctcttct gctctgagta tcgccccaaa atcaaaggag aacatcctg 540
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gctgtccatt ggtgatgttg cgaagaaact

570

<210> 283

<211> 366

<212> DNA

<213> Homo sapiens

<220>

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<220>

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<222> (10)

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<222> (32)

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<222> (39)

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<222> (327)

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<220>

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<222> (333)

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<220>

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<222> (337)

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<220>

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<222> (348)

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<220>  
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<400> 283  
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agcggatttc acacatgcct agcagaccag aactctcggc agttgctaca agggaagaaa 120  
ggactatgtg gatcccttgt ggctatgcag atacctacct cacagagttg ttgtagaaga 180  
ctggtgggttt ggttcaaacc ttgtgattaa agagtttgtc aagcatttta ttcttttgaa 240  
taaaagcaac atatctaaaa catttaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 300  
aaaaaaaaaa aaaaaaaaaa aaagggnggc cgntttnaag gatccaanct tacgaancgt 360  
gcatgc 366

<210> 284  
<211> 414  
<212> DNA  
<213> Homo sapiens

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<220>  
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<222> (394)  
<223> n equals a,t,g, or c

<220>  
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<223> n equals a,t,g, or c

<220>  
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<222> (398)  
<223> n equals a,t,g, or c

<220>  
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<222> (407)  
<223> n equals a,t,g, or c

<400> 284  
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gggtggggccc cgatgggtcac acctggtcac tcttcccaga ccaccccccc ctacaggagc 120  
gggagaagat tgtgggtccc atcagtgact ccccgaaagcc accgccacag cgtgtgaccc 180  
tcacgctacc tgtcctgaat gcagcacgaa ctgtcatctt tgtggcaact ggagaaggca 240  
aggcagctgt tctgaagcgc attttggagg accaggagga aaacccgctg cccgccgcct 300

gggccagccc cacaccggga aactgtgctg gtcttggacg aggcggccgc cgcttctgac 360  
cgtgcccttc gagaaacatt ccactttgna actnngcnca aaggacnccc aaat 414

<210> 285

<211> 551

<212> DNA

<213> Homo sapiens

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<222> (8)

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<222> (22)

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<220>

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<222> (24)

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<220>

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<222> (64)

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<222> (180)

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<222> (225)

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<222> (234)

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<222> (322)  
<223> n equals a,t,g, or c

<220>  
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<222> (324)  
<223> n equals a,t,g, or c

<220>  
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<222> (325)  
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<220>  
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<220>  
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<220>  
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<222> (410)  
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<222> (482)  
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gctatcttag cggcacaaag actaggagaa gatgtggaga cttccaataa atgggctgcn 180  
ggccanaaca aacaacattc tattaccaag aacacggcca agctngaccg gganacagag 240  
tgctgcacca tgacaggtga ccctgaagtg ngtaagtga tccagcaagt cggcananca 300  
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atganagngg tacggccata cccaataacc agtgcttggc aaaatcgacn ggaccattgg 420  
ctccaagctc cgggaaagac attggaaaac ccatcgagaa gggcctaggc gaaatgaaca 480  
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tccaactgta tacctgcac agtgtcattc ctttgtgtga tttcttaatg ctgtatttgt 180  
tcattctaaa cctagatgta tacagctctg agttataaat ggttataaag ctccctgttac 240  
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aaaaatgaaa agctgcatgc atctacagca ggcatggatt gtttatgtcg tatgatatcc 420  
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gtcctatcag taccttgtag agagtatccg aaggtttccg nctcangaag agttcangga 240  
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tcgtcgcgct ccccggggtg ncagncanca tnetgnatgt ntacctnaag tcncaccacg 240  
gagagcacga ganaccgag ttcacgtct acccntatct ncgtatcagg ancaagcnnt 300  
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ccagagtggg actgcctgcg cctgctcctg ttatcaatag caaatatgga ctgagagaaa 180  
cagataaacg tttaaatagg cttaaaaagt taggtgacag cagcaaaaat tcagacagtc 240  
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accgaaaatc ttcagttggc gtaaaaaaga atagcaagag cagaacgta acgaggcaat 360  
ctatgtcaag aattccagct tcttccaact ctacctcatc taagcttaac tcatataaat 420  
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cancctggnt gcttcaagac agagtcagtg aagaaacgtg gggttcantgg gaaaagcgcc 180  
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acatccagct gacctgcca tcaaaggagg gtcaccaac ccctccagta cagctggaaa 180
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gttctccctt aaaaaatata tcccacagaa cacatcnggt ttatantctt gttcctccca 300
gcaataagaa nggaaaccnn ttctgcaac ttcacggtgg ccttncaaat ctcccccca 360
taaaantttg ccntttttt tgnctcccc gggggggttt tttttcacc ccccttatcc 420
ntngngncan cnccttang ngcngcnc caggggaaag annnaacccc naaaaaaagg 480
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<210> 296

<211> 572

<212> DNA



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ccatgcagcc aagtcactgg ccatgattgt ggggatTTTT gccctgtgct ggtagcctgt 180

gcatgctggt aactgtgtca ctcttttcca gccagctcag ggtaaaaata agcccaagtg 240  
ggcaatgaat atggccattc ttctgtcaca tgccaattca gttgtcaatc ccattgtcta 300  
tgcttaccgg aaccgagact tccgctacac ttttcacaaa attatctcca ggtatcttct 360  
ctgccaaagca gatgtcaaga gtgggaatgg tcaggctggg gtacagcctg ctctcggtgt 420  
gggcctatga tctangctct cgcctnttca ngagaagatc aaatncacaa gaaacaaaga 480  
ggacacggnt ggttttattg ngaaagatag ctacacctta caaggaaatg gactggctnt 540  
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<211> 334

<212> DNA

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tggggcaaga nagtgaattg aattacaaaa ccaccaagac ctcccgnntg cccatnnatc 180  
gatgtggccc ccttgaacg ttggtgcccc aaaccaggna attcggnttc gaacgttggg 240  
ccctgtttgg ttctctgtaa aantcccttc cattcccaac ctggggtccc tnnccaaccc 300  
aaccaaattt ttccnnncna acccgggaaa cagg 334

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gagtacgaga acgatctggg gatcacagcc gtcgccctgt acgantacca ggctgcgggc 180
gatgatgaga tctcatttna ccctgatgac atcatcacca acatcgagat gattgangac 240
ggctggtggc gcgggggtgtg caagggccgc ttcagggagc tcgcattctc ttg      293
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<211> 418

<212> DNA

<213> Homo sapiens

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ccccaccgac nttggntnag gataactcca ggtacacaca ctctctgacc cagnactatg 120  
atgccaaacc acagggccgg gatgacagat actntgaaag catcatgnng agacggggcc 180  
tgacctgacc ctgcaaagac atcaacacat ttnttcatgg naacaagcgc agattcaagg 240  
ncatctgtga aaacaaggan tggaaacctt tacagggnaa cctnagggtt angnaagttt 300  
tttttttcca ggnaaccatt tggaaagttt aatngggggg ttcccnnggg tntnnaanga 360  
ctttccgggg gcnaaangng ggnttaaaaa annttttttt ttttttnga aaaagggtt 418

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<213> Homo sapiens

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<223> n equals a,t,g, or c

<220>  
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ttacatggag ctgcacttca ccaaagacat tgtggatgcg ggactggctg gggacaccaa 180  
tctctactac atggcgctca tcgaaagggg cacagccaaa ctgcaggccg ctgtggtgtt 240  
gaaccctggc tactcctcca tcccacctgt tttccanctc tgtttgaact ggaaanggga 300  
gaaaaccaac agcaacnatin acaacattcn gggccatgga gggcga 346

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<213> Homo sapiens

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aaaaanttggt tactaccagn tattggttcg tttaacaatta ttgatggaaa tcaagtcanc 120  
ggacaaaatn ctggaaacaa ttcttcctt caaaaaatct tatcngcaan aaccgactga 180  
agctgccata gatttcctta cnagaattaa ata 213

<210> 302

<211> 440

<212> DNA

<213> Homo sapiens

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<222> (342)

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<222> (382)

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<400> 302

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ttcaccatgg accgggaagt gcgcaaaatc aaacaaggcc tgggcttgaa atttgctgag 120
ntgggtgtata ccggtttctg gcacagccct gagtgtgaat ttgtccgccca ctgcatcgcc 180
aagtcacgagc agcgagtggc agggaaagt caggtgtccg tcctcaaggc ccaggtgtac 240
atcctcggcc gggagtcccc actgtctctc tacaatgagg agctgggtgag catggatgag 300
aacctcatgc acatcagcta cganctgga atcctggaga ancccaagaa ccaagcgctc 360
cangtcttaa acgaagaccc angacccagc caaagcccca acaaccctga catctccgag 420
atcgagttca aaaaagggtc 440
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<210> 303

<211> 495

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (22)

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<400> 303

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ccggggcctt gcggagactc accccttcag cgtcgtgcc ccagctcag ctcttactgc 180
gggcccgtcc acggcgggtc atcctgggtg gagcacagta aggactattg ctatggatgg 240
tacagaaggc ttggttagag gccagaaagt actggattct ggtgcaccaa tcaaaattcc 300
tgttggtcct gagacttttg gcagaatcat gaatgtcatt ggagaacctt ttgatgaaag 360
aggtcccacg aaaaccaaac aatttgctcc cattcatgct gaggtccag agttcatgga 420
aatgagtgtt gagcaggaaa tcttgtgact ggtatcaagg ttgtcgatct gctagcttcc 480
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tatgcccaagg gtggc

495

<210> 304

<211> 293

<212> DNA

<213> Homo sapiens

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aaacggattg ccagagaatt ggcagaagat gacagcatat taaagtgagt gaccctgcga 180  
cccactcttt ggaccagcag cggatgaata aagcttcctg tgttgtgtga aaaaaaaaaa 240  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaagggg cggnctntnt tna 293

<210> 305

<211> 261

<212> DNA

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gggtgcgcaa aacgaccgcc caaggcaacg gaggtcacg agaatcagca tgattcttca 180  
naggctcttn aggttctcct ctgtnattcg gtcagccgtc tcagtcatt tgcgaggaa 240  
cattggtggt acagcagttg g 261

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caactaacct cctcggactc ctgcctcact catctacacc aaccacccaa ctatctataa 120  
tcctagccat ggccatcccc ttatgancgg gcgcagtgat tatangcttt cgntctaaga 180  
ttaaanaatgc cctagcccac ttcttatcaa aangcacacc tacacccctt atccccatac 240  
tagttattat ggnaaacatn atcctactcn ttcnaccaat agccctgggc gtnagcctaa 300  
tcgettacat tactgnaggg cacntactca tgcacctcat tggaancgtc ccctacaata 360  
tcaatcatta aacttcctc tacacttata tcttcacatt ctattctaac ttaatatcct 420  
aanaaattcc ttttcncttt attccaagcc caactttttc cnactttntt cttaaaccctc 480  
ttactttncg aaaaaccttt tt 502

<210> 307  
<211> 119  
<212> DNA  
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<212> DNA

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tggacacggc tgcggtgggc ggggtcttcg acgtctccaa cgctgaccgc ctgggcttct 120  
cagagggtgga gctggtgcag atggtgggtg acggagtga gctgctcatc gagatggagc 180  
agcggctgga gcaggggccag gccatcgacg acctcatgcc tgcccagaaa tgaagcccgg 240  
cccacacccg acaccagccc tgctgcttcc taacttattg cctgggcagt gcccaccatg 300  
caccctgat gttcgccgtc tggcgagccc ttagccttgc tgnagagat tccgttcaac 360  
cttggtanaa tttanttttt tgatgggna agatattgctg atg 403

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<211> 559  
<212> DNA  
<213> Homo sapiens

<220>  
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gagtagccgg taacaaacga gggttcccg gattggaccg acgcagccat gcctctgcga 180  
cttgatatca aaagaaagct aactgctaga tctgacgag ttaagagtgt ggatctgcat 240  
cctacagagc catggatggt ggcaagtctt tacaatggca gtgtgtgtgt ttggaatcat 300  
gaaacacaga cactggtgaa gacatttgaa gtatgtgatc ttctgttctg agctgcaaag 360  
tttgttgcaa ggaagaattg gggtgtgaca ggagcggatg acatgcagat tagagtgttc 420  
aattacaata ctctggagag agttcatatg tttgaagcac actcagacta cattcgctgt 480  
attgctgttc atccaacca gcctttcatt ctaactagca gtgatgacat gcttattaag 540  
ctctgggact gggataaaa 559

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<212> DNA  
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<223> n equals a,t,g, or c

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<223> n equals a,t,g, or c

<220>  
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<222> (245)  
<223> n equals a,t,g, or c

<220>  
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<223> n equals a,t,g, or c

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ggctatccag cgctactcaa agattcaggt ttactcacgt catccagcag agaatggaaa 120  
gtcaaatttc ctgaattgct atgtgtcttg gtttcatcca tccgacattg aagttgactt 180  
actgaagaat ggagagagaa ttgaaaaagt ggagcattca gacttgnctt tcagcaagga 240  
ctggncttct tatctcttgt actacactga attcaccccc actgaaaaag atgagtatgc 300  
ctgccgtgtg aacctatgtga ctttgtcaca gcccagata gttaagtggg atcgagacat 360  
gtaagcagca tcatggaggt ttgaagatgc cgcatttgga ttggatgaat tccaaattct 420  
gcttgcttgc tttttaatat tgatatgctt atacacttac actttatgca caaaatgtag 480  
ggttataata atgntaacat ggacatgatc ttctttataa t 521

<210> 311  
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<220>  
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<222> (52)  
<223> n equals a,t,g, or c

<220>  
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<223> n equals a,t,g, or c

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<222> (537)  
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<223> n equals a,t,g, or c

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<223> n equals a,t,g, or c

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<223> n equals a,t,g, or c

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ggattcctga agctgacagc attcgggccc agatgtctcg ctccgtggcc ttagctgtgc 120  
tcgcgctact ctctctttct ggcttgagg ctatccagcg tactccaaag attcagggtt 180  
actcacgtca tccagcagag agtggaagt caaatttcct gaattgctat gtgtctgggt 240  
ttcatccatc cgacattgaa gttgacttac tgaagaatgg agagagaatt gaaaaagtgg 300  
agcattcaga cttgtctttc agcaaggact ggtctttcta tctcttgatc tacactgaat 360  
tcacccccac tgaaaaagat gagtatgcct gccgtgtgaa ccatgtgact ttgtcacagc 420  
ccaagatagt taagtgggat cgagacatgt aagcagcatc atggagggtt gaagatgccc 480  
gcatttggat tggatgaatt caaattctgc ttgcttggtt tttaatantg atatgcntat 540  
acacttacct ttatgcncaa aanggtaggg ntataataat ggtaacatgg g 591

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<212> DNA  
<213> Homo sapiens

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<223> n equals a,t,g, or c

<220>  
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<222> (576)  
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aaaaaaaaaa aaaagggcgg ccgttctaga ggatccaagc ttacgtacgc gtgcatgcna 120  
cgtcatagct cttctatagt gtcacctaaa ttcaattcac tggccgtcgt tttacaacgt 180  
cgtgactggg aaaaccctgg cgttacccaa cttaatcgcc ttgcagcaca tcccccttcc 240  
gccagctggc gtaatagcna anaggcccgc accgatcgcc ctcccccaaca gttgcgcanc 300  
ctgaatggcn aatgggacgc gccctgnann ggcgcatata gcgcggcggg tgaggtggtt 360  
acgcncagcg tgaccgctac acttgccagt gccctagcgn ccgctccttt cgctttcttc 420  
cctncctttc tcgccangtt cgccggcttt ccccgtaag ctctaaatcg ggggctccct 480  
ttagggttcc gatttagtgc ttacggnac cttecgacccc aaaaaanttg attanggtga 540  
tggttcacgt aantgggcca tcgcccttga tagacnggtt tttc 584

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<211> 763

<212> DNA

<213> Homo sapiens

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<222> (52)

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<222> (54)

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atccaagctt acgtacgcgt gcatgcgacg tcatagctct tctatagtgt cacctaaatt 120  
caattcactg gccgtcgctt tacaacgtcg tgactgggaa aaccctggcg ttaccaact 180  
taatcgccct gcagcacatc cccctttcgc cagctggcgt aatagcgaag aggcccgcac 240  
cgatcgccct tcccaacagt tgcncagcct gaatggcgaa tgggacgcgc cctgtancgg 300  
cgcattaagc gcggcggttg tgggtggttac ncgcagcgtg accgttacac ttgccagcgc 360  
cctagcgcgc gntcctttcg ctttcttccc ttctttctc gccacgttcg ccggctttcc 420  
ccgtcaagct ntaaatcggg ggctcccttt agggttccga tttagtgtt tacggcacct 480  
cgaccccaaa aaactngatt aggggtgatg ttcacgtagt gggccatngn cctgatagac 540  
ggtttttcgc cctttgacgt tggagtcac gttcttaata gtggactntt gttccaaact 600  
ggaacaacac ttaaccctat ctcgggctat tcttttgatt nataagggat tttccnatt 660  
tcgggcctat tgggtnaaaa aatgaagctt gttttaacaa aaaatttaac gcgnaatttt 720  
accaaaaatn nttaaacggc ttanaattta agggggggcc ctt 763

<210> 314  
<211> 761  
<212> DNA  
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tcatanctct cctatagtgt cacctaaatt caatncactg gccgtcgttt tacaacgtcg 180  
tgactgggaa aaccctggcg ttaccaact taatcgctt gcaanacatc cccctttcgc 240  
cagctggngt natancnaaa aggcccgcac cgatcgccct tcccaacagt tgcgcancct 300  
gaatggcaaa tgggacgcgc cctgttacg cgcattaanc ccgnggggtg tgggtggttac 360  
ccccaangtt naccgctaca cttgcnagcg ccctagngcc cgctcctttc gctttcttcc 420  
cttcctttct cgccaanttc ngccggnttt ccccgtaaan ctctaantcg ggggcccctt 480  
tanggttcca atttatgctt tacggcaccn caacccaaaa aacttnnnta aggtnatggt 540  
ccacntatgg gccatcncct aataaanggt ttccccctt ngaaattgga atccanttct 600  
taaaagggaa nctgttccaa atggaaaaaa anccaaccct atcncgggct ntncctngan 660  
ttanaaaggg aattnggnca attccggcct antgggttta aaaaattgaa actgaattta 720  
aanaaaatt taaacgcaaa attntaaaaa aaattnttta a 761

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<211> 540  
<212> DNA  
<213> Homo sapiens

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cttctatagt gtcacctaaa ttcaattcac tgcccgctcg tttacaacgt cgtgactggg 180  
aaaaccctgg cggtaccctaa cttaatcgcc ttgcagcaca tcccccttc gccagctggc 240  
gtaatagcga anaggcccgcc accgatcgcc ctcccaaca gttgcgcagc ctgaatggcg 300  
aatgggacgc gccctgtagc ggcgcattaa gcgcggcggg tgtggtggtt acgcgcagcg 360  
tgaccgntac acttgnaagc gccctaagc ccgntccttt cgctttcttc ccttcctttc 420  
tnccacgttc gnccggtttc ccgtcaagct ctaaactcgg ggctccttta aggggtccnaa 480  
ttantggntt tacgggacct tgancccaaa aaaacttgat ttaggggnga aggggttcacg 540

<210> 316  
<211> 513  
<212> DNA  
<213> Homo sapiens

<220>  
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<220>  
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<222> (420)  
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<220>  
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<223> n equals a,t,g, or c

<220>  
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<222> (483)  
<223> n equals a,t,g, or c

<220>  
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<222> (496)  
<223> n equals a,t,g, or c

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cttatttttc atataaaaat ctaaatgtgt taataaatca ttccatacaa aagtacatta 180  
ttaaataaacc acattattaa aataaaaaaa aaaaaaaag ggccggccgct ctgaggatc 240  
ccaagcttac gtacgcgtgc atgcnacgtc atagctcttc tatagtgtca cctaaattca 300  
attcactggg ccgtcgtttt acaacgtcgg tgactgggaa aaccctggcg ttacccaact 360  
taatccgcct tgcagcacat ccccttttcg ccagctggcg taatagcgaa gagggccgcn 420  
ccgatcgccc ttccaacag ttgcgcgtgc tgaatggcga atgggacncg ccctgtancg 480  
ggngcattaa agcgcngcgg gtgtggtggt tac 513

<210> 317  
<211> 389  
<212> DNA  
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ggcgccgcgn tntanaggat ccaagcttac gtacgcgtgc atgcnacgtc ntagctcttc 120
tatagngtca cctaaattca attcactggc cgtcgtttta caacgtcgtg actgggaaaa 180
ccctggcggt acccaactta atcgccctgc agcacatccc cctttcgcca gctggcgtaa 240
tagcgaaanag gcccgccaccg atcgcccttc ccaacagttg cncagcctga atggcnaatg 300
ggacgcgccc tgtagcgccg cattaagcgc ggcgggtgtg gnggttacnc ncagcgngac 360
cgttacactt gccagcgcgc tagcgcccg 389
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<211> 388

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cgggtcgacc cagcggtccg gtnnanaccn atgngggggn agntctcngg nggnaaggaa 180  
aatcgtgcaa agaggnanta atgaatgtgg atcacgagga tancnntta gtgnaggaan 240  
tncatcgttt gggntntaaaa aatgctgatg gaaagttaan tgtgaaaatt ggggtcctct 300  
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tttgttttca agatgggtgtt atcttttgaa ttcttgataa atgactgttt ttttctgcct 120  
aatagtaact ggtaaaaaaa caaatgttca tatttattga ttaaaaatgt ggttgcttaa 180  
ttcctaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaagggcg gccgntctan 240  
aggatccaag cttacgtacg cgtgcatgcg acgtcatagc tcttntatag tgtcacctaa 300  
attcaattca ctggccgctg ttttacaacg tcgtgactgg gaaaaccctg gcgttaccca 360  
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<210> 320  
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<212> DNA  
<213> Homo sapiens

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cacgcgtccg natccccagt gtgagggttaa tgagcaaaat tggctcttgg ggcccttttt 120  
gtccaagccc cactgaaagg cctcttcaga aaactattat cttaaagcc ctactttaac 180  
tccttaattc cagcatacag ctaaaactgg atgtatatcc tggcaagtaa aggctgagga 240  
ctcctcttta ntcctcagat ctagataact catgacattt tatttgacca acatagcaca 300  
tgatgagata tcaaggtaat taaaatagca tgcttgaaaa aaaatacgta atctgtttca 360  
cctgtaactg ttaagccaa taaacttttc aaaattttaa aaaaaaaaaa aaggcgcgcc 420  
gctctagagg atccaagctt acgtacgcgt gcatgcgacg tcatagctct tctatagtgt 480  
cacctaaatt caattcactg gccgtcggtt tacaacgtcg tgactgggaa aaccctggcg 540  
ttaccctaact taatcgctt gcagcacatn cccctttcgc agctggcgta atancnaaga 600  
ggcccnaccg atcgcccttt ccaacagttg cgcagcctga atggcgaatg ggacgcgccc 660  
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<210> 321  
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<212> DNA  
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ggggataagc ccttaggcac cagcttagac acctncaaga accaggcccc gctgatgcaa 180  
ganggcagan cngataccca tnagagcccc gagaat 216

<210> 322  
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<212> DNA  
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agaagcctcc ccgaccccc aagctatttg ctcacattaa caaattaaag tgcctgaagc 180  
ataattcatt ctttacctgt atactaaaaa ccctgttgta ttgatttttt tataataagc 240  
ctttttacct ctgtgtaaaa aatataatata caagtgtatg atgtanattt tagttcttaa 300  
ctttttttta tggtttctaa tatgtatgac caatgtagcc attgctttta aatgtaccgt 360  
gtaaatataa acacatccta tcagaaaaaa aaanaaaaaa gggcgggccgc tctanaggat 420  
ccaagcttac gtacgcgtgc atgcgacgtc atagctcttc tatagtgtca cctaaattca 480  
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taatnnggcn ttgcngg 557

<210> 323  
<211> 145  
<212> DNA  
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<222> (145)

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<400> 323

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gcacgtcata gctcttctat agtgtcacct aaattcaatt cactggccgt cgttttacaa 120  
cgtcgtgact gggaaaaacnn tntan 145

<210> 324

<211> 353

<212> DNA

<213> Homo sapiens

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<223> n equals a,t,g, or c

<220>  
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<223> n equals a,t,g, or c

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ctccacctca atcacactac tccccatata tagcaacgta aaaataaaan gacagtttga 120  
acatacaaaa ccnaccocat tcctcnccac actcatcgcc cttaccacgc tactcctacc 180  
tatctcccc tttatactaa taatcttata aaaaanaana aaaangggcg gncgntctag 240  
aggatccaag cttacgtacg cgngcatgcg acgtcatagc tcttctatag ggtcacctaa 300  
attcaattca ctggcgcgctg tttacaacg tngngactgg gaaaaccng gcn 353

<210> 325  
<211> 553  
<212> DNA  
<213> Homo sapiens

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<220>  
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<222> (381)  
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<220>  
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<222> (406)  
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<222> (481)

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<400> 325

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tcactgcagt ctcaaccttc cggactcaag tgatgggtccc gcttcagcta cttgggaggc 120
tgaggcagga gaatcgcttg aaccggggag gcggaggttg cggggagccg ggattgtgcc 180
actgcactcc accctagagt gagactccct ctcaaaaaaa aaaaaaaa actcgagggg 240
gggcccggta cccaattcgc cctatagtga gtcgtattac aattccactg gccgtcgttt 300
tacaacgtcg tgaactggaa aaccctgggc gttacccaac ttaaatcgcc ttgcagcana 360
tcccctttcg ccagctgggt naattagcga agaggcccg accgantcgc cttcccaaca 420
gttgcgcagt ggaatggcga atggcaantg taagcttaaa ntttgtttaa aattcgcggt 480
naaatTTTTg gttaaatacag ctcatTTTTt aancataagg ccgnaatcgg gaaaatccct 540
tattaaatcc aaa                                     553
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<210> 326

<211> 628

<212> DNA

<213> Homo sapiens

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<220>  
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atcattgcta gaactgagag accagcctgg ctagaacttc agggcggtcc attcattctt 120  
tcagtaaatg tttgcagcac atgtgttaca tgtcaggcag tgaaaccccc cacagcagcc 180  
ttccctctca gaggatacat ttgtaacctat tacacagtca tcagaggaat aatttttttt 240  
aatcaccagt gtgcacacag tcatggagtt gggatttccc agctaccagg gaggctgagg 300  
tgggaggatt gcttgatgcc aggagttagg gaatatagt caccgtgatt ggacttgcca 360  
atagccactg cactgcggcc tggacgacgt agtgataccc tgactcttat aaataaataa 420

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atgaataaac acannanaaa aaaaaaaggg cgcccgctct agangatcca agcttacgta 480
cgccgtgcat gcgacgtcat aactcttcta taggggcacc taaattcaat tcaactggccc 540
gccgtttaca acgtctgact gggaaaaccc tggcgttacc caacttaatc gnettgcaga 600
anacccccctt ttnccaactg gnggnata 628
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<210> 327

<211> 416

<212> DNA

<213> Homo sapiens

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gggtgtgattt acttatgtaa attatgtaca aatttaagtt caatgaaaca ctgatttaaat 120  
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tattatcttc aatattagaa taaatgctaa attattttca aaaaaaaaaa aaaaaaaaaa 240  
aaaaaaaaaa gggnggangn tctanaggat ccaagcttac gtacncgtgc atgcaangnn 300  
atagntcttc tatagtgtca cctaaattca attnactggc cgtcgattna caacgtcgtg 360  
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nattttccac ccgggtgggg taccaggtaa gtgtacccaa ttcgccctat agtgagtcgt 360  
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aacttaatcg ccttgacgca catccccctt tcgccagctg gcgtaatan gaaaaaggcc 480  
gcancgatcg cccttcccaa cagtttgccg ancctgaaat ggcgaatgga aatcaatttt 540

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aattcactgg ccgtcgtttt acaacgtcgt gactgggaaa accctggcgt taccctaactt 180  
aatcgccctt cagnacatcc ccctttcgcc agatggcgta atagcnaaaa ggccccgcnc 240  
gatcgccctt cccaacagtt gngcagntctg aatggcnaaa gggangcgcc ctgtngcggc 300  
gcattaagcg cggcgggtgt ggtggttacg cnnagggtna ccgctncact tnccancgcc 360  
ctagegcccg gncctttcgn tttcttccct tcctttctcg ccacnttcgc cggntttccc 420  
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tgggaaaacc ctggcggtac ccaacttaat cgccttgacg cacatcccc tttcgccagc 240  
tgggcgaata gcgaaaaggc cgcaccgat cgccttccc aacagttgag cagcctgaat 300  
ggcgaatggg acgcgcctg tancggngca ttaagcgagg cgggtgtggt ggttacgcgc 360  
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agtcactggc tgcaacaggg ccacagtcaa gacgatgcat agtcactgag ctaagtccag 180  
tagtagcaaa gcccctaaatc aaagccagca agaccacagt cacaggagat taaggactct 240  
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tcaaaaaacc aggggtnttc ccgtcctnng ggggnttnga aggtttntcc ccnggggnaa 360  
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tctgcatttc gggaagaccg gcagctcagg accactccaa tgaccacact aacaagatga 180  
atgaagttac ttatnctacc ctgaactttg aagnccanca acccacacaa ccaacttcag 240  
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gcaacatcat cctggacttc cctgcagctg ggtcaacttg cccgagggat gtgcagaatg 240  
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acctgggaat gaatggtact tgaacatctg ggcttgncag ccacaaggaa aggccaancc 360  
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tactaagggt actgctgctg ctgctgctgc tgctgctgct gctgctaaan tccancnaaa 180  
aanatcaccg ccganttaa aagntccncc caaaagtcct gcccaaaaan cccaggccaa 240  
aaacacgctg ctccaaactc anaggtcaaa actcncccaa aaccctctcc aangctctgc 300  
aaaaagctta ttgcatcnta aaattataag gtctnn 336

<210> 337  
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<220>

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<222> (267)  
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tgananngan aactcagtag aagataatgg caagtccaga ctggggatat gatgacaaan 120  
atggtcctga acaatggagc aagctgtatc ccattgccaa tggaaatnac cagtcccctg 180  
ttgatattnn gnccagtga accaaacatg acacctctct ganacctatt agtgtctcct 240  
acaacccanc cacagnnaaa gaaattntcc aatgtggggg cattccttcc atgtaaaatt 300  
ttg 303

<210> 338  
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<212> DNA  
<213> Homo sapiens

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<220>  
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<222> (433)  
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<220>  
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ttcagaaaaa gaaaactcag tagaagataa tggcaagtcc agactgggga tatgatgaca 120  
aaaatggtcc tgaacaatgg agcaagctgt atcccattgc caatggaaat aaccagtccc 180  
ctgttgatat taaaaccagt gaaaccaaac atgacacctc tctgaaacct attagtgtct 240  
cctacaaccc agccacagcc aaagaaatta tcaatgtggg gcattccttc catgtaaatt 300  
ttgaggacaa cgatnaccga tcaagtgtg aaaggtgggc ctttctctga cagctcaggc 360  
tctttcagtt ccattttcac tggggcagtc aaaatgagca tgggttaana acattccagt 420  
ggnntgggag tcnaaatatt ctggccgagc ttnacgtaa 460

<210> 339  
<211> 416  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> n equals a,t,g, or c

<400> 339

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ggcaaacaca acggacctaa gcactggcat aaggacttcc ccattgccaa gggagagagc 120  
ccagtncccc tgttganatc gacactncat acagccaagt ntgaaccctt ccntgaaagc 180  
ccctgtttgt ttccatgaa tcaagcaact tccctgagga tcctcaacaa tggcatgct 240  
ttcaacgtgg gagtttgnat gactctnnag gacaaagcag tgcttcaagg gaaggacccc 300  
tgggttgggc actttacaga ttggttttca ttttttcaat tttcaatggg ggtttcaatt 360  
tgatgggaca aggtttcnga ggcataattg tgggttaaaa agnaatntgg ntgcng 416

<210> 340

<211> 362

<212> DNA

<213> Homo sapiens

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<220>

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<222> (76)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (117)

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<220>

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<222> (201)

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<222> (204)

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<220>

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<222> (233)

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<222> (332)

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<222> (335)

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<222> (338)

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<222> (339)

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<220>

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<222> (357)

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<400> 340

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ataccaggtc aaacanttgc acctgcactg gtccgacttg ccatataagg gctcggngca 120  
cagcctcgaa tgggngcac ttgtccatgg gagatgcaca tagtacatgn gaaaagagaa 180  
ggggacatcg aggaatgtga naanagggcc caggaaacct gaagacgaaa ttncggtgct 240  
gggccttttt ggtgggaggc tgggaaccca ggtgaaacga gggctttcca gccactggtg 300  
ggaggcactn tcttaatat ccccaaacct nnggntgnng cattacgatt ggcaganagg 360  
ca 362

<210> 341

<211> 328

<212> DNA

<213> Homo sapiens



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<220>  
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<223> n equals a,t,g, or c

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<220>

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<220>  
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<400> 341  
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gancgtgttg cctctgccga ctttcagcct gtccctanca ttgttgggtg caacaacaat 120  
gaattcgggt ggctcatccc caaggtcatg angatctatg ataccagaa ngaaatggac 180  
aganangcct ccangctgc tctgcagaaa atgttaacgc tgctgatttg cctcctacat 240  
ttggtgacct gctgaaggaa gaattcattt gggganaatn gggatcccca aaacccccaa 300  
acncatttcc nggaaaataa ttgcnгаа 328

<210> 342  
<211> 140  
<212> DNA  
<213> Homo sapiens

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<220>  
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<223> n equals a,t,g, or c

<220>  
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<223> n equals a,t,g, or c

<400> 342  
aangggactt nccagtgatg cacccaagag ctntttatcc ccaacatcac tgtgaataat 60  
aggggatccn atncgtgcc agcccataac tctacactgg ccttaatagg agcacagtca 120  
cgaatatcnn agtctatgcn 140

<210> 343  
<211> 477  
<212> DNA  
<213> Homo sapiens

<220>  
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<400> 343  
gggacagcag agctgacagt cacagcagcc ctgacaagag agttcctgga gcccaagctc 60  
ttctccacag aggacaagca ggcagcagag accatgggggt ccccttcagc ctgtccatac 120  
agagtgtgca ttccctggca ggggctcctg ctcacagcct cgcttttaac cttctggaac 180  
ctgccaacaac gtgcccagac caatattgat gtcgtgccgt tcaatgtcgc agaaggggaag 240

gaggtccttc tagtagtcca taatgagtc cagaatcttt atggctacaa ctggtacaaa 300  
ggggaaaggg tgcattgcaa ctatcgaatt ataggatatt gtaaaaaata taagtcaaga 360  
aaatgcccac ggcccacac aacgtcgaga gacatntacc caatggaacc ttgtgttcca 420  
nacgtaccac atgncagga ttttctccta ctataaaana aanttgatg agaatac 477

<210> 344

<211> 389

<212> DNA

<213> Homo sapiens

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<220>  
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<400> 344  
nnnnnnnnnt ntcgcacgnc nngccagcca anccntcact aaaggggaaca aaagctggag 60  
ctccaccgcg gtgcgaccgc tctagaacta gtggatcccc cgggctgcag gaattcggca 120  
cgaggccggc cggggctggc acgnncgccg cggcggggnc tggaggcgcg accgggccc 180  
cccgagcggg aatcagaacg ncgccgaggg gaccagatca acgccagcaa gaacgaggag 240  
gacgcgggaa aaatgttcgt tgggtggcctg agctgggata ctagcaaaaa agatttataa 300  
gactatttta ctaaatttgg agaggtcgtt gactgtacaa taaaaatgga tcccaacact 360  
ggacgggtcaa gaggggttng gtttatcct 389

<210> 345  
<211> 152  
<212> DNA  
<213> Homo sapiens

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<220>  
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<222> (34)  
<223> n equals a,t,g, or c

<220>  
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<222> (42)  
<223> n equals a,t,g, or c

<220>  
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<222> (48)  
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<220>  
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<223> n equals a,t,g, or c

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<222> (64)  
<223> n equals a,t,g, or c

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<223> n equals a,t,g, or c

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<222> (87)  
<223> n equals a,t,g, or c

<220>  
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<223> n equals a,t,g, or c

<400> 345  
tcgacccacg ngtcgggggc gcaccatggc ccgnggggct gngctggngc tgctgctctt 60  
nggncgtgctg ggtgttcttg tcgncgncgc ggatggtggt ttcgatttat ccgatgccct 120  
tcttgacaat gaaaacaaga aaccactgc aa 152

<210> 346  
<211> 634  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (32)  
<223> n equals a,t,g, or c

<220>  
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<222> (38)  
<223> n equals a,t,g, or c

<220>  
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<222> (284)  
<223> n equals a,t,g, or c

<220>  
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<222> (491)  
<223> n equals a,t,g, or c

<220>  
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<222> (586)  
<223> n equals a,t,g, or c

<220>  
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<222> (588)  
<223> n equals a,t,g, or c

<220>  
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<223> n equals a,t,g, or c

<220>  
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<222> (613)  
<223> n equals a,t,g, or c

<220>  
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<223> n equals a,t,g, or c

<400> 346  
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catatcccaa gtcattctcag aaattgatgg taacaggatg accttgagcc aagaaggagc 120  
acaagattcc ttccctcttc agcagaagat cttgggtttgc tctttgatgc tcttgatcag 180  
gcagttgaaa atcaaagagg tcaactctggg gaagtatat gaagcctaca gtaaagtctg 240  
tcgcaaacag caggtggcgg ctgtggacca gtcagagtgt ttgncacttt cagggtcttt 300  
ggaagccagg ggcatttttag gattaaagag aaacaaggaa acccgtttga caaagggtgtt 360  
tttcaagatt gaagagaaaag aaatagaaca tgctctgaaa gataaagctt taattggaaa 420  
tatcttagct actggattgc cttaaattct tctcttacac cccaccgaa agtattcaag 480  
ctggcattta nagagctaca ggcttcattt taaggcttta cacattcggg cctgaaaaca 540  
aatatgacct tttttacttg aagccaatga attttaatct atagancntt aaaattanca 600  
cagaataata tcnttggggc ntactatttt accc 634

<210> 347  
<211> 363  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (228)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (233)



<223> n equals a,t,g, or c

<220>  
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<222> (242)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (268)  
<223> n equals a,t,g, or c

<220>  
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<222> (319)  
<223> n equals a,t,g, or c

<220>  
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<222> (322)  
<223> n equals a,t,g, or c

<220>  
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<222> (323)  
<223> n equals a,t,g, or c

<220>  
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<222> (324)  
<223> n equals a,t,g, or c

<220>  
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<222> (325)  
<223> n equals a,t,g, or c

<220>  
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<222> (328)  
<223> n equals a,t,g, or c

<400> 347  
ggcacgagag gaatatggag aggctgactc ttgcttggtg tggggtggcc ctgaattcctt 60  
ttgaggacct aagtcctgac tgcttgggac atgcaggact tgtatatgag tatacattgg 120  
gagaagttca cctttattga gaagtgtaac aaccctcgtt ctatcacatt attgatcaaa 180  
ggaccaaata agcccacact tagatcaaag atgcagtaaa gggatgggct tgnagggctg 240  
tncaaaaatg ctgttgatga tggctgtntg gttccgggtg ctggtgctgt ggaagtggca 300  
atggcagaag ccctggatna annnnaantc catgtaaagg gcaaggcaca gttgggggtcc 360  
agc 363

<210> 348  
<211> 388  
<212> DNA  
<213> Homo sapiens

<220>  
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<220>  
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<222> (339)  
<223> n equals a,t,g, or c

<220>  
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<222> (344)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (364)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (382)  
<223> n equals a,t,g, or c

<400> 348  
aatcggcac gagctgaagg ctagcaaacc gagcgatcat gtcgcacaaa caaatttact 60  
attcggacaa atacgacgac gaggagttag agtatcgggt agtgctggcg cgggagcaat 120  
agcgaagggtc gtgagctttg gccgctgagg gcacaaggaa ttagtaacag gaactgaggc 180  
gatagaattg gcgcatgcgt atganacatg tcatgctgcc caaggacata gccaaagctgg 240  
tccctaaaac ccattctgatg tctgaatctg aatggaggaa tcttggcgtt cagcagagtc 300  
agggatgggt ccattatatg atccatgaac cagaacctna aatnttgctg ttccggggcc 360  
attnccagga accaaggaat tnagtttc 388

<210> 349  
<211> 194  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc feature  
<222> (38)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature

<222> (51)  
<223> n equals a,t,g, or c

<220>  
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<223> n equals a,t,g, or c

<220>  
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<222> (60)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (67)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (69)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (74)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (83)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (91)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (124)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (127)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (140)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (180)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (191)

<223> n equals a,t,g, or c

<400> 349

gagttgttgc ctgggctgga cgtgggttttg tctgctgngc ccgctcttag ngetctngtn 60  
taatttnang cagngcgcca gcnggatggt ncacaagcag atatactact cggacaagta 120  
cttngangaa cactacgagn accgggatgg tatgttacc agagaacttg acaacaagn 180  
acctaaaact natc 194

<210> 350

<211> 524

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (9)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (11)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (14)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (17)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (29)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (85)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (98)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (101)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (148)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (240)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (258)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (484)

<223> n equals a,t,g, or c

<400> 350

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ttaacctnt naanggnaca aagtctggnt ctccaccagg tggaggaccg ctccctagcaa 60
ctagtgggtc ccccgggcct gcagnaattc ggcagtgncg naaagcccta cggcgtcact 120
gcaatgtgct ggaactggga gcaagtgnca gcggctggac ggcattcctga gtcgagacca 180
ttccgattca cgggcgcggc aacttcccca cgctcgagct gcagccgagc ctgtatcgtg 240
aaggtggtgc ggcggcggnct tgccgagaag cgcctcggcg tccgcgacgt gcgcctcaac 300
ggctcggcag ccagccatgt cctgcaccag gacagcggcc tgggctacaa ggacctggac 360
ctcatcttct gcgccgacct gcgcggggaa ggggagtttc agactgtgaa ggacgtcgtg 420
ctggactgcc tgttggactt cttacccgag ggggtgaaca aagagaagat cacaccactc 480
acgntcaagg aagcttatgt gcagaaaatg gttaaagtgt gcaa 524
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<210> 351

<211> 352

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (21)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (261)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (291)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (295)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (328)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (348)

<223> n equals a,t,g, or c

<400> 351

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ccttgcttaa tcgtagctgc aaagtcagac ctgcatgaag ttaaacaaga atacagtatt 120
tcacctactg atttctgcag gaaacacaaa atgcctccac cacaagcctt cacttgcaat 180
actgctgatg cccccagtaa ggatatcttt ggtaaattga caacaatggc catgtatccc 240
catgcccgtg tacgctgtat ntgcacctgc aacagggtga cattttgcat ntgtnaaaac 300
ttctcgaact tatactttgc tgcaaatntg gtaaaagaac aaaaatcntt tc 352
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<210> 352

<211> 632

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (3)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (4)

<223> n equals a,t,g, or c

<220>

<221> misc feature  
<222> (8)  
<223> n equals a,t,g, or c

<400> 352  
agnnaganac caaccctcac taaaggaac aaaagctgga gctccaccgc ggtgcggccg 60  
ctctagaact agtgatccc ccgggctgca ggaattcggc acgaggtgtg tcagaacaat 120  
cttgaatcat gaagctacta accagagccg gctctttctc gagattttat tccctcaaag 180  
ttgccccaa agttaaagcc acagctgccc ctgcaggagc accgccacaa cctcaggacc 240  
ttgagtttac caagttacca aatggcttgg tgattgcttc tttggaaaac tattctcctg 300  
tatcaagaat tggtttgttc attaaagcag gcagtagata tgaggacttc agcaatttag 360  
gaaccaccca tttgctgctt cttacatcca gtctgacgac aaaaggagct tcattcttca 420  
agataaccgc tggaaattgaa gcagttgttg gcaaattaag tgtgaccgca acaagggaag 480  
acatggctta tactgtggaa tgcctgcggg gtgatgttga tattctaag gagttcctgc 540  
tcaatgtcac cacagacca gaatttcgtc gttgggaagt agctgacctt cagcctcagc 600  
taaagattga caaagctgtg gcctttcaga at 632

<210> 353  
<211> 440  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc feature  
<222> (435)  
<223> n equals a,t,g, or c

<400> 353  
ctttaactcc accattagca cccaaagcta agattctaatt ttaaactatt ctctgttctt 60  
tcattgggaa gcagatttgg gtaccaccca agtattgact caccatcaa caaccgctat 120  
gtatttcgta cattactgcc agccaccatg aatattgtac ggtaccataa atacttgacc 180  
acctgtagta cataaaaacc caatccacat caaaaccccc tccccatgct tacaagcaag 240  
tacagcaatc aaccctcaac tatcacacat caactgcaac tccaaagcca cccctcacc 300  
actaggatac caacaaacct acccaccctt aacagtacat agtacataaa gccatttacc 360  
gtacatagca cattacagtc aaatcccttc tcgtcccat ggatgacccc cctcagatag 420  
gggtcccttg accancatcc 440

<210> 354  
<211> 609  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc feature  
<222> (3)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (5)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (8)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (11)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (139)  
<223> n equals a,t,g, or c

<400> 354  
aanncnganac naaccctcac taaagggaac aaaagctgga gctccaccgc ggtgcggccg 60  
ctctagaact agtggatccc ccgggctgca ggaattcggc acgagccgga ggggtgtgtgt 120  
tgggcaaaagc cggaggagna ggaggacgat tgttttacgg atcccgatgat cggcccgctcc 180  
ttctccctct tccccctcc ctaccgcccc tgtcccgccg gggagcggcg gcggccttg 240  
actttgctgt ctttcctcgc ggagacagat ttcaacacta cacttgcaca atgtctttga 300  
aaccaagagt agtagatttt gatgaaacat ggaacaaaact ttgacgaca ataaaagccg 360  
tggtcatggt ggaatacgtc gaaagagcaa catggaatga ccgtttctca gatattctatg 420  
ctttatgtgt ggcctatcct gaacccttg gagaaagact ttatacagaa actaagattt 480  
ttttggaaaa tcatgttcgg catttgcata agagagtttt ggagtcagaa gaacaagtac 540  
ttgttatgta tcataggtac tgggaagaat acagcaaggg tgcagactat atggactgct 600  
tatataggt 609

<210> 355  
<211> 466  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc feature  
<222> (348)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (368)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (450)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature



<222> (451)

<223> n equals a,t,g, or c

<400> 355

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gctccattat tgatcgggtc atgcagaata attgtgtgcc caagaagatg ctgcagctgg 60
ttggtgtcac tgccatgttt attgcaagca aatatgaaga aatgtaccct ccagaaattg 120
gtgacttttc ttttgtgact gacaacactt atactaagca ccaaatcaga cagatggaaa 180
tgaagattct aagagcttta aactttggtc tgggtcggcc tctaccttg cacttccttc 240
ggagagcatc taagattgga gaggttgatg tcgagcagca tactttggcc aaatacctga 300
tggaactaac tatgttggaac tatgacatgg tgcactttcc tccttctnaa attgcagcag 360
gagctttntg cttagcactg aaaattctgg gataatggtg aatggttatg cagcacctgg 420
ctaagaatgt agtcatgggt aaatcaaggn nttacaaagc acatgc 466
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<210> 356

<211> 447

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (269)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (375)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (380)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (436)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (440)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (446)

<223> n equals a,t,g, or c

<400> 356

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ggtgatgagg aggcttgtcc agaggacaag ggaccccagg acccacaggc actggcgctg 60
gacaccaga tccctgcaac ccctggaccc aaaccctgg tccgcaccag ccgggagcca 120
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gggaaggacg tcacgacctc aggttactcc tccgtcagca ccgcaagtc cacaagctcc 180  
gtggacggtg gcttgggggc cctgcccaca cctacctcag tgctgtccct ggacagtgc 240  
tcgcacacac agccctgccca ccatcaggnc aggaagtcac gtttacagtgc tcgtccccc 300  
agtcccccgc agagcagtggt tccccagcaa caggtgaagc ggataaacta tgcatacaca 360  
gtgaagagga ggacntgaan ctgggcttgt gaagctgtaa gtgtgtcagc acatttgcgc 420  
agtggatttt actgangggg tgaagng 447

<210> 357

<211> 510

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (2)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (453)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (486)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (491)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (496)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (500)

<223> n equals a,t,g, or c

<400> 357

tnccacgcgt ccgcccacgc gtccgcccac gcgtccgcag attccctccg tcgcccgc 60  
gatgatgtgc ggggcgccct ccgccacgca gccggccacc gccgagacc agcacatgc 120  
cgaccagggt aggtcccagc ttgaagagaa agaaaacaag aagttccctg tgtttaaggc 180  
cgtgtcattc aagagccagg tggtcgcggg gacaaactac ttcataaagg tgcacgtcgg 240  
cgacgaggac ttcgtacacc tgcgagtggt ccaatctctc cctcatgaaa acaagccctt 300  
gaccttatct aactaccaga ccaacaaagc caagcatgat gagctgacct atttctgac 360  
ctgactttgg acaaggccct tcagccagaa gactgacaaa gtcacccctc gtctaccaga 420  
gcgtgcactt gtgacccata aataagcttc atntccgggc tgtgccccctt ggggtggaag 480

gggcangatt ntgcantgn ttttgcattt

510

<210> 358

<211> 240

<212> DNA

<213> Homo sapiens

<400> 358

ggtcttgac tcatgagctg tccccacatt aggcctaaaa acagatgcaa ttcccggacg 60  
tctaaaccaa accactttca ccgctacacg accgggggta tactacggtc aatgctctga 120  
aatctgtgga gcaaaccaca gtttcatgcc catcgtccta gaattaattc ccctaaaaat 180  
ctttgaaata gggcccgat ttaccctata gcacccctc tacctcctct agagccaaaa 240

<210> 359

<211> 340

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (320)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (331)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (334)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (335)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (338)

<223> n equals a,t,g, or c

<400> 359

ggcagagct cataaggaaa tctacccta tgtcatccag gaacttagac caactttaa 60  
tgaactggga atctccactc cggaggaaact gggccttgac aaagtgtaaa ccgcatggat 120  
gggcttcccc aaggatttat tgacattgct acttgagtgt gaacagttac ctggaaatac 180  
tgatgataac atattacctt atttgaacaa gttttccttt attgagtacc aagccatgta 240  
atggtaactt ggactttaat aaaaaggaaa tgagtttgaa ccggaaaaaa aaaaaaaaaa 300  
aaaaaaaaa aaagaaaaan aaagaaggga nagnnaanaa 340

<210> 360  
<211> 501  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc feature  
<222> (147)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (148)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (192)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (242)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (244)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (348)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (364)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (384)  
<223> n equals a,t,g, or c

<220>  
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<222> (455)  
<223> n equals a,t,g, or c

<220>

<221> misc feature  
<222> (465)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (469)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (474)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (491)  
<223> n equals a,t,g, or c

<400> 360  
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taacaggggc cctctcagcc ctccaatga cctccggcct agccatgtga tttcacttcc 120  
actccataaa gctcctcata ctaaggnta ctaaccaaca cactaaccat ataccaatga 180  
tggcgcgatg tnacacgaag aaagcacata ccaagggcac cacacaccac ctgtccaaaa 240  
angncttcga tacgggataa tcctatttat tacctcagaa gtttttttct tcgcaggatt 300  
ttctgagctt ttacactcca gcctagccct acccccaact aagaaggnaac tggccccaac 360  
aagnatcacc cgctaaatcc ctanaatcca ctccataaca ctccgtatat cgatcaggat 420  
atcatcactg actcacatat ctaatagaaa aaacngaaac aatantcanc atgnttatta 480  
aatttatggt ntctatttac c 501

<210> 361  
<211> 393  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc feature  
<222> (357)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (359)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (364)  
<223> n equals a,t,g, or c

<220>

<221> misc feature  
<222> (367)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (390)  
<223> n equals a,t,g, or c

<400> 361  
gccccattat tcctagaacc aggcgacctg cgactccttg acgttgacaa tcgagtagta 60  
ctcccgattg aagcccccat tcgtataata attacatcac aagacgtctt gcactcatga 120  
gctgtcccca cattaggctt aaaaacagat gcaattcccg gacgtctaaa ccaaaccact 180  
ttcacogcta cacgaccggg ggtatactac ggtcaatgct ctgaaatctg tggagcaaac 240  
cacagtttca tgcccatcgt cctagaatta attcccctaa aaatctttga aataggggccc 300  
gtatttacct tatagcacc cctctacccc ctctagagcc aaaaaaaaaa aaaaagntnc 360  
aagnttnaaa aaactgaaaa tcagaaaaagn ttt 393

<210> 362  
<211> 664  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc feature  
<222> (308)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (535)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (551)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (567)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (642)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (660)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (662)

<223> n equals a,t,g, or c

<400> 362

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acgccctcat aatcattttc cttatctgct tcctagtccct gtatgccctt ttcctaacac 120
tcacaacaaa actaactaat actaacatct cagacgctca ggaaatagaa accgtctgaa 180
ctatcctgcc cgcacatcc tagtcctcat cgcctccca tccctacgca tcccttacat 240
aacagacgag gtcaacgac cctcccttac catcaaatca attggccacc aatgggtactg 300
aacctacnaa gtacaccgac tacggcggac taatcttcaa ctctacata cttccccatt 360
attcctagaa ccaggcgacc tgcgactcct tgacgttgac aatcgagtag tactcccgat 420
tgaagcccc attcgtataa taattacatc acaagacgct ttgcactcat gagctgtccc 480
cacattaggc ttaaaaacag atgcaattcc ccgacgtcta aaccaaacca ctttnaccgg 540
tacacgaacc nggggtatta ctacggncaa tgctctgaaa tctggggagc aaaaccacag 600
gttcatgccc atcgtccctag aaataaatc ccctaaaaat cnttgaaaaa aggggcccgn 660
antt 664
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<210> 363

<211> 595

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (466)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (467)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (485)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (515)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (552)

<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (557)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (559)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (568)  
<223> n equals a,t,g, or c

<400> 363  
gcgcaagtag gtctacaaga cgctacttcc cctatcatag aagagcttat cacctttcat 60  
gatcacgccc tcataatcat tttocttata tgcttccctag tcctgtatgc ctttttccta 120  
acactcacaa caaaactaac taataactaac atctcagacg ctcaggaaat agaaaccgtc 180  
tgaactatcc tgcccgcctat catcctagtc ctcacgcgcc tcccatccct acgcatcctt 240  
tacataacag acgaggtcaa cgatccctcc cttaccatca aatcaattgg ccaccaatgg 300  
tactgaacct acgagtacac cgactacggc ggactaatct tcaactccta catacttccc 360  
ccattattcc tagaaccagg cgacctgcga ctccttgacg ttgacaatc gagtagtact 420  
cccgattgaa gccccattc gtataataat tacatcacaa gacgtnnttg cactcatgag 480  
ctgtncccac attaaagctta aaaacagatg cattnccgga cgtctaaacc aaaccacttt 540  
caccgatata cnaaccngng ggtatacnac cggccaatgc ttctgaaatc ttgtg 595

<210> 364  
<211> 441  
<212> DNA  
<213> Homo sapiens

<400> 364  
acaagacgct acttccccta tcatagaaga gcttatcacc ttctatgatc acgccctcat 60  
aatcattttc cttatctgct tcctagtccct gtatgccctt ttcctaacac tcacaacaaa 120  
actaactaat actaacatct cagacgctca ggaaatagaa accgctctgaa ctatcctgcc 180  
cgccatcatc ctagtccctc tcgccctccc atccctacgc atcctttaca taacagacga 240  
gggtcaacgat cctcccttt accatcaaat caattgggcc accaatggta ctgaacctac 300  
gagtacaccg actacggcgg actaatcttc aactcctaca tacttcccc attattccta 360  
gaaccaggcg acctgcgact ccttgacgtt gacaatcgag tagtactccc gattgaagcc 420  
cccattcgta taataattaa c 441

<210> 365  
<211> 367  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc feature  
<222> (347)  
<223> n equals a,t,g, or c



<220>  
<221> misc feature  
<222> (362)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (363)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (366)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (367)  
<223> n equals a,t,g, or c

<400> 365  
catacttccc ccattattcc tagaaccagg cgacctgcga ctcccttgacg ttgacaatcg 60  
agtagtactc ccgattgaag cccccattcg tataataatt acatcacaag acgtottgca 120  
ctcatgagct gtccccacat taggcttaaa aacagatgca attcccggac gtctaaacca 180  
aaccactttc accgctacac gaccgggggt atactacggt caatgctctg aaatctgtgg 240  
agcaaaccac agtttcatgc ccatcgtcct agaattaatt cccctaaaaa tctttgaaa 300  
tagggcccggt atttacccta tagcaccccc tctaccacct ctagagncaa aaaaaaaaaa 360  
annagnn 367

<210> 366  
<211> 460  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (51)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (154)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (211)  
<223> n equals a,t,g, or c

<220>

<221> misc feature  
<222> (322)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (336)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (340)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (355)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (356)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (378)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (411)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (413)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (415)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (453)  
<223> n equals a,t,g, or c

<400> 366  
ttttcgaggc caacgatccc tcccttacca tcaaatcaat tggccaccaa nggtaccgaa 60

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cctacgagta caccgactac ggcggactaa tcttcaactc ctacatactt cccccattat 120
tcctagaacc aggcgacctg cgactccttg acgntgacaa tcgagtagta ctcccgattg 180
aaacccccat tcggataata attacatata nggacgtctt gcactcatga gctgccccac 240
attaggctta aaaacagatg caattcccgg acgtctaaac caaaccacta tcaccgctac 300
acgaccgggg gtatactacg gncaatgctc tgaaanctgn ggagcaaacc acagnntcat 360
gcccatcggc ctagaatnaa tccccctaaa aatctttgaa atagggcccc nanthaccct 420
atagcaccce ctctaccccc tctagagcca aanaaaaaaa 460
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<210> 367

<211> 610

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (6)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (13)

<223> n equals a,t,g, or c

<400> 367

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gcaagntgac acnaaccctc actaaaggga acaaaagctg gagctccacc gcggtgcggc 60
cgctctagaa ctagtggatc ccccgggctg caggaattcg gcacgaggga atggcggctt 120
ccatctctga ggcgagcgac gctatggatc ccacagtggg ttgctaagaa ggccattttc 180
aactctccac tggaggctgc tatggcgctc cctcacctgc agcagcccag ctttctactg 240
gtagcctga aagctgactc tataaataag ccctttgcac agcagtgcc aagacttggt 300
aaagtcattg aggactttcc agcaaagtct gaaccaatca ggtccttgt gactggagca 360
gctggtcaaa ttgcatattc actgctgtac agtattggaa atggatctgt ctttggtaaa 420
gatcagatgt catcgcaaca gataaagaag acgttgcctt caaagacctg ggatgtggcc 480
attcttgtgg gctccatgcc aagaagggaa ggcatggaga gaaaagattt actgaaagca 540
aatgtgaaaa tcttcaaata ccagggtgca gccttagata aatacggcaa gaagtcagtt 600
aaaggttatt 610
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<210> 368

<211> 548

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (370)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (378)

<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (384)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (412)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (429)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (449)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (471)  
<223> n equals a,t,g, or c

<220>  
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<222> (490)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (495)  
<223> n equals a,t,g, or c

<220>  
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<222> (528)  
<223> n equals a,t,g, or c

<400> 368  
ggcacgagga gcactctatt tattgtactg tgaataatga tgaaggagag tggagtggcc 60  
caccacctga atgcagagga aaatctctaa cttccaaggt cccaccaaca gttcagaaac 120  
ctaccacagt aaatgttcca actacagaag tctcaccaac ttctcagaaa accaccacaa 180  
aaaccaccac accaaatgct caaggtacag agactccatc agttcttcaa aaacacacca 240  
cagaaaatgt ttcagctaca agaaccctac caactcctca gaaaccacc acagtaaatg 300  
tcccagctac aatagtca ccaacacctc agaaaccac cacattaatg ttccagttac 360  
aggagtctcn tcaacacntc aagnacacc tagtaatgtt tcagttacag gncctaccac 420  
ttttcganc ccaccgggc aatgttcgnc accattcccg cgcgttcggc ntttcttca 480  
aaaccttttn caagnccttt tgcgttagat cctgtggcat gttttgtnc cggcccttac 540  
ggccaggt 548

<210> 369  
<211> 538  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc feature  
<222> (12)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (423)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (449)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (466)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (521)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (531)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (538)  
<223> n equals a,t,g, or c

<400> 369  
gatggcgcgg anccgggacg cgcgtacgcc ctgctgcttc tcctgatctg ctttaacggt 60  
ggaagtggac ttcacttaca ggtcttaagc acaagaaatg aaaataagct gcttcctaaa 120  
catcctcatt tagtgcggca aaagcgcgcc tggatcaccc ccccccgtggc tcttcgggag 180  
ggagaggatc tgtccaagaa gaatccaatt gccaaagatac attctgatct tgcagaagaa 240  
agaggactca aaattactta caaatacact ggaaaaggga ttacagagcc accttttggg 300  
atatttgtct ttaacaaaga tactggagaa ctgaatgtta ccagcattct tgatcgagaa 360  
gaaacaccat tttttctgct aacagggtta cgctttggat gcaagaggga acaatgtaga 420  
ganacccttt agagctacgc attaagggnt cttgatatcc aattgncaac ggaaccagtg 480  
gttcacacag ggatgtcttt gttggggcct gttgaagagt ngaggtgcag nacatacn 538

<210> 370  
<211> 538  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc feature  
<222> (401)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (492)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (500)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (536)  
<223> n equals a,t,g, or c

<400> 370  
gagctcagtc cccatcccga agcacagggc aggacgtcgc ggcggagtgg ggaagcgagg 60  
agtcctgtgc cgggagcttg gaggctgagt ttgagaaagc tgcagaggag gttaggcacc 120  
ttaagaccaa gccatcggat gaggagatgc tggtcatcta tggccactac aaacaagcaa 180  
ctgtgggcca cataaataca gaacggcccg ggatgttga cttcacgggc aaggccaagt 240  
gggatgcctg gaatgagctg aaagggactt ccaaggaaga tgccatgaaa gcttacatca 300  
acaaagtaga agagctaaag aaaaaatacg ggatatgaga gactggattt gggtactgtg 360  
ccatgtgttt atcctaaact gagacaatgc cttgttttt nctaataccg tggatggtgg 420  
gaatccggga aaataaccag ttaaccagc tactcaaggc tgctcaccat acggtcttaa 480  
cagattaggg gntaaaacgn ttactgactt ccttgagtag ttttacctga aaccantt 538

<210> 371  
<211> 224  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc feature  
<222> (21)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (26)  
<223> n equals a,t,g, or c

<220>  
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<222> (48)  
<223> n equals a,t,g, or c

<220>  
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<223> n equals a,t,g, or c

<220>  
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<222> (68)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (90)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (108)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (113)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (123)  
<223> n equals a,t,g, or c

<220>  
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<222> (141)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (171)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (192)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (204)  
<223> n equals a,t,g, or c

<220>  
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<222> (215)  
<223> n equals a,t,g, or c

<400> 371  
gcctgtgcct acacaccacc ntcgcnagaa gctgtgcagc gcattgcnga gtctcaccng 60  
cagtc tanca gcaatttgaa tgagaaccan gcctcagagg aggagganga gcngggggag 120  
ctncggggagc tgggttatcc nagagaggaa gatgaggagg aagaggagga ngatgaagaa 180  
gaggaagact angaggacag ccangctgaa gaccngagcg gaga 224

<210> 372  
<211> 459  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc feature  
<222> (6)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (52)  
<223> n equals a,t,g, or c

<220>  
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<222> (90)  
<223> n equals a,t,g, or c

<220>  
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<222> (105)  
<223> n equals a,t,g, or c

<220>  
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<220>  
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<220>  
<221> misc feature  
<222> (208)  
<223> n equals a,t,g, or c

<220>  
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<222> (328)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (394)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (429)  
<223> n equals a,t,g, or c

<400> 372  
aacttnccca atgccgaact gggaggcccc tttaccaga tgaacggagt gnccggaaat 60  
ggcatgaaca acattgacat gactggagan aagaagtcgt tgganctccc atatcccagc 120  
agctttgtct ccgtctctnn acctagaaac cagaccttca cttacatggg caagtntctcc 180  
attgacctct agtacctctg tgccagcngc taccagaag gcataatcaa tattgtgagt 240  
gcaggcatct tgcaaggggt cacttcccca gcttcaacca cagcctcatc cagcgtcacc 300  
tctgcctccc ccaaccact ggccacanga cccctgggtg tgtgcacccat gtcccagacc 360  
cagcctgacc tggaccacct gtactctccg ccancgcctc ctccctctta ttctggctgt 420  
gcaggaganc tctaccagga cccttctgcg ttctgtta 459

<210> 373  
<211> 422  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc feature  
<222> (27)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (47)  
<223> n equals a,t,g, or c

<220>

<221> misc feature  
<222> (60)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (66)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (70)  
<223> n equals a,t,g, or c

<220>  
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<222> (78)  
<223> n equals a,t,g, or c

<220>  
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<222> (87)  
<223> n equals a,t,g, or c

<220>  
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<222> (105)  
<223> n equals a,t,g, or c

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<222> (267)  
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<222> (331)  
<223> n equals a,t,g, or c

<220>  
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<222> (351)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (359)  
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<220>  
<221> misc feature

<222> (393)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (401)  
<223> n equals a,t,g, or c

<400> 373  
ggcagacctg aggcccatcc ccaaggngcc cagccgtagc ttcaggntct ccgccagggg 60  
ccctcncggn tgcttctngt ttttaanact tccagatcga tectntcctc ggtaccgtgg 120  
gctttgggtc tggcctccac ggggtgggcct tcaccctgaa agcagtttgc cgagaatgta 180  
tgtgagccaa gttcgccgcc aagggggagg gccagttggg agcctgccga gcgggccaag 240  
aaagtagagg acatgatgaa gaagctntgg ggtgacaggt gagccccggg gaatatggtg 300  
ggggattcct gaaaactggg ggtagtggca ncaacgtagg ggcgtggtgt nctattcana 360  
attggttcaa gccacacaagt ttgcccaca atnttcctt ngggaccaac ttccaagta 420  
at 422

<210> 374  
<211> 342  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (4)  
<223> n equals a,t,g, or c

<220>  
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<222> (16)  
<223> n equals a,t,g, or c

<220>  
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<222> (17)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (20)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (24)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (292)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (301)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (305)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (325)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (332)

<223> n equals a,t,g, or c

<400> 374

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gcanaacatc agcgcnacn gganataaaa agattatcca cagagcattc cagtgtatca 60
gagtatcatc cagccgatgg ctatgcgttc agtagcaaca ttacacaag aggatccac 120
ctggaccaag gggaagctgc tgttgctttt aagccaactt ctaatcgcca tattagattg 180
aaattatgaa ccaactccaa acacaacca agaaatatgc ccaatcccag ttatgacttt 240
gtttgccagg ggaaacaaca gttgagctct ccgggttcct taaggaaatga tntttttaga 300
naatnccttg aatgaatcg gaaancatgg tngaaaaagt tt 342
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<210> 375

<211> 387

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (19)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (162)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (305)

<223> n equals a,t,g, or c

<220>

<221> misc feature  
<222> (335)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (365)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (366)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (374)  
<223> n equals a,t,g, or c

<400> 375  
ggcagagctc tgcgcgcant ccgcttgact cagctcaccg agattctgtc aggggggtgtt 60  
tatattgaga agaacgataa gctttgtcac atggacacaa ttgactggag ggacatcgtg 120  
agggaccgag atgctgagat agtgggtgaag gacaatggca gnaagctgtc ccccctgtca 180  
tgaggtttgc aaggggcgat gctgggggtcc tggatcagaa gactgccaga cattgaccaa 240  
gaccatctgt gcttcctcag tgaattggt cactgctttg gggcccaacc ccaaccagtg 300  
gttgncatga tgagtgtggc cgggggttgt ttcanggcc cttcaggac acagactgtt 360  
tttgnntggc cggnatattca atggaca 387

<210> 376  
<211> 492  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc feature  
<222> (110)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (203)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (318)  
<223> n equals a,t,g, or c

<220>  
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<222> (333)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (336)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (405)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (416)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (440)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (444)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (448)

<223> n equals a,t,g, or c

<400> 376

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ggcaccgagaa gcaaaactcaa agcatttggg tcaaaacatc ctgattgttt tatacatggt 60
ttggatgata aattcagtaa agatacaggc ataatcctta tatgcaaata agttgatggg 120
tattttctat ggtgatttca gacaaggaac ctgcagggtca ctctggaaga tggttacatt 180
gaattgagca ccagcgatag ggncggccca atttttaaat ctccacagac gtatatggat 240
ggtttactgc attatgtatc tgtaataaag gacaactctg ggtgagtcga ataaataactt 300
ctgtcagagc tgtgagtnga gttttactct ctnttngttt taatggaatt ttctggtgtc 360
tttttgcaaa aaatttgtcc ttgattacca aaaatacttt cactnataag tcttgnocct 420
ctttcctttt ttcccatatn caanttttct tcataaaaaa aataaaacttg ccacacatgg 480
gtgggcttca tt                                     492
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<210> 377

<211> 336

<212> DNA

<213> Homo sapiens

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cccgcntgtn tgtccccaga gccatggaga gagccagtct gatccagaag gccaanctgg 120  
cagagcaggc cgaacgctat gaggacatgg cagccttcat ganaggcgcc gtggagaagg 180  
gcgaggagtc tcctgcnaag agcgaaacct gctctcagta gcctatnana ncgtggtggg 240  
cggccagang gctgcctgga ggggtgctgc cagtattgan cagaaaagca angaggaggg 300  
gttcgganag gagaaggggc ccgangtgcg ttgaat 336

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tgccttgctc ggaagggggc gageggctgc tgcccaccca gaagcagccc gggggcggcc 120  
aggtaactc cagccgctac aagacggagc tgtgccgcc ctttgaggaa aacgggtgcct 180  
gtaagtaagg ggacaagtgc cagttcgac acggcatcca cgagctccgc agcctgaccc 240  
gccaccccaa gtacaagacg gagctgtgcc gcacctcca caccatcggc ttttgccct 300  
acggggcccg ctgccacttc atccacaacg ctgaagagcg ccgtgccctg gccggggccc 360  
gggacctctc cgctgaccgt ccccgccctc agcatagctt tagtttgctg ggtttcccag 420  
tgccgctgcc accgccgctg ccaccgggct gctggacagc ccacgtccat caacccaacc 480  
cctatttt 488

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gcantaacag ccaggagtcc aaaactactt acctggaaga ccttccacca cccctgagt 180  
atgaattggc cccgtccaag ttagaagagg aagtggatga tgtctttctc attcgagctc 240  
aaggactgcc ctgggtcatg gcactatggg aagatgtggc ttttaacttt tttttccaga 300  
cttgcagaat ccggcaacgg ttgagtaatg ggaattacat tttntccct aaaaacaaga 360  
gatgggggaa aacgtaaggg ggtnnntggc cttnaatt 398

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tcgtgtcccg ccccaccgag aaaaccgtct tcaccgtctt catgctagct gcctctggca 120  
tctgcatcat cctcaatgtg gccgaggtgg tgtacctcat catccgggcc tgtgcccgcc 180  
gagcccagcg ccgctccaat ccaccttccc gcaagggtc gggcttcggc caccgcctct 240  
cacctgaata caagcagaat gagatcaaca agctgctgag tgagcaggat ggctccctga 300  
aagacatact gcgcncaacc ctggcacggg ggctgggctg gctgaaaaaa acgaccgtgc 360  
tcggntgtga tgccacatac caggcaacct cccatccac cccgaccttg cctggggcga 420  
nccctccttc tccctgcccg tncccanng ctcac 455

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gggatcgact acaacccctg ggtggagttt gtgaantggc cagtgcgcat gacgtcgtga 180  
acttgggcca nggcttcccg gatttcccac caccagactt tgccgtggaa gcctttcagc 240  
acgctgtcag tggagacttc atgcttaacc agtacaccaa gacatttggt taccaccac 300  
tggacgagga tcctggcaat ttctttgggg gagctgctgg gtcaaggata agaccggttc 360  
agggatgtgc tggtgactgt tggtggnat gggggccngt ttcaaaagcn ttncaggcc 420  
n 421

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ctctagaact agtggatccc cggggctgca ggaattcggc acgagcggcg gcggcggcgg 120  
cggcccaagtc ggtgtatgcc ttctcggcgc gcccgctggc cggcggggag cctgtgagcc 180  
tggtctccct gcggggcaag gtactactta tcgagaatgt ggcgtccctc tgaggcacca 240  
cgttccggga ctacaccag atgaacgagc tgcagcggcg cctcggaccc cggggcctgg 300  
tggtgctcgg cttcccgtgc aaccagtttg ggcacagga gaaacccaag aacgaagaga 360  
ttctgaattc cctcaagtac gtccggcctg gtggtgggtt cgagcccaac ttcattgctct 420  
tcgagaagtg cgaggtgaac ggtgcggggg cgcaccctct cttcgncttc ctgcgggagg 480  
ccctgccagc tcccagcgac gacgncaccg cgcttatgac cgaccccaag ctcatcacct 540  
ggtct 545

<210> 383  
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gatttcaata cgtctcgggg cagggccgtg ctgattgaga atgtggcttc gctctgaggc 120  
acaaccaccc gggacttcac ccagctcaac gagctgcaat gccgctttcc caggcgcctg 180  
gtggctccttg ggcttccctt gcaaccaatt tgggacatca gganaactgt caaaatgagg 240  
anatcctgaa cagttcctaat tatnttccgt cctgggggtgg gnataccaac ccccttccc 300  
cctttttcca aaaattttaa ggttaaatng gcnaaaaaaa acatcctntt tttcccccta 360  
ccttaaanga aaaac 375

<210> 384  
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ctttcccagg cgcttggtgg tccttggtt cccttgcaac caatttgac atcagagcag 120

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gagagacaga agtagcaaac cctctttcga gatgtccctc cagccccaga agtacctnca 180
gcctcacacc atctcttcag cctagcaagt tgctggaggg agtctataac ctaccaggag 240
ccagccagcc atttgatca agaaatagaa atctgcaggg tacagtggct cacacctata 300
atcccagcgc tttgggaggg taagtcttag gacaaaggca aggaagaaaa gcangaactt 360
naaaatccaa ttccttttgg gncctnaaat ttaaccttca agttcaaggg agctnaagta 420
aggcanaagg ccaaanggct ttttacttna acaacaacgg tgccaatttg gaaaggcaag 480
ggcaaggcaa aaaaccagg ggcaagaagg aaaangggaa aaggggntnt 530
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<210> 385

<211> 465

<212> DNA

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<400> 385

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tgacgatctc gaggacctgg aagaagcaga ngagccagac atggaggaag acgatgatca 180
gaaagctgtg aaagatgaac tgtaatacgc aaagccagac ccgggcgctg ccgagacccc 240
tcggggggct gcacaaccag cagcagcgca aggcttccga gccttgnggg ctcggtttga 300
aaagaagggn tngccgggaa acccagggna actctctnga agttganact ncancctag 360
aaaacgtccg ttnaaccccg ttnccttctt ctgcttttcg ggtttttgga aaagggattc 420
atttcagggc aggccaanct tgttggggnn tgttcctgaa accat 465
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cacttcgagc tgaagcacct ctccagcggg gacctgctcc gggacaacat gctgcggggc 120  
acagaaattg gcgtgttagc caaggctttc attgaccaag ggaaactcat ccagatgat 180  
gtcatgactc ggctggccct tcatgagctg aaaaatctca ccagtatag ctggctgttg 240  
gatgggtttc caaggacact tccacaggca gaagccctag atagagctta tcagatcgac 300  
acagtgatta acctgaatgt gccctttgag gtcattaaac aacgccttac tgctcgtcgg 360  
attcatcccg ccagtggccg agtctataac attgaattca accctcccaa aactgtgggc 420  
attgatgacc tgactgggga gcctctcatt cagcgtgagg atgataaacc agagacgggt 480  
atcaagagac taaaggctta tgaagaccaa acaaagccag tcctggaata ttaccagaaa 540  
aaaggggtgc tggaaacatt ctccggaaca gaaaccaaca agatttgcc ctatgtatat 600  
gcttttctac aactaaagt ncacaaaagaa gccagaaagc ttaattact tcatgaggag 660  
aaatgtgtgt aactattaat agtaagaang gcaaaccctc tantccttgg atttaaaact 720  
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ntacaagaaa tctggaaaac ttgtattctt caggcttggg taatgtcagg caaaaccact 120  
gtngttgcac atngcttcaa aggtgcgcag ntngtgggnc aacattgttt cccaacactt 180

<210> 388  
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<212> DNA  
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<221> misc feature

<222> (427)

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<400> 388

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aagatcgaga agcagctgca gaangacaan caggtctacc gggccacgca cgcctgctg 120
ctgctgggtg ctggagaatc tggtaaaagc accattgtga agcagatgag gatcctgcat 180
gttaatgggt ttaatgnaga cagtgagaag gcaaccaaag tgcaggacat caaaaacaac 240
ctgaaaagagg cgattgaaac cantgtggcc gccatgagca acctnnngtc ccccgtgga 300
gctggnaaac ccgagaaac cagttcagag tggactacat cctggagtgt tatgaacgtg 360
cctggntttt gacttcctc cggattctat ggcnggcaa ggtctgtgga ggtnaagntt 420
ctgctgna 428
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<211> 454

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<222> (309)

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<220>

<221> misc feature

<222> (369)

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<220>

<221> misc feature

<222> (402)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (424)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (426)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (437)

<223> n equals a,t,g, or c

<400> 389

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gggtgggaaa ctcaggaact ttgcacccat ccctggtgaa cctgtggttc ccatcctctg 120  
tagcaaccgc aactttccag aagaactcaa gcctctctgc aagagcccaa tgcccaggag 180

```
ntanttcaga ggctggagga aatcgctgna ggacccgggg cacatgtgga aatctgtgcn 240
tacgctggcc tgtaccgat gctaagggg cttgccactg gcnggcntcc cntccgcagc 300
aggggaagnc ttttcntcnt gcagaaagg ccacccatga tattccattc cccagcagtt 360
caactaacnt ggttccattc gggaaggagc agccggggaa gnattgggtt gattggaagg 420
cttngnccca aatggtnctt tccctggcaa tttt 454
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<210> 390

<211> 553

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (7)

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<220>

<221> misc feature

<222> (29)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (30)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (58)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (77)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (414)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (417)

<223> n equals a,t,g, or c

<400> 390

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gctctagaac tagtgntcc cccgggctgc aggaattcgg cacgagcagg gacgctaaga 120
ttgctacctg gactttcgtt gaccatgctg tcccgggtgg tactttccgc cgccgccaca 180
gcgcccctc tctgaagaat gcagccttcc taggtccagg gaccctatgt actcggaact 240
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```
gggcttatct tgtacgcttt atccaaagaa atatatgtga ttagcgcaga gaccttcact 300
gccctatcag tactaggtgt aatggtctat ggaattaaaa aatatggtcc ctttgttgca 360
gactttgctg ataaactcaa tgagcaaaaa cttgcccaac tagaagaggc gaanagngct 420
tccatccaac acatccagaa tgcaattgat acggagaagt cacaacaggc actgggtcag 480
aagcgccatt accttttttg atgtgcaaa gaaataacatt gctatggctt tggaagtta 540
ttaccggga acg 553
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<210> 391

<211> 632

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (12)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (586)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (613)

<223> n equals a,t,g, or c

<400> 391

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cgctctagaa ctagtggatc ccccgggctg caggaattcg gcacgaggtc ctgtgcggtc 120
acttagccaa gatgcctgag gaaaccacaga cccaagacca accgatggag gaggaggagg 180
ttgagacgtt cgcctttcag gcagaaattg cccagttgat gtcattgatc atcaatactt 240
tctactcgaa caaagagatc tttctgagag agctcatttc aaattcatca gatgcattgg 300
acaaaatccg gtatgaaagc ttgacagatc ccagtaaatt agactctggg aaagagctgc 360
atattaacct tataccgaac aaacaagatc gaactctcac tattgtggat actggaattg 420
gaatgaccaa ggctgacttg atcaataacc ttggtactat cgccaagtct gggaccaaag 480
cgttcatgga agctttgag gctggtgcag atatctctat gattggccag ttcggtgttg 540
gtttttattc tgcttatttg gttgctgaga aagtaactgt gatcancaaa cataacgatg 600
atgagcagta cgnttgggag tcctcagcag gg 632
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<210> 392

<211> 600

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (6)

<223> n equals a,t,g, or c

<220>



<221> misc feature  
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<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (518)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (571)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (572)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (587)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (590)  
<223> n equals a,t,g, or c

<400> 392  
gctcanatct gccttctgga gactgcgccg tcctcccggg agagccagaa agaggacatg 60  
gctgctgggc agcggggaagc gaggccccag gtgtcactga cattcgagga cgtggctgtg 120  
ctctttacct gggatgagtg gagaaagctg gctccttctc anagaaactt gtaccgggat 180  
gtgatgctgg agaactatag gaacctggtc tctactgggac tctcatttac caaaccaaaa 240  
gtcatctccc tgttcagca aggagaagat ccctgggagg tggagaaaga cagttctggt 300  
gtctcctctc taggatgtaa gagcacacct aaaatgacaa agtcaactca aactcaggat 360  
tcatttcagg agcagataag gaaaagattg aaaagggatg aaccctggaa ctcatatca 420  
gaaagatcct gcatatatga agagaaatta aagaaacagc aggacaaaaa tgaaaattta 480  
caaataattt cagttgcccc tacaaaaatc cttactgnag atagaagcca taaaaatgtt 540  
gaatttgccc aaaacttcta cctgaaatca nncttcatta agcaccngan aattgcctaa 600

<210> 393  
<211> 531  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc feature  
<222> (63)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (267)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (352)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (376)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (394)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (395)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (400)  
<223> n equals a,t,g, or c

<220>  
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<222> (451)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (464)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (471)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (476)  
<223> n equals a,t,g, or c

<220>

<221> misc feature  
<222> (512)  
<223> n equals a,t,g, or c

<400> 393  
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ggnccccccg gacagtggct ctgacggcgt tactgatggt gctgctcaca tctgtggttc 120  
cagggcaggg ccaactccaga gaattacctt ttccagggac ggcaggaatg ctacgcgttt 180  
aatggtaaca gccagaagga catcctggag gagaaagcgg gcagtgccgg aacaggatgt 240  
gcagacacaa cttacggagc tgggcgngcc catggaccct gcagcgccga gttccagcct 300  
aggggtggaat gttttccccc tccaagtagg gggcccttgg cagcaacaca anctgcttgt 360  
ttggccaagt gacggntttt taccagga gcannnggtan tcctgtcaac tggattggag 420  
gcacatttga ttttgcgccg ttagacatga nggggttggg ttcngtttgt naaatntggg 480  
ttgggaattt taatgaaaaa ggggggcaaa gnaattttaa aggggggttt t 531

<210> 394  
<211> 404  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (269)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (295)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (330)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (382)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (387)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (390)  
<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (399)

<223> n equals a,t,g, or c

<400> 394

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gggactcttaa ttctgtaata tatcaaggaa tctcgtaaaa ccgacactaa aacgtccctg 60
cctacaaatc atccggccaa attatgagtt cattgtatta tgcgaatgct ttattttcta 120
aatatccagc ctcaagttcg gttttcgcta ccggagcctt cccagaacaa acttcttgty 180
cgtttgcttc caacccccag cgcccgggct atggagcggg ttccggcgct tccttcgccc 240
cctcgatgca gggcttgtag cccggcggng ggggcatggc gggccagagc gcggncggcg 300
tctacgcggc cggctatggg ctcgagccgn gttccttcaa catgcactgc gcgccctttg 360
agcagaaacc tctcgggggt gngcccnggn gaattccgnc aagg 404
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<210> 395

<211> 499

<212> DNA

<213> Homo sapiens

<220>

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<222> (10)

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<220>

<221> misc feature

<222> (89)

<223> n equals a,t,g, or c

<220>

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<222> (90)

<223> n equals a,t,g, or c

<220>

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<222> (93)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (95)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (98)

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<220>

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<222> (112)

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<220>

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<222> (115)

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<220>

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<222> (119)

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<220>

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<222> (125)

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<222> (149)

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<220>

<221> misc feature

<222> (172)

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<220>

<221> misc feature

<222> (211)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (223)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (225)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (299)

<223> n equals a,t,g, or c

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<220>  
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<222> (442)  
<223> n equals a,t,g, or c

<220>  
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<222> (443)  
<223> n equals a,t,g, or c

<220>  
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<222> (445)  
<223> n equals a,t,g, or c

<220>  
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<222> (457)  
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<220>  
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<222> (470)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (477)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (484)  
<223> n equals a,t,g, or c

<400> 395  
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agctgcacct tcacgtacct gctgggtggn agngngtncc gggaggccgt tntgntcggn 120  
ccagnccctgg aaacagcgcc tcgggatgnc cagctgatca aggagctggg gnttcggctg 180  
ctctatgctg gcgttgaga ccagggccag ncctggccac aantnaggct gtgtcacctt 240  
cgttctgaat gaccacagca tggccttcac tggagatgcc ctgttgatcc gtgggtgtng 300  
gcggacagac ttccagcaag gctgttgcca agaccttgta accattcggg ccatgaaaag 360  
atctttcaaa atttccagga gactgtcttg atctaacctg gttcaagggt accatggggg 420  
ttaaantgtt caacgtggag gnnngggagg acctttnaaa cccttggttn aaccttnaat 480  
tttnaggagt ttttcaaaa 499

<210> 396  
<211> 526  
<212> DNA  
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<220>  
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<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (502)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (508)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (519)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (523)  
<223> n equals a,t,g, or c

<400> 396  
gggtccccgtc acgctgactt tccgtgcagt gctgtggtgc gaaaatgcct cgccgctcct 60  
ggtagacgaa gaggaagaca aacctacagt cgcttccaaa ctctagagtt ggaaaaggaa 120  
tttcttttta acccctatct gaccaggaaa agaagaatcg aggtttccca cgccctagcc 180  
ctcaccgaga gacaggtaaa aatctggttc cagaacagga gaatgaaatg gaaaaaggaa 240  
aacaacaagg acaaatttcc cgtttcccg caggaggtga aggacgggga aacgaaaaag 300  
gaagcccaag agctggagga agacagagcc gaaggcctga caaattaact tctaccttta 360  
aaatttacca cagactatta aaactaataa tcaccatag ctgtggacac cacctatatt 420  
ctttggtgga aaggacctta cctgngtttc aagctacctt catgtcactg gtcttgaggg 480  
tttctgggct tttagagagg antttgngg tttaaaaang ttntag 526

<210> 397  
<211> 443  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc feature  
<222> (94)  
<223> n equals a,t,g, or c

<220>  
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<222> (443)  
<223> n equals a,t,g, or c

<400> 397  
gccccacgct cggggtgctc cttacctccc cggtgggtcgg gcgcgaatta ctggaaattg 60  
gcttttcccg ttggggccga agtaccttcc ctgnggcggc gactcagcgg ggtgtcgttc 120  
ggccggcgtg acgcagccgg atcggcgcca gacggaaaacc tagcgggtgac tgtatctgaa 180  
ttttgcagct gcagaatgtg tagtacctta aaagggttggc aacaatgagt aaaccagaat 240  
taaaaggaaga caagatgctg gaggttcact ttgtgggaga tgatgatgtt cttaatcaca 300  
ttctagatag agaaggagga gctaaattga agaaggagcg agcgacttt tggtcaaccc 360  
caaaaaaata ataaagaagc cagaatatga ttggaggaa gatgaccagg aggtcttaaa 420  
agatcagaac tatgtgaaa ttn 443

<210> 398  
<211> 652  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (14)  
<223> n equals a,t,g, or c

<220>  
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<220>  
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<222> (21)  
<223> n equals a,t,g, or c

<220>  
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<222> (31)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (64)  
<223> n equals a,t,g, or c

<220>  
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<220>  
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<223> n equals a,t,g, or c

<220>  
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<222> (88)  
<223> n equals a,t,g, or c

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<223> n equals a,t,g, or c

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<222> (100)  
<223> n equals a,t,g, or c

<220>  
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<222> (103)  
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<220>  
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<222> (111)  
<223> n equals a,t,g, or c

<220>  
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<222> (116)  
<223> n equals a,t,g, or c

<220>  
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<222> (134)  
<223> n equals a,t,g, or c

<220>  
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<222> (261)  
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<220>  
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<222> (325)  
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<220>

<221> misc feature  
<222> (383)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (387)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (397)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (549)  
<223> n equals a,t,g, or c

<220>  
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<220>  
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<222> (594)  
<223> n equals a,t,g, or c

<220>  
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<222> (606)  
<223> n equals a,t,g, or c

<220>  
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<222> (620)  
<223> n equals a,t,g, or c

<220>  
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<222> (639)  
<223> n equals a,t,g, or c

<400> 398  
gcccacgcgt ccgnanacgc ntccgtttgg nccaagatgg catggaatga ggaaggcgcgt 60  
tccttgngga ctggtggnct tggcgtnct ncgggctgtn agnacctcat ntatgngcac 120  
ttaccaaaag cggntgaaaa ttgtggaagt tggccccga gatggactac aaaatgaaaa 180  
gaatatcgta tctactccag tgaaaatcaa gctgatagac atgctttctg aagcaggact 240  
ctctgttata gaaaccacca nctttgagtc tcctaagtgg gttccccaga tgggtgacca 300  
cactgaagtc ttgaagggca ttcanaagtt tcctggcatc aactaccag tcctgacccc 360

aaatttgaaa ggcttcgagg cancggnacc atgactnctg tgaggatgca gcactccctg 420  
gcaggtcaga cctatgccgt gcccttcac cagccagacc tgcggcgaga ggaggccgtc 480  
cagcagatgg cggatgccct gcagtacctg cagaaggctc tggagacatc ttcagcaagt 540  
gggtgctgnc actcaccccc acctgatgag agggccatnc ctgtctgggc aatnccagca 600  
acacancctt tgggagcaan ccccttgggg aatcccggnc tggggaaccc at 652

<210> 399

<211> 341

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (39)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (84)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (137)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (153)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (302)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (310)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (332)

<223> n equals a,t,g, or c

<400> 399

ggcacgagag gacctggata aagcacttct aaaggcctnt caggacatgt tcgacaagaa 60  
aaccaaggct tccctttacc tctnactca caatgggaac atgtacacct catccctgta 120  
cgggtgccctg gccctgnttc tgtccacca cnttgcccaa gaactggctg gctccaggat 180  
tggtgccttc tcttatggct ctggttttagc agcaagtttc ttttcatttc gagtatcccg 240

tctaaagggtg ttctgcagat ccatggaaaag cttctgggaa acgtatgcta gcagagcttc 300  
tncccggtgan tcatatTTTT aagatcccac tnttagctgg a 341

<210> 400  
<211> 604  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc feature  
<222> (392)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (484)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (502)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (509)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (559)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (593)  
<223> n equals a,t,g, or c

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tacaatcaac caacaagtca ttattaccct cactgtcaac ccaacacagg catgctcata 120  
aggaaagggtt aaaaaaagta aaaggaaactc ggcaaatctt accccgcctg ttaccacaaa 180  
acatcacctc tagcatcacc agtattagag gcaccgcctg cccagtgaca catgtttaac 240  
ggccgcggta ccctaaccgt gcaaaggtag cataatcact tggttcctta ataggacact 300  
gtatgaatgg cttcacgagg gttcagctgt ctcttacttt taaccagtga aattgacctg 360  
cccgtgaaga ggcggcatga cacagcaaga cnaagaagac cctatggagc ttttaattat 420  
taatgcaaac agtacctaca aaccacacagg tcctaactac caaacctgca ttaaaaaatt 480  
cggntggggc gacctcggac anaaccaanc tccagcagta catgctaaac ttaccagcaa 540  
acgactatat ctaattganc atacttgaca aggacaagta cctaggaaca ggnaatcttt 600  
ttaa 604

<210> 401  
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<212> DNA  
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acgagaagac cctatggagc tttaatttat taatgcaaac agtacctaac aaaccacag 180  
gtcctaaact accaaacctg gcattaaaaa ttctgggttg ggcgacctcg gagcagaacc 240  
caacctccga gcagtacatg ctaagacttc accagtcaaa gcgaactact atactcaatt 300  
gatccaataa cttgaccaac ggaacaagtt accctaggga taacagcgca atcctattct 360  
agagtccata tcaacaatag ggtttacgac ctcgatgttg gatcaggaca tcccgatggt 420  
gcagccgcta ttaaagggtc gtttgttcaa cgattaaagt cctacgtgat ctgagttcag 480  
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cctctcctac ttggataact gtggtaattc tagagctaata acatgccgac gggcgctgac 180  
ccccttcgag ggggggatgc gtgcatttat canatcanaa ccaacccggt canccctct 240  
ccggcccccgg ccggngggcg gcgnc 265

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ttctcgaggag gagcttnnag aactacaaga ggcatttaata aaaatagata tnnacaatag 180  
tgggtatgtc agtgactatn aacttcaaga cctgtttaag gaagcaagcc ttcctctgcc 240  
tggctacaag gtgcgcgaga ttntggagaa aattctatca gttgctgaca gcaacaaaga 300  
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<211> 540  
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atccctccat tcccatcttt cccagcaat taccagctct ggctgggtcg ccacaacttg 180  
tttgacgacg aaaacacagc ccagtgtgtt catgtcagtg agagcttccc acaccctggc 240  
ttcaacatga gcctcctgga gaaccacacc cgccaagcag acgaggacta cagccacgac 300  
ctcatgctgc tccgcctgac agagcctgct gataccatca cagacgctgt gaaggtcggg 360  
aagttgcccc ccaggaacc cgaagtgggg gagcacctgg ttggcttccg gctggggcaa 420  
gcattgaacc agaagaattt cttaatttca gaagatcttc aaatggtgng ganccttcaa 480  
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cggggcgcgct ctgcctgccc tgctggacga gcagcaggta aacgtgctgc tctacgacat 180  
gaacggctgt tactcacgcc tcaaggagct ggtgcccacc ctgccccaga accgcaagtg 240  
aagcaagggtg gagattttcc agcacgtcat cgactacatc agggacttta atttgnantt 300  
naatcggant ccnaatttg 319

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<212> DNA  
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ccacgtgaaa gcactacacg attccnagcc aggatgtaac tgtgcccctg cccagttccc 120  
ncancttccc catgctgcca ncccngattn tggctgaaac gaccggccct ngaggacctg 180  
gtcttaggtt cagaagcgaa gcatcacgtg acacantgac cggcctgaga gaatgcctct 240  
ggtgaccact ntnacctggg acgcenttaa agtgggaaga gcncgtgttc aaggaccacc 300  
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<210> 407

<211> 437

<212> DNA

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cccatgcccc tcatgcccag cacctgaatt tcctgggggg accatcagtn ttctgtgtcc 120  
ccccaaaacc caaggacact ctcatgaatc tcccggaccc ctgaagggtca cgtgcgtggt 180  
ggtggacgtg aagccaggga agaccccagag gtccagtcca actggtacgt ggatggcgtg 240  
gaggtgcata atgccaagac aaagccgcgg gnggagcagt tcaacagcac gtaccngtgg 300  
ttcagcgtcc ttcaccgtcc tgcaccagga tggcttgaac ggcaaggagg ttacaagtgg 360  
caaggttttn caacaaaggg cttcccgtnc ttcttgggg aaaaccttt tncaaaggcc 420  
aaggggcagn cccgngg 437

<210> 408  
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ggcgaaagga ccacggtcac cgtctcctca gcctccacca anggccatc ggtcttcccc 120  
ctggcgccct gctccangaa cacctccgaa aacacagcgg cctgggctg cctgggtcaag 180  
gactacttcc ccgaaaccgg tgacggtgtc ttggaactca gggggctctg accagcgggg 240  
tgcacacctt cccagctgtc ctacagtcct caggaancta ctccctcanc accntggnga 300  
cgntgcctcc 310

<210> 409  
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<400> 409

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actctggctc ccanatacca ctggagaaat actgatgacg cagtctccag ccaccctgct 120
tgtgtctcca ggggaaagag tcaccctctc ctgcagggcc gggcagagtg ttacagcaa 180
cttagcctgg tatcagcaga aacctggcca ggctcccagg ctctcatgt atggntcatc 240
caccanggcc actgatgtcc cagtcagggt cagtggcant gggctctggga cagagttcac 300
tctcaccatc agcagcctgc agtctgacga ttctgcagtc tatttntgct agcagtatat 360
tatgtggcct ggaaccttcg gncnagggac caagggggaa atcanacgaa ctggggntgc 420
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<210> 410

<211> 448

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<213> Homo sapiens

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ggctacatca aacttcgcaa gattcgagca gccagaata tctccaagac gatcgccaca 180  
tcacagaatc gtatctatct cacagctgac aaccttgagc tgaacctaca ggatgaaagt 240  
ttcaccaggg gaagtgcag cctcatcaag ggtaagaaat gagcctagtc accaagaact 300  
ccaccccccag aggaagtggg tctgcttctc cagttttgga gnaccaccag gggtcagaa 360  
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<212> DNA  
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<220>  
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cttcggagac cctgtccntc a 141

<210> 412  
<211> 473  
<212> DNA  
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tccagtgtga agtgcagctg gtggagtctg ggggagccgt agtacagcct ggggggtccc 180  
ttagactctc ctgtgaagcc tctggattca cctttgacaa ttatgccatg cactgggtcc 240  
gtcaagctcc ggngaagggt ctggagtggg tctgtctcat cagtcgggat ggtcgtgaga 300  
catattttgc agactctatg aagggtcggg tcaccatctc cagagacaac agcaaaaact 360  
gcctgtatct ccaagtgaac agtctgagag ttgaggacac cgncttgat tactgtgcaa 420  
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tgcaagctggt ggagctctgg ggaggcttgg tccaagccgg gggggtcctt gagactctcc 180  
tgngcannct ctggcttccc cctttataac catgggatga cctgggtncg ccaggctcca 240  
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<210> 414  
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gtgcagctgg tggagtctgg gggaggcttg gtacagccag ggcgggtccct gagactctcc 180
tgtacaactt ctggattcac ctttgagat tattctatga gctgggtccg ccaggctcca 240
gggaaggggc tggagtgggt aggtttcatt agaagcaaag cgcattgggtg gacaacagaa 300
tacgcccggt ctgtgaaaag gcagattcac catctcaaag agatgattcc acaggcatcg 360
nctatctggc aaatgaacag cctgaaaccg aggacacaga cattattact gtctagacat 420
gactacaggc acaccctgg ctactggggg cagggaaccc tggtcaccgn cttctctggc 480
ttccaccaag ggccatcgtc ttccccctgg ngcccttgtt ccaggancac ttccgaaanc 540
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cgccaagttg caggaanaang tctggaatgg gtctcangta ttgatcctgc tggtaacaca 180
aactatccan gctccgtgaa nggccgatto atcatctcca gagaaaatga caagagctcc 240
tcgtatcttc aaaatgaatg ggctgacanc cggggaaaac ngtgtgtaat attgtnnaaa 300
nanaaattgc anttcctggt aantgggtan ntncgatctc ttggggccgn nggaancctt 360
ggttaaatgt nttcctcaag aattnccga accaagnccc caaagggttt tcccgcctta 420
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gaagacacgg ctgtnntatta ttgtncgagg ggattttttg gggaccgtga ttactactac 180  
tactactaca tggacgtctg gggcaaagg accacggtca ccgtctctc agcatccccg 240  
accagcccc aggtcttccc gctgagcctc tgcagcaccc agccagatgg gaacgtggtc 300  
atcgctgct tngtccaggg cttcttcccc caggagccac ttcagtgtgg acctggagcg 360  
aaaggggnaca gggcgtgacc gccagaaaat tcccacccag ccaggatgcc tccgggggac 420  
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tctgggacag atttcaactct caccattagc agtctgcaac ctgaagattt tggcacttac 180  
ttctgtcaac agaattacaa tgtcccgtgg aacgttcggc caggggaacn aangtgga 240  
atgaaaccga actgtggctg caccatctgt cttcatcttc ccgccatctg atgagcagtt 300  
gaaatcttga actgcctctg ttgtnttgcc tgctgaataa cttctatccc anaaaaggcc 360  
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ggacgcn 427

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tgacctcct angtcagccc aaggctgccc cctcgggtcac tctgttcccg ccctcctctg 180  
angagcttca agccaacaag gccacactgg tgtgtctcat aaatgacttc taccggggaa 240  
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tgtgctgacg cagccgcctt cagtgtcttg gggcccaggg cagaggggtca ccatctcctg 180  
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aggaacagcc cccaaagtcc tcatctatgg taacagcaat cggccctcag gggtccttga 300  
ccgattctct ggctccaagt ctggcacctc agcctccctg gccatcactg ggctccaggc 360  
tgaagatgan gttgattatt actgccagtc ctatgacagc agcctgggtg gttcgggtgt 420  
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ccccgggcag agggtcacca tctcttggtc tggaagcagc tccaacatcg gaactaatta 180  
tgtatactgg taccagcagc tcccaggaac ggcccccgaa gtcctcatct ataagaatga 240  
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cgaccctccg ggatccctga gagattctct ggctccacct cagggacatt ggccaccgtg 180  
attatcagtg gggcccaggt ggacgatgat actgacttct actgtcagtc aacacacagt 240  
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angacagacg gccangatca cctgntctgg agatgcattg ccagaacaat ctattttttg 180

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gtatcaacag aagccaggcc aggccctgt attggtgatt tataaagtcc atgagaggcc 240
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acaatntagg cnatgtaggg tctgttcccc caaatccaga tctgtcgnaa acantnttgg 180  
atcaatacnt tgccatggnc ncanaaaanc atgggtncaa catggaacan gctcttgga 240  
tgctcttctg gcataancnt aatatccaaa antcatnggc tgatttgccc aacttnaccc 300  
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gccccgaaa cnaaacggga cgggaagaga ncnacgatga actggaacaa gcaaatggaa 540  
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ttgaggaacc ngaaacanaa aat 143

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ggaaaacttt gaagccttca tgaaggcaat cggtctgccg gaagagctca tccagaaggg 120  
gaaggataatc aaggggggtgt cggaatcgt gcagaatggg aagcacttca agttcaccat 180  
caccgctggg tccaaagtga tccaaaacga attcacggtg ggggaggaat gtgagctgga 240  
gacaatgaca ggggagaaag tcaagacagt gggtcagttg gaaggtgaca ntaactggt 300  
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aacgtcgnga ctggnaaaac cctggngtta cccaacttaa tcgccttgca gnanatcccc 240  
ntttcgccag ntggcgtaat ancnaaaag cccgnaccga tcgcctttcc naacagttgc 300  
ncagcctgaa tggcaaattg gacnccccct gtagcggngc attaagcncg gcgggtgtgg 360  
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tcttcccttc ctttttcgcc acgttcgccg gttttccccg taaagcttta aatggggggc 480  
tcccttnagg gttccgattt agggctttac gggaccttga ccccaaaaaa ctttgnttag 540  
ggggatgggt cagctagnng ggccattgcc cttgatanac gggtttttcg cccttttgac 600  
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ccccccagtc ttgctcaagc ccctcaagct cctggaaaac accactttgt gcctgttctg 240  
cgcttactcc tgattaatac aatgaatttt cttgggcatt ttacaatttc caacacttta 300  
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nttcttcac aaccggcagc gctctagcac tgccatgaca gtgatggccg acctgggcga 180  
gcgcatggtc agggagaacc tcaaagtgtg gatctatccc gaggggtactc gcaacgacaa 240  
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tgtngcgcaa ganaaccagg gcatcttctt ctcgggggac tcctacctag tgctgcacaa 180  
tggcccagaa gaggtttccc atctgcacct caacacactg ctgggagagc ggcctgtgca 240  
gcaccgcgag gtaaggggca atgagtctga cctcttcatg agctacttcc cacgggggctt 300  
caagtaccag gaaggtgggt tggantcagc atttcacaag acttccacag gagccccagt 360  
tgccatcaag aaantntacc aggtgaaggg gaanaanaaa tccgtccaac gagngggcat 420  
gaattgggaa anttnaaatn ggggttgttt acctggaatn ggcaaaaatt tnnctgggtt 480  
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tggcattgcta actagttacg cgacccccga gcggtcggcg tcccccaact tcttagaggg 180  
acaagtggcg ttcagccacc cgagattgag caataacagg tctgtgatgc ccttagatgt 240  
ccgggggtgc acgcgcgcta cactgactgg ctccagcgtgt gcctacccta cgccggcagg 300  
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gaacgaggaa ttcccagtaa gtgcgggtca taagcttgcg ttgattaagt ccctgcccct 420  
tcaacccttc tggnccttcg gaccactgng acttttccat ctttcttaaa cggaggctgg 480  
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acacacgtaa gcagaagaac ggcttcccg ccaacttcat ccactcgctg gactcctccc 180  
acatgatgct caccgccctg cactgctaca ggaagggcct gaccttcgtc tctgtgcacg 240  
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tgcccaagcc aggggccttc gacctggagc aggtgaagcg ttccacctac ttcttcagct 480  
gacaccccggt gaggccttgc agtgtgtaaa taaagctctt ttgccacccc aaaaaaaaaa 540  
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gangattatg nngaaaactt ncaagtcatt agatttgcgg aagtgactca agaagttgaa 180
gtagcaagac ctgtagacaa ggtaatatgt ggtttaacgc cnngnaggag atacagaaac 240
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gagcaagttg acaactttac tctggatata aatactgcct atgccagact cagaggaatc 180  
gaacaggctg ttcagagcca tgcagttgct gaagagggaag ccagaaaagc ccaccaactc 240  
tggttttcag tggaggcatt aaagtacagc atgnaagacc tccatctggc agaaacacct 300  
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ttacatggaa gagaaccctt agggcccgtt ttcncatggt ggtttccaaa aattggggccc 480  
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ccctgctcca ccgtccccgt caccacggag gtttcgtacg ccggtgcac caagaccgtc 60
ctcatgaatc attgctccgg gtctgcggg acatttgta tgtactcgg ccaagcccag 120
gccctggacc acagcttct cctgctgcaa aganganaaa accagccagc gtgaggttg 180
tcctgagctt gccccaatgg cggctcgtt gacacacacc tacaccaca tcgaaganct 240
gccagtgcc agaacacnnt cntgggggnt tccccaacng gaacttccc cgggggccg 300
ggggcttncc ccttagcatc tggaacgtag gtttttnnnn nnnnnngnn aaanccccct 360
ttcaattgcc cttcnaaaan ttttacctcc ccccgaaact ctttaaaact cttaaactcg 420
ggttcctctt cttccaaata ttatgttcta atttttttt tcatccctgc tttcccaata 480
taaactcagg gggaaatnca aaaaaaaaaa aaatccangg gggg 524
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<210> 436

<211> 384

<212> DNA

<213> Homo sapiens

<220>

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<222> (5)

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<220>

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<222> (79)

<223> n equals a,t,g, or c

<220>

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<222> (124)

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<220>

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<222> (177)

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<222> (341)

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<222> (349)

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<220>

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<222> (366)

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<220>

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<222> (374)

<223> n equals a,t,g, or c

<400> 436

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ttacttcacg cagttcagna ccagctcggg gtccgcggaa gaggcagccc tactggagtc 120  
tcgnattcctt taccctaaaga ggaagcagca gtgcctgcaa tttttctata aaatgancgg 180  
ggaagtcctt ncagacagac ttcgttgtct gggtnccagga ggggatgaca gcacaggcaa 240  
tgttcgcaat tgggtgaagg gcagactttt caaggagatg atgaccacaa tttggaaaat 300  
tggcccatgt ggggtgcttcn aagaggaaca gaatttcggg naccttttnc caggggcaca 360  
aaaggnggac ctnagagct tcaa 384

<210> 437  
<211> 390  
<212> DNA  
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<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (317)  
<223> n equals a,t,g, or c

<220>  
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<222> (372)  
<223> n equals a,t,g, or c

<220>  
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<222> (385)  
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<220>  
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<222> (386)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (390)  
<223> n equals a,t,g, or c

<400> 437  
cttgctcaat gacgccgtca ctgtggctct gtatcacctc ttgaggagt ttgccaaacta 60  
cgaacacgtg ggcacgtgg acatcttctt cggtctcttg agcttcttcg tgggtggcct 120  
gggcgggggtg cttgtgggcg tggctacgg ggtcatcgca gccttcacct cccgatttac 180  
ctccacatc cgggtcatcg agccgtctt cgtcttctc tacagctaca tggcctactt 240  
gtcagccgag ctcttcacc tgtcaggcat catggcgctc atagcctcag gagggtgat 300  
gcgncctat gtgggangcc aacacttcca caagttccca caacaacatc aaataatttc 360  
ctggaagatg tnggagcagc gtcannaagn 390

<210> 438  
<211> 234  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (21)  
<223> n equals a,t,g, or c

<220>  
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<222> (24)  
<223> n equals a,t,g, or c

<220>  
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<222> (47)  
<223> n equals a,t,g, or c

<220>  
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<222> (82)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (114)  
<223> n equals a,t,g, or c

<400> 438  
nccccggact tttagtgttaa ngcncctacc ccctgcaggt accggtncgg aattcccggg 60  
tttgactcca cgcgttttgc tncattaaca acataaaacc ctcatggaca cganaaaaca 120  
ccctcatgtt catacaccta tccccattc tctctctatc cctcaacccc gacatcatta 180  
ccgggttttc ctcttaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 234

<210> 439  
<211> 144  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> n equals a,t,g, or c

<220>  
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<223> n equals a,t,g, or c

<220>  
<221> misc feature



<222> (36)  
<223> n equals a,t,g, or c

<220>  
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<222> (43)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (105)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (114)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (135)  
<223> n equals a,t,g, or c

<400> 439  
nnctatcgat ggggagcaag agtcttttaa ataagnccat ttnagtcctt ggtaacaag 60  
ggtttaaagt ggagcgaatg cacatcacag acatgaaatt ggctnacctg cctngcttag 120  
aagcccttgg tgttnaggtc aaca 144

<210> 440  
<211> 411  
<212> DNA  
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<220>  
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<222> (69)  
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<220>  
<221> misc feature  
<222> (86)  
<223> n equals a,t,g, or c

<220>  
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<222> (132)  
<223> n equals a,t,g, or c

<220>  
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<222> (209)

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<220>

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<222> (230)

<223> n equals a,t,g, or c

<220>

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<222> (246)

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<222> (276)

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<220>

<221> misc feature

<222> (340)

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<220>

<221> misc feature

<222> (346)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (390)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (404)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (410)

<223> n equals a,t,g, or c

<400> 440

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gccaaagtcc accccaactc tgtgcacatc tgtgcggtgg ttgtggagta cgagaccaag 60
gctggccgna tcaacaaggg cgtggncacc aactggctgc gggccaagga gcctgccggg 120
gagaacggcg gncgcgcgct ggtgcccatg ttcgtgcgca agtcccagtt ccgcctgccc 180
ttcaaggcca ccacgcctgt catcatggng ggccccggca cgggggtgtn acccttcata 240
ggcttnatcc aggagcgggc ctggctgcga cagcanggca aggaggtggg ggagacgctg 300
ctgaactacg gctgccgccg ctcggatgag gactacctgn accggnagga gctggcgcgag 360
ttccacaggg acggtgcgct caccagctn aacgtggcct tctnccgggn a 411
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<210> 441  
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<212> DNA  
<213> Homo sapiens

<220>  
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<223> n equals a,t,g, or c

<220>  
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<222> (73)  
<223> n equals a,t,g, or c

<220>  
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<223> n equals a,t,g, or c

<220>  
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<222> (162)  
<223> n equals a,t,g, or c

<220>  
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<222> (232)  
<223> n equals a,t,g, or c

<220>  
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<222> (252)  
<223> n equals a,t,g, or c

<220>  
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<220>  
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<222> (360)  
<223> n equals a,t,g, or c

<220>  
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<222> (365)  
<223> n equals a,t,g, or c

<220>

<221> misc feature  
<222> (407)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (435)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (449)  
<223> n equals a,t,g, or c

<220>  
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<222> (472)  
<223> n equals a,t,g, or c

<220>  
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<222> (495)  
<223> n equals a,t,g, or c

<220>  
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<220>  
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<222> (504)  
<223> n equals a,t,g, or c

<220>  
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<222> (509)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (538)  
<223> n equals a,t,g, or c

<220>  
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<222> (560)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature

<222> (586)  
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<220>  
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<222> (587)  
<223> n equals a,t,g, or c

<220>  
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<222> (619)  
<223> n equals a,t,g, or c

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tggtggggcc tancctgtt gggggctctg catgcccagg cccaggactc cacctcagac 120  
ctgatccag cccacctct nagcaagtc cctctgcagc anaacttcca cgacaaccaa 180  
ttccacggga agtggtatgt ggtacgcctg gcacggaatg caattctcag anaacacaaa 240  
gaccgcgaaa anatgtatgc caccatctat gagctgaagg aaacaaganc tacaatgtcc 300  
ctccgcctgt ttaagaaaaa aaaatgtgac tacttggatc aggaattttg gtccaaggtn 360  
gccanccggc gaattccacc ttggggacct ttaaaattgc cttggantaa ccaatttcct 420  
ccttccaatt gttancacca attacaacng ccttcttttg gtttcttcc anaaaatttc 480  
tccaaacaag gaatncttcc ananccccc ttccggaaaa acaaggaatt aattccgnac 540  
ttaaaggaaa aattctccgn tctcccattt cttgggcccc ctaaanncaa attcgtcttc 600  
ccttttccaa ccaacattnt ttt 623

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<211> 211  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (47)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (58)  
<223> n equals a,t,g, or c

<220>  
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<222> (77)  
<223> n equals a,t,g, or c

<220>  
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<222> (93)  
<223> n equals a,t,g, or c

<220>  
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<222> (121)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (131)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (178)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (195)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (207)  
<223> n equals a,t,g, or c

<400> 442  
tgggcagcca cactgcacgc aggctgggcc gactgagggg ctcagangcc aggctctnag 60  
gcccacgcag ggcctanggt gggaagatgg cangtggggg cggcgacctg agcaccagga 120  
ngctgaatga ntgtatttca ccagtagcaa atgagatgaa ccattcttct gcacacanc 180  
acgatttgca aaggntgttc acggaanacc a 211

<210> 443  
<211> 399  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (316)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (347)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (358)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (376)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (391)  
<223> n equals a,t,g, or c

<400> 443  
gtctgagtgg atggacactg cctcttagaa ctagaactta gaactttatc ttgaaaatgt 60  
accactgttg cagaagctcc tcacagagta tgtgtcaggc atttttaacc tgctaaaggc 120  
aagaagaagt gttcaccaca tagttgcaaa ggtcttcaac ttgccacagc caacagaaaa 180  
atcaaaatga ttgaaccctt tgggaatcaa gtatattgtg gccaggccag tgtattctac 240  
aaatgctttt gaggaaaatc ataaaaagac aggaagacat cataagacat ttctggatca 300  
tctcaaagtg tgttgnaact gttccccaca aaaggcaaga gaattgncct ctctttgntt 360  
cccatagcat tttggntgcc agcataccgg nttaaagaa 399

<210> 444  
<211> 465  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc feature  
<222> (376)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (390)  
<223> n equals a,t,g, or c

<400> 444  
gcgggactcc aaatgggtcg cagtcgcagc cgctctccac ggagggaacg taggcgttcc 60  
cggtccacat cccgggagag agaacgcagg cgccgagaaa ggtccaggtc tcgggagaga 120  
gatcgagaaa ggagccgctc gcgatccccg caccgaagac gctcccgatc tccaagacga 180  
catagatcca catctccttc cccttctcga ctgaaaagaaa gaagagatga ggaaaagaaa 240  
gaaacaaaaag aaacaaagag caaagaacgg cagattactg aggaagactt agagggcaaa 300  
acagaggaag aaatagaaat gatgaagtta atgggatttg cctcctttga ctccacaaaa 360  
ggtaagaagg tggatngctc tgtaaatgcn tatgccataa atgtctctca gaagaggaag 420  
tacaggtatg catagcccc atttttgttt gaactaataa atcag 465

<210> 445  
<211> 297  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (7)

<223> n equals a,t,g, or c

<400> 445

ggcagtntct ctgccaggct ggggatgatt ccaatagtaa taagaagaat gctgacctcc 60  
aaagtgctaaa gcccgagccc gagctgggtt atgaagacct gaggggctca gtgaccttcc 120  
actgtgccct gggccctgag gtggcaaacg tggccaaaat tctgtctggc agagagtggg 180  
gaaaagacgc ggtttccagc ttgcagattt gttaagtttc tcaggcagat ttgactttc 240  
agcctttcat acttgtttaa gcaactattt gtattaaatg aagtttttg aaaaaca 297

<210> 446

<211> 448

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (21)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (22)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (24)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (306)

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<220>

<221> misc feature

<222> (366)

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<222> (369)

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<220>

<221> misc feature

<222> (435)

<223> n equals a,t,g, or c

<220>



<221> misc feature  
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<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (448)  
<223> n equals a,t,g, or c

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gcagtctgtc gcctcagtggt taaattcggg gccacactca aaatcagcag gcttctcttg 120  
gaacggggcga gagagctgaa tattgacatc atcgggtgtca gcttccacgt gggaagtggc 180  
tgcaccgatc ctggagacct tcgtgcaagc catctccgat gcccgctgtg tcttcgacat 240  
ggggagctga gggttggttc aacatgtatc tgcttgatat cgggtggtggg ctttcctggg 300  
atctgnagga tgtgaaactt aaatttggaa gagatcacca tgttatcaac ccagccctgg 360  
gacaantant tcccggggccg aattcggggcg tggacattca tagccgagcc cgggcaggat 420  
aattaagttg gcttncagcn ttcaagcn 448

<210> 447  
<211> 268  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (10)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (21)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (36)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (43)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (45)  
<223> n equals a,t,g, or c

<220>  
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<222> (60)  
<223> n equals a,t,g, or c

<220>  
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<222> (99)  
<223> n equals a,t,g, or c

<220>  
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<222> (132)  
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<220>  
<221> misc feature  
<222> (135)  
<223> n equals a,t,g, or c

<220>  
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<222> (140)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (141)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (159)  
<223> n equals a,t,g, or c

<220>  
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<222> (183)  
<223> n equals a,t,g, or c

<220>  
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<222> (192)  
<223> n equals a,t,g, or c

<220>  
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<222> (206)  
<223> n equals a,t,g, or c

<220>  
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<222> (222)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (243)

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<220>

<221> misc feature

<222> (260)

<223> n equals a,t,g, or c.

<220>

<221> misc feature

<222> (262)

<223> n equals a,t,g, or c

<400> 447

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ggcacgaggn agtgtcccag ncggttcgt gtcgcnatgg ggnanatcga gtgggccatn 60
tgggccaacg agcaggcgct ggcgtccggc ctaatcctna tcaccggggg catcgtggcc 120
acagctgggc gnttnaccn ntgggtacttt ggtgcctant ccattgtggc gggcgtgttt 180
gtntgcctgc tngagtacc cgggnaaag aggaagaagg gntccaccat ggtgcgatgg 240
ggncagaagt acatgaccgn cntggtga 268
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<210> 448

<211> 425

<212> DNA

<213> Homo sapiens

<400> 448

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gacaccttca tccgtcacat cgcctgctg ggctttgaga agcgcttcgt acccagccag 60
cactatgtac atgttcctgg tgaaatggca ggacctgtcg gagaaggtgg tctaccggcg 120
cttcaccgag atctacgagt tccatctccc aagtggtttg acgggcagcg ggccgccgag 180
aaccaccagg gcacacttac cgagtactgc ggcacgtca tgagcctgcc caccaagatc 240
tcccgctgtc cccacctcct cgacttcttc aagggtgcgc ctgatgacct caagctcccc 300
acggacaacc agacaaaaa gccagagaca tacttgatgc ccaaagatgg caagagtacc 360
gcgacagaca tcaccggccc catcatcctg cagacgtacc gcgccattgc caactacgag 420
aagac 425
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<210> 449

<211> 88

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (25)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (26)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (71)  
<223> n equals a,t,g, or c

<220>  
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<222> (73)  
<223> n equals a,t,g, or c

<400> 449  
tcgttgccct gttactgtct gtggnnatgt gcatgggtcaa ttatcatgatc ttatgggaact 60  
ctttagaatt ngnggaaaat caccggat 88

<210> 450  
<211> 214  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc feature  
<222> (8)  
<223> n equals a,t,g, or c

<220>  
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<222> (26)  
<223> n equals a,t,g, or c

<220>  
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<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (49)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (53)  
<223> n equals a,t,g, or c

<220>  
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<222> (68)  
<223> n equals a,t,g, or c

<220>  
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<222> (71)  
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<220>  
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<222> (91)  
<223> n equals a,t,g, or c

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<223> n equals a,t,g, or c

<220>  
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<223> n equals a,t,g, or c

<220>  
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<223> n equals a,t,g, or c

<220>  
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<222> (205)  
<223> n equals a,t,g, or c

<400> 450  
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taccgganta ngtgnggatg gtgactgant nttcaaataa antacganac tgnnccaacc 120  
tctctgccac ggacatccaa ntgcttgac gcanatacca gttggaagca gagtttggtg 180  
gggtgtctca acnaaaagtt gagnaagca acgt 214

<210> 451  
<211> 473  
<212> DNA  
<213> Homo sapiens

<220>  
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<220>  
<221> misc feature  
<222> (444)  
<223> n equals a,t,g, or c

<220>  
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<222> (469)  
<223> n equals a,t,g, or c

<400> 451  
gcggacgcgt ggggcaagac ttttgcgcgg tacctttcat tccggcgtga caacaatgag 60  
ctgttgctct tcatactgaa gcagtttagt gcagagcagg tgacatatca gcgcaaccgc 120  
tttggggccc agcaggacac tattgaggtc cctgagaagg acttggtgga taaggctcgt 180  
cagatcaaca tccacaacct ctctgcattt tatgacagt agctcttcag gatgaacàag 240  
ttcagccacg acctgaaaag gaaaatgatc ctgcagcagt tctgaggccc tatgccatcc 300  
ataaggattc cttgggattc tggtttgggg tggtcagtgc cctctgtgct ttatggacac 360  
aaaaccagan cacttgatga actcggggta ctagggtcag ggcttatagc aggatgtctg 420  
gctgcacctg gcatgactgt ttgnttctcc aacctgcctt gtgcttctna cct 473

<210> 452  
<211> 397  
<212> DNA  
<213> Homo sapiens

<220>  
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<220>  
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<220>  
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<223> n equals a,t,g, or c

<220>  
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<222> (376)  
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<220>  
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<222> (387)  
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<220>  
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<222> (389)  
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tcgttttggc attgcagcta aatatcagtt ggatccact gcttccattt ctgcaaaagt 120  
caacaactct agcttaattg gagtaggcta tactcagact ctgaggcctg gtgtgaagct 180  
tacactctct ggctctggta gatgggaaga gcattaaatg ctggnaggcc acaagggttg 240  
ggctcgccct gggagttggg aggcttaatc cagctgaaag aaacctttgg ggaatgggat 300  
atccagaaga tttgggcctt aatataattn ccattgtgga ccagcagcag gctttttttc 360  
cccccaagaa gattgntcca aaccnangnt gatctcc 397

<210> 453  
<211> 463

<212> DNA  
<213> Homo sapiens

<220>  
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<220>  
<221> misc feature  
<222> (393)  
<223> n equals a,t,g, or c

<220>  
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<223> n equals a,t,g, or c

<220>  
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<222> (426)  
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<220>  
<221> misc feature  
<222> (435)  
<223> n equals a,t,g, or c

<220>  
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<222> (453)  
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tacggggaca tcgtgatgac ccagtctcca gactccctgg ctgtgtctct gggcgagagg 120  
gccaccatca actgcaagtc cagccagagt gttttataca gtcacaaca taagaactac 180  
ttaacttggg accagcagaa accaggacag cctcctaagc tgctccttta ctgggcatct 240  
acccgggaat ccgggggtccc tgaccgattc agtggcagcg ggtctgggac agatttcact 300  
ctcaccatca gcagntgca ggctgaagat gtggcagatt attactgtca gcaatattat 360  
actactccct ggacgttcgg ccactggacc aangtgaaa tcanacgaaa ctgtggctgc 420  
accatntgcc tcatntttcc gccatctggg gancagttga aat 463

<210> 454  
<211> 332  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc feature  
<222> (95)



<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (332)

<223> n equals a,t,g, or c

<400> 454

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ccacttcgta tgctggttga aacagctcag gaganaaatg aaacgctttt tccagctctc 120
atttactcct caacaatggt gtggttggtg aatatggcag aaggagaccc ggaagctcaa 180
aggagagtat ccaaaaattc caagtataat gcagaaaagca cagaaaggag tcacaagaca 240
ctgttgacaga gaatgatgat ggcgggttca gtgaggaatg ggaagcccag aaggacagtc 300
atctagggcc tcatcgctct acacctgaat cn 332
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<210> 455

<211> 429

<212> DNA

<213> Homo sapiens

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<221> misc feature

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<220>

<221> misc feature

<222> (11)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (12)

<223> n equals a,t,g, or c

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<221> misc feature

<222> (99)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (105)

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<222> (107)

<223> n equals a,t,g, or c

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<222> (346)  
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<220>  
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<222> (392)  
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cgtgggttcca gagagcggtt ttgaccgcca cattaccant ttttnancng agggtcggct 120  
ctaccaagta ggaatatgct ttnaaggnta ttaaccangg tggacttaca tnagtagctg 180  
atcagcggga aagactgtgc agtaattgtc acacagaaga aagtacctga caaattattg 240  
gantccagca cagtgactca cttattcaag ntanctggaa acattgggtg tntgaagacc 300  
ggaatgtcag ctgncagcag atcccaggta cagagggcac gctatnaggc agctaacttg 360  
gaatacaagt atggctatga gnttcctgtg gncatgcctg tgtaaaagga tttccgggtat 420  
ttctcaggt 429

<210> 456  
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<212> DNA  
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<222> (352)  
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<222> (588)

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<222> (604)

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<400> 456

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gccggttgcc aggccaagga gtggactagg gtgcggggg aagcggttg ggagagccca 120
tggtgactgc gtgagtggag cccagctgtg tggatgccc agcatggatg actacatggt 180
cctgagaatg attggggagg gctcgttcgg cagagctctt ttggttcaac atgaaagcag 240
taatcaagat gtttgccatg aaagaaataa ggcttccaag tctttctcta atacacagaa 300
ttctaggaag gaggtgttgc ttttagccaa aatgaaacac cctaattattg gngccttcaa 360
agaatcattt gaaagctgca ggacacttgt atattgtgat ggaatactgt gatggacggg 420
atctaattgca aaagattaaa cagcagaaaa ggaaaagtta tttcctgaag acatgatact 480
tnaatgggtt acccaaagt gccttgaggt aaaatnacat ttaccaagaa acgtgtgctn 540
cccaagagat ttnaaagtc ccaaaaaatn tttttcctta acctcaanaa ttgggaaaaa 600
gttnaaaatt ggggaaaaac ttt 623
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<210> 457

<211> 441

<212> DNA

<213> Homo sapiens

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<222> (13)

<223> n equals a,t,g, or c

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<222> (432)

<223> n equals a,t,g, or c

<400> 457

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ggetgcactt gcttgcttcc acttatgctt gttctcagaa cacaaacaaa acctgtgaag 120
agtgcctgaa aaacgtctcc tgtcttttgt gcaacactaa caagcttgtc ttggactacc 180
agttncaaaг tcttgccacc ggcttccctt tgттааттаа ctnccttgac ctngggaatt 240
ttgttgggtn aaacttagaa gcgctgaatc atcacatgtt cggtagtccg gggaaaccctc 300
ctcctggggc attggcatct gctgcttgct tgcttgctgc aagaagaaaa aaagaaccctc 360
aaacccgгac aggaattaaa gaaaaaaggc nttgcgttna accgгaaaga aaaagcngaa 420
taccggccgg angaacггaa a 441
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<210> 458

<211> 419

<212> DNA

<213> Homo sapiens

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<222> (278)

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<222> (408)

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<222> (409)

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<220>

<221> misc feature

<222> (410)

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<400> 458

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agagcgagag actctgcagg cctggaagga gcgcgtgggg caggagctgg accgcgtggt 120  
ggctttcttg atggagcact cccacgacca ggagcacggg ggcttcttca cgtgccttgg 180  
ccgcgagggg cgggtgtatg atgacctcaa gtatgtgtgg ctgcagggga ggcaggatatg 240  
gatgtattgt cngcctgtac cgcactttcg agcgcttncg ccatgctcag cttctggacg 300  
cagcanaagc aggtggtgag ttcttgctgc ggtatgcccg ggtggcacct tctggcaaga 360  
agtgtgcctt tgtgctgact cggtgacggc cgcccgggtca angngcannn aaccatctt 419

<210> 459

<211> 509

<212> DNA

<213> Homo sapiens

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<220>  
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<223> n equals a,t,g, or c

<220>  
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<400> 459  
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tatattaaag gcttcccaac tgatgcaact cttgatgaca taaaagaatg gttagaagat 120  
aaaggtcaag tactaaatat tcagatgaga agaacattgc ataaagcatt taagggatca 180  
atthttgttg tgthttgatag cattgaatct gctaagaaat ttgtagaggc ccctggccag 240  
aagtacaaag aaccagacct gctaatactt ttcaaggccg gttnccttgc caaaaaatga 300  
ggaagaanca aataagtga gctaattagg nttacagggc agagcaacca agttgaggag 360  
tcctgatgna ctctggngaa gttggtcctt ctnatttcgg ggttngtgcg gccttgggng 420  
ttcncacttt tcctcagggn taatgtgctc ccaggccagg gtttttttag anccggcttg 480  
taccngtcan tgnccctng cnggtcttg 509

<210> 460  
<211> 468  
<212> DNA  
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<220>  
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<221> misc feature  
<222> (445)  
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<220>  
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<222> (459)  
<223> n equals a,t,g, or c

<220>  
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<222> (465)  
<223> n equals a,t,g, or c

<220>  
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<400> 460  
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gtgggtgtgtt cttgactccg ctgctcgcca tgtcttctca caagactttc aggattaagc 120  
gattcctggc caagaaacaa aagcaaaatc gtcccattcc ccagtggatt cggatgaaaa 180  
ctggaaataa aatcaggtac aactccaaaa ggagacattg gagaagaacc aagctgggtc 240  
tataaggaat tgcacatgag atggcacaca tatttatgct gtctgaaggc cacgatcatg 300  
ttaccatatt aagctgaaaa tgtcaccact atctggagat ttcgacgtgt tttcctctct 360  
gaatctgtta tgaacacgtt gggtggctgg attcagtaat aaatatgtaa ggcctttctt 420  
tttaaaaaaa aaaaaaaaaa aaaaanaaan acaaaaaana tcaanaaa 468

<210> 461  
<211> 580  
<212> DNA  
<213> Homo sapiens

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<220>  
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<220>  
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<222> (54)  
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<220>  
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<220>  
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<223> n equals a,t,g, or c

<220>  
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<220>  
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<222> (575)

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<400> 461

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cgcttgcagg taccgggtccg gaattcccgg gtcgacccac gcgtccgtcg acccacgcgt 120
ccgcccacgc gtccgcccac gcgtccgccc acgcgtccgc tgtgtcgtaa aatgggggtc 180
ccttactgca ttatcaaggg aaaggcaaga ctgggacgtc tagtccacag gaagacctgc 240
accactgtng ccttcacaca ggtgaactcg gaaagacaaa ggcgctttgg ctaagctggg 300
ggaagctatc aggaccaatt acaatgacag atacgatgan atccgcccgt ccactggggg 360
tggaatgtt ccctgggtcc ctaattcttg ttgctccgta tcgcccact ccgaaaaagg 420
caaaagntta aanaactttg ccacttaaac tngggttaaa tnttcnctgn tnaatttncc 480
ctgttccctt aaaaataatt gaaattatnn aatttcccc tccccaaaaa aaaaaaaaaa 540
gggggggccc ttaaanattc cccccnaag gggcnaatta 580
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<210> 462

<211> 549

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (3)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (5)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (8)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (11)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (13)

<223> n equals a,t,g, or c

<400> 462

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acngnganac nancctcact aaaggggaaca aaagctggag ctccaccgcg gtgcggccgc 60
tctagaacta gtggatcccc cgggctgcag gaattcggca cgaggcgccg ccacaatggt 120
gcgcatgaat gtcctggcag atgctctcaa gagtatcaac aatgccgaaa agagaggcaa 180
acgccagggtg cttattaggc cgtgctccaa agtcatcgtc cggtttctca ctgtgatgat 240
gaagcatggt tacattggcg aatttgaaat cattgatgac cacagagctg ggaaaattgt 300
tgtgaacctc acaggcaggc taaacaagtg tggggtgatc agccccagat ttgacgtgca 360
actcaaagac ctggaaaaat ggcagaataa tctgcttcca tcccgccagt ttggtttcat 420
tgtactgaca acctcagctg gcatcatgga ccatgaagaa gcaagacgaa aacacacagg 480
agggaaaaatc ctgggattct ttttctaggg atgtaatata tatatttaca aataaaatgc 540
ctcatggac 549
```

<210> 463

<211> 480

<212> DNA

<213> Homo sapiens

<220>

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<222> (7)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (130)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (320)

<223> n equals a,t,g, or c

<220>

<221> misc feature  
<222> (410)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (416)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (450)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (455)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (456)  
<223> n equals a,t,g, or c

<400> 463  
gcctctngcg ggccctgttc aagcgggaatc ctgccaaccg gctcgggtcc ggccctgatg 60  
gggcagagga aatcaagcgg catgtcttct actccaccat tgactggaat aagctatacc 120  
gtcgtgagan cagccacccc ttcaagccag cagtgggtca gcctgatgac accttctact 180  
ttgacaccga gtacacgtcc cgcacaccca aggattcccc aggcattcccc cccagcgctg 240  
gggcccacatca gctgtttccgg ggcttcagct tcgtggccac cgccctgatg gaagacgacg 300  
gcaagcctcg tgccccgcan gcaccctgc actcgggtgg acagcaactc catgggaaga 360  
acctgggttt tagtgacggc tacgtggtaa aggagacaat tgggtgtgggn tcctantctg 420  
agtgaagcg ctgtgtccac aaagggccan aacannaata atgcaatagg ggaggtaaca 480

<210> 464  
<211> 220  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (16)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (17)  
<223> n equals a,t,g, or c

<220>  
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<222> (18)  
<223> n equals a,t,g, or c

<220>  
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<222> (30)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (42)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (58)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (63)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (67)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (72)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (105)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (129)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (147)  
<223> n equals a,t,g, or c

<220>  
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<222> (157)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (170)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (213)

<223> n equals a,t,g, or c

<400> 464

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agggacacgt cccatnnngt ggcgggcgcg ctgcggccct tngtgcaggc cacggtgncc 60
gcnaccngaa gncagcctgt ttggaccta aagcggccct tcctnagccg ggagtcgctg 120
agcggccang cctgcgatcg acttgtngtc gactccntgg gtgctcaatn tccctgcttc 180
tttttgtaa ttccacaca gacatcaagg tgnctgattt 220
```

<210> 465

<211> 438

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (330)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (366)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (383)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (403)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (414)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (428)



<223> n equals a,t,g, or c

<400> 465

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ataggcatga gccaccacgc caggccggga atgccctatt ctaattcaca taaagactcc 60
atgtgggcta gcaggcatgt gaaatgtctg ccagtgcac aacagctata taactaagaa 120
gttatctttt tcaactgtctt ctggtactct tcatttcact tgggtttttt agcaattcag 180
gaagctggaa tggttgaatg ggttttagct tgataccttc ttctttttcc catttggcag 240
ataataccac tagtctgacg gataaacacc tggacccaat cagggaaaat ctgggaaaagc 300
actgggaaaa actgtgcccg taaactgggn ttcacacagt ctcagattga tgaattgacc 360
atgacnatga gcgagatgga tgnaagaaag gttaccagat gcnccaaaat gggngatgag 420
gaaggctnaa ggggcccg                                     438
```

<210> 466

<211> 127

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (21)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (53)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (87)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (94)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (118)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (122)

<223> n equals a,t,g, or c

<400> 466

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gcacgattca tgcaaaaagg naactaagca ctatgagatg cttgctaadc gancagctgc 60
aaatgggtcac tgcattgata tttatgnttg tgcncctgat caaactggac ttttgganct 120
gnagtgt                                     127
```

<210> 467  
<211> 439  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc feature  
<222> (40)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (194)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (295)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (409)  
<223> n equals a,t,g, or c

<400> 467  
gctggaatct ttacaggaga accacttcca agaagatgan cagtttcttg gagccgttat 60  
gccaaaggctt ggcattggaa tggatacttg tgcattcct ttgaagcacg gtgggctttc 120  
cttggttcaa accacagatt acatttacct gatcgtagac gacccttaca tgatgactcc 180  
tgcagttgct gaantcaggc ctgtcccctg cccacacttg gcactgggca taaagcaatt 240  
agggaggaag caggaaaagcc ctctgctgct gttgcaactg aatacatgct ggcangataa 300  
catgtgccaa tgtcctcagt gactctatgc aatgggggtc acggaatgtg acaatatgct 360  
gatgctcctt ggaatcataa taaaatgacc gacaggaaaa ggataaatna tcctctgatt 420  
atccaagggtt ttaaaacca 439

<210> 468  
<211> 484  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (350)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (399)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (412)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (415)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (449)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (463)  
<223> n equals a,t,g, or c

<400> 468  
gagcaggccc gttggaagtg gttgtgacaa cccagcaat gtggagaagc ctggggccttg 60  
cctggctctc tgtctcctcc catcgggagg aacagagagc caggaccaa gctccttatg 120  
taagcaaccc ccagctggac ataagagatc aagatcaatg ctaaaactcca atgggttcagt 180  
gactgtggtt gtcttcttca agccagctga tacctgtcat actgcaggca tctaaattag 240  
aaacctgcga gtaaaactga agaaagaagg atattctaata attcttataat tgtgtaatat 300  
taaggaaatct cttctcgata aaatcacaca tctaagaata aggttaaaan atatttctgt 360  
tataccagaa gaaacaacaa tgctgactct ttaatgaana aataactctat antanatggg 420  
cgctgaatac tgttgctttc tcacttcang aaaacataat gtntgaaaat ggacgtttca 480  
ttaa 484

<210> 469  
<211> 489  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc feature  
<222> (308)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (348)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (368)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (371)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (387)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (417)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (420)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (458)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (468)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (477)  
<223> n equals a,t,g, or c

<400> 469  
cgccctggcga ttaccggtct caccatggag cggaaagtgc ttgcgctcca ggcccgaag 60  
aaaaggacca aggccaaagaa ggacaaagcc caaaggaaat ctgaaactca gcaccgagggc 120  
tctgctcccc actctgagag tgatctacca gagcaggaag aggagattct gggatctgat 180  
gatgatgagc aagaagatcc taatgattat tgtaaaggag gttatcatct tgtgaaaatt 240  
ggagatctat tcaatgggag ataccatgtg atccgaaagt taggctgggg acacttttca 300  
acagtatngg ttatcatggg gtattccagt taagttttta ttggttcntg taaaaagatt 360  
agtttaganga ngtctaaaag ggtttgntct agttccatgg tggacccagg ttcaacnacn 420  
ctagccggtc cattaccaga atttgttgtt ggcaaaagncc cgatcctngg ggaaccnttt 480  
ctttcggaa 489

<210> 470  
<211> 318  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc feature  
<222> (2)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (12)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (21)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (32)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (73)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (102)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (103)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (106)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (114)  
<223> n equals a,t,g, or c

<220>  
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<222> (151)  
<223> n equals a,t,g, or c

<220>

<221> misc feature  
<222> (188)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (223)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (258)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (264)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (280)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (281)  
<223> n equals a,t,g, or c

<400> 470  
cntcactata tntgaggagc nggtaccct gnaggtaccg gtccggaatt cccgggtcga 60  
cccacgcgtc cgntatgaca acctgatcac accagccatg annggngccg gctncctgca 120  
ggggaacgtc gattcttgcc agggtgacag nggagggcct ctggtcactt cgaagaacaa 180  
tatctggngg ctgatagggg atacaagctg gggttctggc tgngccaaaag cttacagacc 240  
aggagtgtac ggggaatgnga tggnatcac ggactggatn natcgacaaa tgagggcaga 300  
cggctaattcc acatggct 318

<210> 471  
<211> 455  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc feature  
<222> (306)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (417)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (426)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (431)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (440)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (446)  
<223> n equals a,t,g, or c

<400> 471  
ggagtataca ccatgagcaa agctcaccct cccgagttga aaaaatttat ggacaagaag 60  
ttatcattga aattaaatgg tggcagacat gtccaaggaa tattgcgggg atttgatccc 120  
tttatgaacc ttgtgataga tgaatgtgtg gagatggcga ctagtggaca acagaacaat 180  
attggaatgg tggtaatacg aggaaatagt atcatcatgt tagaagcctt ggaacgagta 240  
taaataaatgg ctgttcagca agagaaaccc atgtcctctc tccatagggc ctgttttact 300  
atgatnttaa aaattaagtc atgtacattt tcatattaaa ctttttgta aataaaacttt 360  
tgtaataatc aaaaaaaaaa aaaaaaaaaa aaaccaagg gggggcccg tccccantcc 420  
ccccntttt nattcctttn aaaatncctt ggccc 455

<210> 472  
<211> 676  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc feature  
<222> (605)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (669)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (672)  
<223> n equals a,t,g, or c

&lt;400&gt; 472

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gctccaggag tgggacggag ggagctggcc gggatgaagt ctgagactat gtcctgagaa 60
gaaagagtgt atcgtattgg ttgaaaagtt ggtggggtcg ggcttaagcg gaggaggggg 120
ctctctggcc cttactcggc agatggggcc ggagagagga cgggaggtgc cgggagaaca 180
tcgagggacc ggtggaggaa gggtagctgg atgagttttg attcatcatg gataatctgt 240
catcagaaga aattcaacag agagctcacc agattactga tgagtctctg gaaagtacga 300
ggagaatcct gggtttagcc attgagtctc aggatgcagg aatcaagacc atcactatgc 360
tggaatgaaca aaaggaacaa ctaaaccgca tagaagaagg cttggaccaaa ataaataagg 420
acatgagaga gacagagaag actttaacag aactcaacaa atgctgtggc ctttgtgtct 480
gccccatgtaa tagaacaagg aactttgagt ctggcaaggc ttataagaca acatggggag 540
atggtggaga aaactcacct tgcaatgtag tatctaaaca gccaggcccg gtgacaaatg 600
gtcanccttta gcaaccaaca acaggagcag ccagtgggtg atacattaaa cccataacta 660
atgatcccng anaaga 676
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&lt;210&gt; 473

&lt;211&gt; 512

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (1)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (403)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (457)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (487)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (495)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (500)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; misc feature



<222> (506)

<223> n equals a,t,g, or c

<400> 473

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ntcgacagaa ggggtacggct gcgagaagac gacagaaggg tacggctgcg agaagacgac 60
agaagggggc agcatggcgt acccggggca tcctggcgcc ggcggcgggt actaccag 120
cgggtatgga ggggctcccg gagggcctgc gtttcccgga caaactcagg atccgctgta 180
tggttacttt gctgctgtag ctggacagga tgggcagata gatgctgatg aattgcagag 240
atgtctgaca cagtctggca ttgctggagg atacaaacct tttaacctgg agacttgccg 300
gcttatgggt tcaatgctgg atagagatat gtctggcaca atggggttca atgaatttaa 360
agaactctgg gctgtactga atggctggag acaacacttt atnaattttt gacactgcag 420
gaatggaaca agtagacca caagaattgg ataaagnccc tgacaacaat gggatttaag 480
gtttgantcc ccaanctggn gaattnaatt gc 512
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<210> 474

<211> 272

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (18)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (59)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (69)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (74)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (104)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (122)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (129)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (150)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (185)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (186)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (191)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (234)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (249)  
<223> n equals a,t,g, or c

<400> 474  
ggcacagcgg cgggccnngt cgtccggcgg ttgcggatgt cgggctgggc ggacgagcnc 60  
ggcgtcgang gccnacgggc gcatctacgt ggggaacttc cgancgacgt gcgcgagaag 120  
gnacttgga ggacctgttc tacaagtacn gccgcatccg cgagatcgag ctcaagaacc 180  
ggcannccctc ntcctgtcgg cttcgtgcg cttcgaggaa ccccgagat gcanaggatg 240  
ctatttatng gaagaaatgg ttatgattat gg 272

<210> 475  
<211> 338  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc feature  
<222> (1)  
<223> n equals a,t,g, or c

<220>

<221> misc feature  
<222> (8)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (15)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (16)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (36)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (119)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (127)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (170)  
<223> n equals a,t,g, or c

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cgcccggtta ccattctgaa acaaatgcaa gtattacatc cagcagccag aatgctggng 120
gagctgncta aggtcaaga tatagaagca ggagatggca ccacatcagn agncatcatt 180
gctggctccc tcttagattc ttgnaccaag cttcttcaga aagggattca tccaaccatc 240
atttctgagn cattccagaa ggccctggaa aagggcattg aaancttgac tgacatgnct 300
cgacctgngg aactgagnga cagagaaact ttggtaaa 338
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<210> 476

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ttagccagga atggaaggat gagaagcggg atttgctgac tgaaggacaa agtttttagca 180  
gccttgatga agaagccctg ggatcccgcac acaggccaga cctgggccct agcactccat 240  
cactgtttga agctgcttcc ttggcaacca caatttcact tcttctata cgtcaatggg 300  
cattatccac aagacaaggc ctacaatttn ttcaaaccag gtaatatattt ggtgcaattc 360  
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ttgn 424

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aaggcaccga ttcctattga acttggtgtt gtngtancag ccacnttaac ctctcatttt 180  
ggaaaactac atgaaaatta taattcnagt attgctggac atnttccc 228

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<400> 478  
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tgcaggtggc tggcgagacc tacagcttgc acgtgggctg cgacctcata gacagcttcg 180  
ctctggacga gcccttctac gagcacctgc aggcggaaaa gagccgatg tacgtggcca 240  
aaggctctgc cagagagagt cacttcaggg gtttgcttca gaacgtccac ctagtgtttg 300  
aaaactctgt ggaagatatt ctaagcaaga agggttgcca gcaaggccag ggaggtaggt 360  
gtgttgtgaa aaatgcattt tatatactgg cttggatgga tttctattgt gacatgggtg 420  
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ttcctccgca accatgtctg acaaaccgca tatggctgag atcgagaaat tcgataagtc 180  
gaaactgaag aagacagaga cgcaagagaa aaatccactg ccttccaaag aaacgattga 240  
acaggagaag caagcaggcg aatcgtaatg aggcgtgcgc cgccaatatg cactgtacat 300  
tccacaagca ttgccttctt attttacttc ttttagctgt ttaactttgt aagatgcaaa 360  
gaggttggnt caagtttaaa tgactgtgct gcccctttca catcaaagna ctactgacaa 420  
cgaaggccgc gncgtgccttt cccatctgtc tatctatctg gctggcaggg naggaaagaa 480  
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aactgncann cannagtgcg tcctnnggaa cagcgaaatg ncccgnacaa cctccaagtg 180
nctgcnaggc gggncgtgtg cacccttctgc ctctctgccc caatgatgaa ggnggggttc 240
tgccccccagg tgnaacatta aacttttccc aggtngggcc tctgttcggg caccatgcca 300
ggtngt                                     306
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<210> 481

<211> 473

<212> DNA

<213> Homo sapiens

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<222> (411)

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<222> (418)

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<222> (431)

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aaagaaacaa tcatgaacca ggaaaaactc gccaaactgc aggcacaagt gcgcattggt 180  
gggaaaggaa ctgctcgcag aaagaagaag gtggttcata gaacagccac agcagatgac 240  
aaaaaacttc agttctcctt aaagaagtta ggggttaaaca atatctctgg tattgaagag 300  
gtgaatatgt ttacaaacca aggaacagtg atccacttta acaaccctaa agttcaggca 360  
tctntggcag cgaacacttt caccattaca ggccatgctg agacaaagca nctgacanaa 420  
atgctaccca ncatcttaaa ccagnttggt gcggatagnc tgactaagtt taa 473

<210> 482

<211> 571

<212> DNA

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gatgacggtn cggggcgccct ctcccagga cncttggtc aagggtggagt atgcctacag 120  
cgacaacagc ctggaccccg ggctttttgt agaaagcacc cgcaagggga gtgtagtggtc 180  
cagagctaat agcatcggtt ccaccagtgc ctcttctgtc cccaacacag atgatgagga 240  
cagtgattac caccaggagg cctacaagga gtcctacaaa gaccggcggc ggcgcgnaac 300  
acacttnagg cttgagcaga agaggaggga cgccatcaag agaggctatg atgaccttca 360  
gaccatcgtc ccacttgcc agcagcagga cttctccatt ggctcccaa agctcagcaa 420  
agccatcgtc tacaaaagac cattgactac attcagtttt tgcacaagga gaagaaaaag 480  
caggaggagg aggngtcacg ttacgcaagg atgtaccggc ctaaagatca tgaaagtga 540  
ctatgagcan attgtgaagg cacantagna n 571

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<220>  
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acccacgcnt nccggccagg atgctgaatc tgetgctgnt ggcgctggcc gtcctggcga 120  
gccgcgccta cgcggncct gccccaggcc aggcctgca gcgagtgggc atcgtcggng 180  
gtnangaggc cccaggagc aagtggcct ggcangtgag 220

<210> 484  
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cgctctagaa ctagtggatc ccccgggctg caggaattcg gcacgagcag cccagcagcg 120  
gctgaccctc tgcctgcggg gaagggagtc gccaggcggc cgtcatggcg gtgtcggaga 180  
gccagctcaa gaaaatggtg tccaagt tttt taacgatggc agttccaggg aactaatgaa 240  
cctcactgga acaatccctg tgccttatag aggtaataca tacaatattc caatatgcct 300  
atggctactg gacacatacc catataatcc ccctatctgt tttgttaagc ctactagttc 360  
aatgactatt aaaacaggaa agcatgttga ttgnccaaaa aaattngggg gggnaaaaaa 420  
ggggaaaatt ttanttttt 439

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<210> 486  
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tattatgagt aaaagtttgc atgatgatgg ntttactgnt ccacagatta ttgaaatgga 180  
gctggatagt caggagcaag ttgttggtgc aggatcctcc tgtgacttac attcagcaat 240  
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ccaagcctgg gactttggtt caagtgcttg aggctgcaaa gtttgcatag gangagaatc 360  
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tggaatgggg caaaatta 558

<210> 487  
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<212> DNA  
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<220>  
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<220>  
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tcaaggtctc gctcagctna aggcattgtac ctacaaaggt cacaagacag gtggnactgn 120  
agagcanata tgggagatcc agaaggatca acttntatac tatccattct taaaaatgtg 180  
cctttcagca aatgntgagc atncaagctt agtggatgca acccatcana accactccna 240  
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<222> (412)

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<220>

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<220>

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<220>

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<220>

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<222> (440)

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<220>  
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<223> n equals a,t,g, or c

<220>  
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<223> n equals a,t,g, or c

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aaatgacttc tgaagattta gaaaatgctc taaaagcagt catcaatgac aaaagttaca 120  
aggagaacat catncgcctc tccagccttc acaaggaccg cccggtggag ccgctggacc 180  
tgcccggtgt ctgggtggag tttgtgatga ggcacaaggc cgcgccacac ctgcgncccg 240  
cncccccacg acctcacntg gtaccagtac cattnccttg gccgtgantt ggtttccntn 300  
ttggcccttg gtcntgaaat tggccttaat aacctttaa attttgctnt natggttacc 360  
cgaaaatttt ggggnaaaaa agggccnttt aagaaaagccn caaaatnaga cnnccctttg 420  
aaangggtn gganaaaaggn naaaattttt accttncncg gnatttccna atttnaanag 480  
atagngttta aanatttttt ttttttagg 508

&lt;210&gt; 489

&lt;211&gt; 425

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (3)

&lt;223&gt; n equals a,t,g, or c

&lt;400&gt; 489

ccnccggtggg atgttgagct gaggccggag gagaagtagc agtcgctggc agagcacaca 60  
ggctgctctg ggggatgagc tgggtgcgtt aaggaacagg ccagcactgg cattcgcaag 120  
cagtggggaa ggggagagat gccgaggtg tcatgtatcct gactttcaga ggcctttttt 180  
tgtttgtttt aatttttgc agattgatat taaaaactca tgtggaggaa ctcaaggaat 240  
gtttagaaga ccaaaagtcc ccaatgacag gaacaaaagc aaccaatttt taactttctc 300  
ttctcattcc tgttttcatt gatttccac atgtagtcc tttgttcagg aagtccttgg 360  
ggaaattaag gatctttgaa gctctgaaat aggtgatcag gttagtggg tctgtcagct 420  
gtctg 425

&lt;210&gt; 490

&lt;211&gt; 607

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (2)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (5)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (6)

&lt;223&gt; n equals a,t,g, or c

<220>  
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<222> (8)  
<223> n equals a,t,g, or c

<220>  
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<222> (9)  
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<220>  
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<223> n equals a,t,g, or c

<220>  
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gctctagaac tagtggatcc cccgggctgc aggaattcgg cagcagaagc cgtcaaggag 120  
tagaaattgg tatgcttaga agcagattct aaaagcagtt tctcttcaga acatcttttt 180  
tcataccact tgataagcat cttgaaacac catggctgta gctgcagtaa aatgggtgat 240  
gtcaaagaga actatcttga aacatttatt tccagtccaa aatggagctt tatattgtgt 300  
ttgtcataaa tctacgtatt ctctcttacc agatgactat aattgcaacg tagagcttgc 360  
tctgacttct gatggcagga caatagtatg ctaccaccct tctgtggaca ttccatata 420  
acacacaaaa cctatccctc ggncagatcc tgtgcataat aatgaagaaa cacatgatca 480  
agtgtctgaaa accagattgg aagaaaaagt tgaacacctt gaggaaggac ctatgataga 540  
acaacttagc aaaatgtttc ttactacta agcaccgttg gtatcctcat ggacgggtatc 600  
acagatg 607

<210> 491  
<211> 371  
<212> DNA  
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<220>  
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<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (265)  
<223> n equals a,t,g, or c

<220>  
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<220>

<221> misc feature

<222> (339)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (353)

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<220>

<221> misc feature

<222> (364)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (368)

<223> n equals a,t,g, or c

<400> 491

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gattgagttg cttctggagt nggcagggtc actgtgaacg cctacgtgag cctcttctac 120
accataaaagc gggcacaagt ggtcagtcct gaaagagtcg gaagctggca tatcggccgc 180
ccaagtgaac ctgtccagtg tctgcttgcc atcctgccag aacaggccct caagcccaag 240
agccatccca ggcctgtttc agctncagct aaagcctctc tttcatctgg aagaagaggc 300
aagggggcag gagaccaggc tctagctctg gggccntcnt tcagcccca tcnggggaat 360
aaanttantt t 371
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<210> 492

<211> 440

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (347)

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<220>

<221> misc feature

<222> (353)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (397)

<223> n equals a,t,g, or c

<220>  
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<222> (402)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (434)  
<223> n equals a,t,g, or c

<400> 492  
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acctttggga gtaataactga agagaggggt ctgcagaaag gatgtgtatg aagcttagat 120  
aataatggct gtttcgtaaa ctgtttgaga cctattaatg aaaatgacta tttcttgctg 180  
tttttatcca acgtctgcat tttccccctt taaagctgcg gtctcctgtt tgataaaaga 240  
atattggcca gtattgcaga ttttaactgg atttggtga tcctccaggg gaccagtttc 300  
tgtgggcgtg tattggagca ggtttgtctt taactcttaa atggttnggt ccnaattttt 360  
aaaaaggaag ggccccaagt agcccagatt taaaggngta tnccattcc caaagttcct 420  
tggaacaatt accnaaagga 440

<210> 493  
<211> 90  
<212> DNA  
<213> Homo sapiens

<220>  
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<220>  
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<222> (20)  
<223> n equals a,t,g, or c

<220>  
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<222> (27)  
<223> n equals a,t,g, or c

<220>  
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<222> (49)  
<223> n equals a,t,g, or c

<220>  
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<222> (56)  
<223> n equals a,t,g, or c

<400> 493

ngggagctgg cctggagcgn atgggcnccg tgatggatcg catggccanc ggctgncagc 60  
gcatggggccc atcaatctgg agcggatcgg 90

<210> 494

<211> 218

<212> DNA

<213> Homo sapiens

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<222> (30)

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<222> (40)

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<222> (53)

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<220>

<221> misc feature

<222> (78)

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<222> (163)

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<222> (167)

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<222> (192)

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ctcatacaaa attttccnga taaatgnaat ttaancctcg ttttctcct cttcttcgtc 120
ctggttaatc tgggnagtaa cgtaattcgt aactctcttt ggntgtnagc aactgacgcg 180
caaccagttc angtagatta ttcttcttca aatatngt 218
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<210> 495

<211> 148

<212> DNA

<213> Homo sapiens

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<220>

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<222> (83)

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<220>

<221> misc feature

<222> (96)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (111)

<223> n equals a,t,g, or c

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<221> misc feature

<222> (116)

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<220>

<221> misc feature

<222> (122)

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<400> 495

gtttttaaaa aaaacatgtc atgtangttg tctaaaaata aaatgcattt aaactcaaaa 60  
aaaaaaaaaa aaaaaaaaaa aanagggggg gggcgnggga aaaaaaaaaa ngaggntgag 120  
gntttgaaga agggaagggg ggccccc 148

<210> 496

<211> 536

<212> DNA

<213> Homo sapiens

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<220>

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<222> (382)

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<220>

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<222> (412)

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<222> (460)

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<222> (484)

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<222> (534)

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<400> 496

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gaggggaagga gcccgagccag aaagcactac aatcatgggc aagttcccaa ctgagtcac 120
ttgtgagtgga ataatcagga aaaatgagga atccaaaaga caaaaatcaa agaacagatg 180
gggtctgtga ctggatcttc tatcattcca attctaaatc cgacttgaat attcctggac 240
ttacaaaatg ccaaggggggt gactggaagt tgtgggatat cagggtataa attatatccg 300
tgagtggggg gaggggaagac cagaattccc ttggaattgt gtattgatgc cattntaagc 360
ctaaaagatc accttgtatt cncctttacct tctaaaagcc attatttatg gngttagaag 420
aagaggaaga aattcaggtg ccgnaaaaca cttttgttcn gggggggggcc cgtacccaat 480
tcgncccata gtgagtcgta ttacaatcac gggccgctcg ttacacggcg gacnng 536
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<210> 497

<211> 93

<212> DNA

<213> Homo sapiens

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<220>

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<222> (85)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (88)

<223> n equals a,t,g, or c

<220>

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<222> (89)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (91)

<223> n equals a,t,g, or c

<400> 497

gtgaaacatc aataaagacc acttaatgca cgctttcaaa aaaaaaaaaa aaaaaaaaaa 60  
aaaaaaaaaa aaaaaaaaaa aaannaanna nat 93

<210> 498

<211> 392

<212> DNA

<213> Homo sapiens

<220>

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<220>

<221> misc feature

<222> (50)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (104)

<223> n equals a,t,g, or c

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<222> (106)

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<220>

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<220>

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<222> (160)

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<220>

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<222> (180)

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<220>

<221> misc feature

<222> (181)

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<220>

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<222> (245)  
<223> n equals a,t,g, or c

<220>  
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<222> (248)  
<223> n equals a,t,g, or c

<220>  
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<222> (334)  
<223> n equals a,t,g, or c

<220>  
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<222> (351)  
<223> n equals a,t,g, or c

<220>  
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<222> (363)  
<223> n equals a,t,g, or c

<220>  
<221> misc feature  
<222> (377)  
<223> n equals a,t,g, or c

<220>  
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<222> (390)  
<223> n equals a,t,g, or c

<400> 498  
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tgacgcgccc cctgatgatg ggcctccagg ggagctcggg cctnanggcc tgnacggtcc 120  
agaggaaaaag ggccgggatc gtgaccggga ggcacggcgn acaccggagc gagcgcgagn 180  
ncgccgggac cgggatcgtg accgtgaccg tgaccgcgag cacaaacggg gggagcgggg 240  
cattnaancg gggcagggat gaagcccga gttggggcg gtggccagga caacgggttg 300  
gaaggttttg gcaacgacag ccgagaattt tacntgaatt ttaaggcggc nacgttactt 360  
gtnccggaat ttggtnttt attgaagtn cc 392

<210> 499  
<211> 262  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (23)



<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (40)

<223> n equals a,t,g, or c

<220>

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<222> (60)

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<220>

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<222> (76)

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<220>

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<222> (78)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (104)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (114)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (160)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (209)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (212)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (218)

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<220>

<221> misc feature

<222> (219)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (226)

<223> n equals a,t,g, or c

<400> 499

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agccagggga cacagnanag aagccacact ggacacaaca ccanaaaggc ttcntattcg 120
ggtgtggagt cttttcagca acccggtcca gtactgggcn gatacagcca tccaccttac 180
agatgtgtct acgtgacgct ctgccattnc anctcgggna ctatangtaa ttctcaagaa 240
agccctcatt tttataacct gg                                     262
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<210> 500

<211> 437

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (309)

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<220>

<221> misc feature

<222> (317)

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<220>

<221> misc feature

<222> (384)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (398)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (405)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (406)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (418)

<223> n equals a,t,g, or c

<400> 500

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accacaaaagc cccctggag catcttcccg gctggcagga ccatgccatc tctgtggaga 60
agggtgctggg gaggaagtc cttccagtgc cacatggagt gaggccctgc ccatgctggg 120
gactttgggg aggaatttgg tattctgggt gccttgctca gctctcattg agatcttttc 180
ctatcagaat gttagtgaat atacttcgca gctctttgtt cagcaataag gaatattctt 240
tcaattcttg ctcttcaagc caatttacta caccatttg tctttccaaa attcatccca 300
acggtatant tggtttnggt cctccttggg ttcaatctgt ttcctggtaa aattgaacct 360
gtccattgtg aatcctctta attncctcct cccaaaanaa ccagnncttg taaatttntg 420
gccaaactcca ggggccca 437
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<210> 501

<211> 180

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (162)

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<220>

<221> misc feature

<222> (165)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (166)

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<220>

<221> misc feature

<222> (174)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (177)

<223> n equals a,t,g, or c

<400> 501

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atggcccatc gatgagcatt tttaacatac tccatagtct tttcctgtgg tgtaggtct 120
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